EXERCISE CLASS 7 - SPC for non-iid data

EXERCISE 1

Data stored in the file ESE7_ex1.csv contains the measurements of time (in seconds) required to complete a surgical operation.

- 1. Design a control chart for the mean based on moving range estimate.
- 2. Provide an interpretation for out of control data (if any).
- 3. Suggest an adequate process data model.
- 4. Design a control chart for a 'trend' model.
- 5. Design a SCC and a FVC control charts for the process data.

Let's start by importing the required libraries and loading the data.

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

# Import the dataset
   data = pd.read_csv('ESE7_ex1.csv')

# Inspect the dataset
   data.head()
```

Out[]: time 0 600 1 480 2 540 3 240 4 420

Point 1

Design a control chart for the mean based on moving range estimate.

Solution 1

Control chart for individual.

What if we design the control chart without any graphical analysis of the process?

Computation of moving ranges MR:

1. Compute the differences between consecutive observations (lag = 1):

$$D_i = X_{i+1} - X_i.$$

2. Compute the absolute values of the differences: $MR = |D_i|$.

```
In [ ]: # Compute the moving ranges using the diff function
    data['MR'] = data['time'].diff().abs()

# Print out descriptive statistics of MR and time
    data.describe()
```

Out[]:		time	MR
	count	26.000000	25.000000
	mean	325.769231	123.600000
	std	155.413592	114.378028
	min	120.000000	0.000000
	25%	210.000000	30.000000
	50%	300.000000	120.000000
	75%	450.000000	180.000000
	max	690.000000	450.000000

Now let's make the control chart for the mean of the moving ranges.

Remember the formulas for the control limits.

I chart:

- $UCL = \bar{x} + 3\left(rac{ar{MR}}{d_2}
 ight)$
- $CL=ar{x}$
- $LCL = \bar{x} 3\left(rac{ar{MR}}{d_2}
 ight)$

MR chart:

- $UCL = D_4 \bar{M}R$
- $CL = \bar{MR}$
- LCL = 0

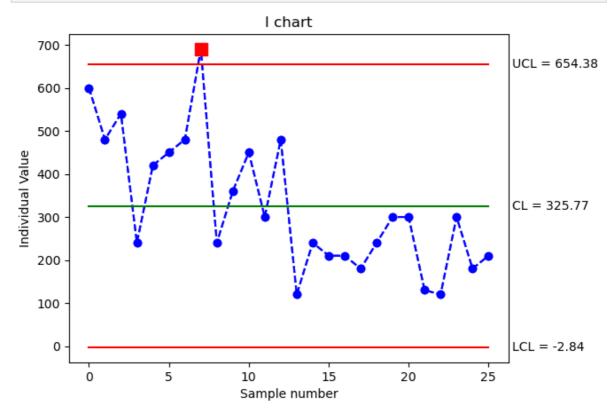
```
In []: # Define the constants for the control limits
    d2 = qda.constants.getd2(2)
    D4 = qda.constants.getD4(2)

# make a copy of the data
    df = data.copy()
# change the name of the column time to I
    df.rename(columns={'time':'I'}, inplace=True)
```

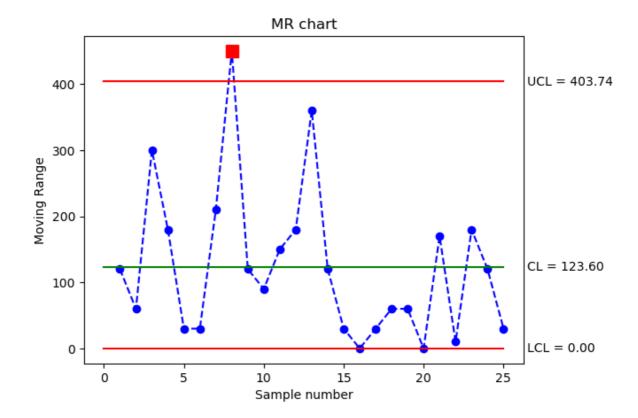
```
# Print the first 5 rows of the new dataframe
         df.head()
Out[]:
                  MR
         0 600
                 NaN
           480 120.0
           540
                 60.0
           240 300.0
         4 420 180.0
In [ ]: # Create columns for the upper and lower control limits
         df['I\_UCL'] = df['I'].mean() + (3*df['MR'].mean()/d2)
         df['I_CL'] = df['I'].mean()
         df['I_LCL'] = df['I'].mean() - (3*df['MR'].mean()/d2)
         df['MR\_UCL'] = D4 * df['MR'].mean()
         df['MR_CL'] = df['MR'].mean()
         df['MR_LCL'] = 0
         # Print the first 5 rows of the new dataframe
         df.head()
Out[]:
              MR
                           I UCL
                                       I_CL
                                                I LCL
                                                        MR_UCL MR_CL MR_LCL
           600
                     654.382175 325.769231 -2.843713 403.743345
                                                                  123.6
                 NaN
         1 480 120.0 654.382175 325.769231 -2.843713 403.743345
                                                                  123.6
                                                                              0
                     654.382175 325.769231 -2.843713 403.743345
           540
                 60.0
                                                                  123.6
                                                                              0
                300.0 654.382175 325.769231 -2.843713 403.743345
         3 240
                                                                  123.6
                                                                              0
           420 180.0 654.382175 325.769231 -2.843713 403.743345
                                                                  123.6
                                                                              0
In [ ]: |
         # Define columns for the alarm rule
         df['I_TEST1'] = np.where((df['I'] > df['I_UCL']) |
                          (df['I'] < df['I_LCL']), df['I'], np.nan)
         df['MR_TEST1'] = np.where((df['MR'] > df['MR_UCL']) |
                          (df['MR'] < df['MR_LCL']), df['MR'], np.nan)</pre>
         # Print the first 5 rows of the new dataframe
         df.head()
Out[ ]:
                  MR
                           I_UCL
                                       I_CL
                                                I_LCL
                                                        MR_UCL MR_CL MR_LCL I_TEST1
                                                                                        MR_TEST1
                                                                  123.6
         0 600
                 NaN
                      654.382175 325.769231 -2.843713 403.743345
                                                                             0
                                                                                   NaN
                                                                                             NaN
           480
                120.0
                      654.382175
                                325.769231
                                            -2.843713 403.743345
                                                                  123.6
                                                                                   NaN
                                                                                             NaN
                                            -2.843713 403.743345
         2 540
                 60.0
                      654.382175 325.769231
                                                                  123.6
                                                                             0
                                                                                   NaN
                                                                                             NaN
         3 240
                300.0
                     654.382175
                                325.769231
                                            -2.843713 403.743345
                                                                  123.6
                                                                              0
                                                                                   NaN
                                                                                             NaN
         4 420 180.0 654.382175 325.769231 -2.843713 403.743345
                                                                  123.6
                                                                              0
                                                                                   NaN
                                                                                             NaN
         # Plot the I chart
         plt.title('I chart')
```

plt.plot(df['I'], color='b', linestyle='--', marker='o')

```
plt.plot(df['I'], color='b', linestyle='--', marker='o')
plt.plot(df['I_UCL'], color='r')
plt.plot(df['I_CL'], color='g')
plt.plot(df['I_LCL'], color='r')
plt.ylabel('Individual Value')
plt.xlabel('Sample number')
# add the values of the control limits on the right side of the plot
plt.text(len(df)+.5, df['I_UCL'].iloc[0], 'UCL = {:.2f}'.format(df['I_UCL'].iloc[0]),
plt.text(len(df)+.5, df['I_LCL'].iloc[0], 'LCL = {:.2f}'.format(df['I_LCL'].iloc[0]),
plt.text(len(df)+.5, df['I_LCL'].iloc[0], 'LCL = {:.2f}'.format(df['I_LCL'].iloc[0]),
# highlight the points that violate the alarm rules
plt.plot(df['I_TEST1'], linestyle='none', marker='s', color='r', markersize=10)
plt.show()
```



```
In []:
    plt.title('MR chart')
    plt.plot(df['MR'], color='b', linestyle='--', marker='o')
    plt.plot(df['MR_UCL'], color='r')
    plt.plot(df['MR_CL'], color='g')
    plt.plot(df['MR_LCL'], color='r')
    plt.ylabel('Moving Range')
    plt.xlabel('Sample number')
# add the values of the control limits on the right side of the plot
    plt.text(len(df)+.5, df['MR_UCL'].iloc[0], 'UCL = {:.2f}'.format(df['MR_UCL'].iloc[0]
    plt.text(len(df)+.5, df['MR_CL'].iloc[0], 'CL = {:.2f}'.format(df['MR_CL'].iloc[0]
    plt.text(len(df)+.5, df['MR_LCL'].iloc[0], 'LCL = {:.2f}'.format(df['MR_LCL'].iloc
    # highlight the points that violate the alarm rules
    plt.plot(df['MR_TEST1'], linestyle='none', marker='s', color='r', markersize=10)
    plt.show()
```



Point 2

Provide an interpretation for out of control data (if any).

Solution

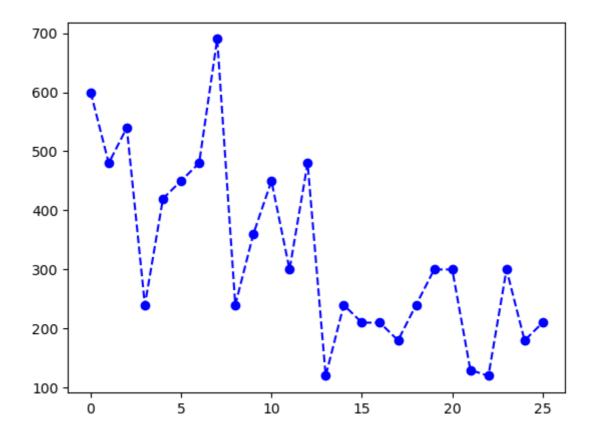
The measured variable (time) is NON NEGATIVE. Thus, LCL = -3 makes no sense. We can set LCL=0, but remind that it can never be violated.

What can we conclude about the process? Nothing, because we made no check of control chart assumptions!

Let's check if:

- The data are random.
- The data are normally distributed.

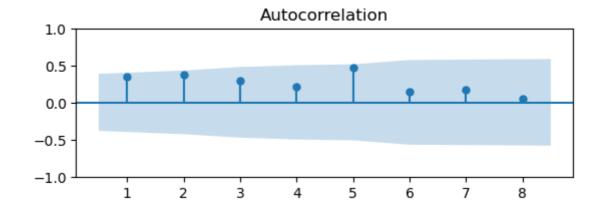
```
In []: # Plot the data first
    plt.plot(data['time'], color='b', linestyle='--', marker='o')
Out[]: [<matplotlib.lines.Line2D at 0x2119d487f08>]
```

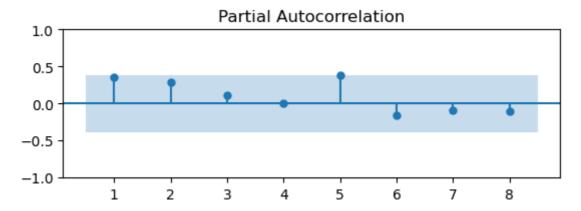


Plot the autocorrelation and partial autocorrelation functions of the data. Use the plot_acf and plot_pacf functions from the statsmodels package.

```
import statsmodels.graphics.tsaplots as sgt

fig, ax = plt.subplots(2, 1)
    sgt.plot_acf(data['time'], lags = int(len(data)/3), zero=False, ax=ax[0])
    fig.subplots_adjust(hspace=0.5)
    sgt.plot_pacf(data['time'], lags = int(len(data)/3), zero=False, ax=ax[1], method plt.show()
```





Perform the runs test to check if the data are random. Use the runstest_1samp function from the statsmodels package.

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

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

Runs test p-value = 0.024

The runs test gives a low p-value, this means that the data are not random. But remember that we have a small sample size. Let's check if the data are normally distributed.

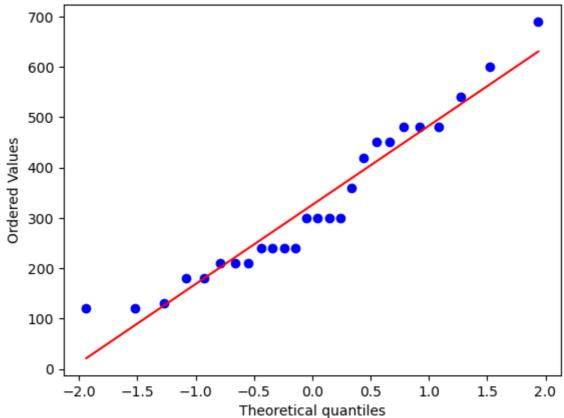
Test the normality of the data.

```
In [ ]: # Perform the Shapiro-Wilk test
_, pval_SW = stats.shapiro(data['time'])
print('Shapiro-Wilk test p-value = %.3f' % pval_SW)

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

Shapiro-Wilk test p-value = 0.081

Probability Plot



Data are barely normal and the process may be not random decreasing trend seems to be present.

It is worth to try fitting a trend model.

Point 3

Suggest an adequate process data model.

```
In [ ]: # Add a column with the sample number to use as regressor
    data['t'] = np.arange(1, len(data)+1)

data.head()
```

```
      Out[]:
      time
      MR
      t

      0
      600
      NaN
      1

      1
      480
      120.0
      2

      2
      540
      60.0
      3

      3
      240
      300.0
      4

      4
      420
      180.0
      5
```

```
In []: # Fit a regression model to the data
import statsmodels.api as sm

# Fit the linear regression model
x = data['t']
```

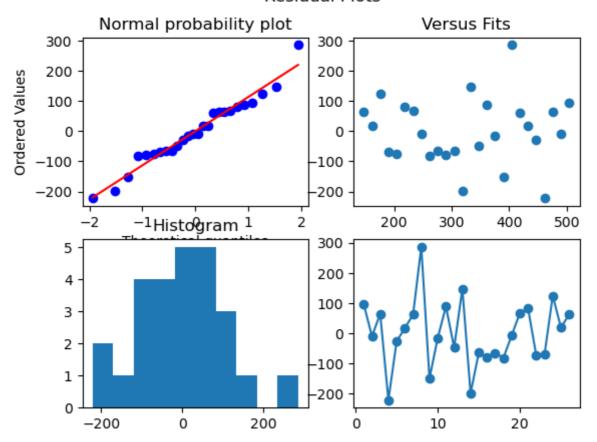
```
x = sm.add\_constant(x)
y = data['time']
model = sm.OLS(y,x).fit()
# Print the model summary
qda.summary(model)
REGRESSION EQUATION
_____
time = + 518.554 const -14.280 t
COEFFICIENTS
Term Coef SE Coef T-Value P-Value
const 518.5538 45.5680 11.3798 3.7191e-11
   t -14.2803 2.9506 -4.8397 6.2424e-05
MODEL SUMMARY
  S R-sq R-sq(adj)
112.8402 0.4939 0.4728
ANALYSIS OF VARIANCE
-----
   Source DF Adj SS Adj MS F-Value P-Value
Regression 1.0 2.9824e+05 2.9824e+05 23.4232 6.2424e-05
    const 1.0 1.6489e+06 1.6489e+06 129.4994 3.7191e-11
       t 1.0 2.9824e+05 2.9824e+05 23.4232 6.2424e-05
    Error 24.0 3.0559e+05 1.2733e+04 NaN NaN
    Total 25.0 6.0383e+05
                                    NaN
                                              NaN
                          NaN
```

Now that we have a trend model, we can check if the assumptions on the residuals are met (randomness and normality).

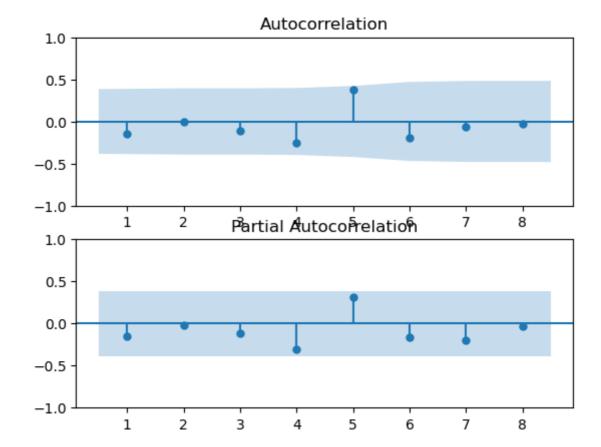
```
fig, axs = plt.subplots(2, 2)
fig.suptitle('Residual Plots')
stats.probplot(model.resid, dist="norm", plot=axs[0,0])
axs[0,0].set_title('Normal probability plot')
axs[0,1].scatter(model.fittedvalues, model.resid)
axs[0,1].set_title('Versus Fits')
axs[1,0].hist(model.resid)
axs[1,0].set_title('Histogram')
axs[1,1].plot(np.arange(1, len(model.resid)+1), model.resid, 'o-')
_, pval_SW_res = stats.shapiro(model.resid)
print('Shapiro-Wilk test p-value on the residuals = %.3f' % pval_SW_res)
```

Shapiro-Wilk test p-value on the residuals = 0.700

Residual Plots



Runs test p-value on the residuals = 0.710



Point 4

Design a control chart for a 'trend' model.

Solution

A TREND control chart will be based on the residuals of the trend model.

$$egin{aligned} UCL &= eta_0 + eta_1 \cdot t + 3rac{ar{MR}}{d_2(2)} \ & CL &= eta_0 + eta_1 \cdot t \ \ LCL &= eta_0 + eta_1 \cdot t - 3rac{ar{MR}}{d_2(2)} \end{aligned}$$

Which MR should I use? To be rigorous, we should use the MR of the residuals. Alwan states that the difference between the MR of the residuals and the MR of the original data is negligible, but let's use the MR of the residuals.

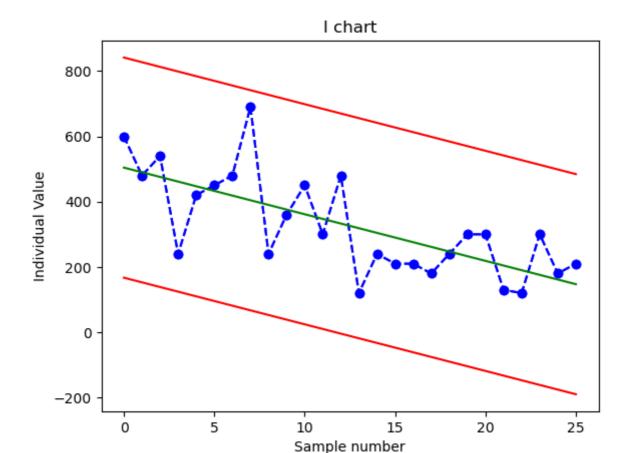
```
In [ ]: df_res = pd.DataFrame({'I': model.resid})
    df_res['MR'] = df_res['I'].diff().abs()

df_res.describe()
```

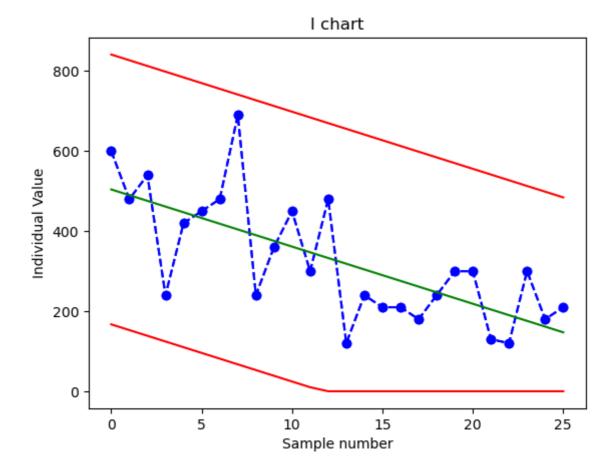
```
Out[ ]:
                                MR
                2.6000e+01
                             25.0000
         count
                 8.9638e-14 126.7985
         mean
                1.1056e+02 109.5280
           std
           min -2.2143e+02
                              4.2803
          25% -6.9026e+01
                             44.2803
          50% -8.6103e+00 105.7197
          75%
                6.6362e+01 194.2803
                2.8569e+02 435.7197
          max
```

Let's create a TREND control chart. We can use the model fits and the MR of the residuals to compute the control limits.

```
In [ ]: # Let's reuse the old dataframe df
        # Replace the I_CL column with the fitted values
        df['I_CL'] = model.fittedvalues
        # Replace the I UCL and I LCL columns with the upper and
        # lower control limits computed from the formula
        df['I_UCL'] = df['I_CL'] + 3 * df_res['MR'].mean() / d2
        df['I_LCL'] = df['I_CL'] - 3 * df_res['MR'].mean() / d2
        # Also update the TEST1 column
        df['I_TEST1'] = np.where((df['I'] > df['I_UCL']) | (df['I'] < df['I_LCL']), df['I']</pre>
In [ ]: # Plot the I chart
        plt.title('I chart')
        plt.plot(df['I'], color='b', linestyle='--', marker='o')
        plt.plot(df['I'], color='b', linestyle='--', marker='o')
        plt.plot(df['I_UCL'], color='r')
        plt.plot(df['I_CL'], color='g')
        plt.plot(df['I_LCL'], color='r')
        plt.ylabel('Individual Value')
        plt.xlabel('Sample number')
        # highlight the points that violate the alarm rules
        plt.plot(df['I_TEST1'], linestyle='none', marker='s',
                 color='r', markersize=10)
        plt.show()
```



Now there are no out of control points. But the LCL has values below 0. This makes no sense, because the time cannot be negative. We can set LCL=0, but remind that it can never be violated.



Point 5

Design a SCC and a FVC control charts for the process data.

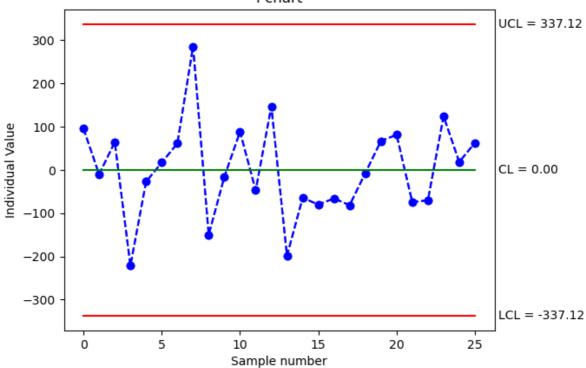
Solution

Let's build the same I-MR chart this time using the model residuals.

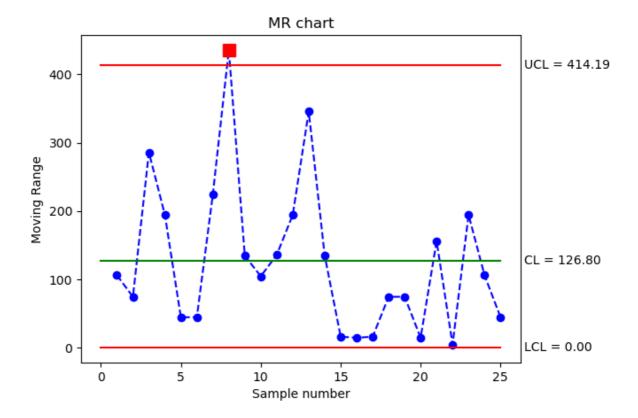
```
Out[ ]:
                           MR
                                  I UCL
                                             I CL
                                                      I_LCL MR_UCL
                                                                      MR_CL MR_LCL I_TEST1 MR_T
                                         8.9638e-
              95.7265
                          NaN 337.1167
         0
                                                  -337.1167 414.1913 126.7985
                                                                                     0
                                                                                           NaN
                                         8.9638e-
              -9.9932 105.7197 337.1167
                                                   -337.1167 414.1913 126.7985
                                                                                           NaN
                                              14
                                         8.9638e-
                       74.2803 337.1167
         2
              64.2872
                                                   -337.1167 414.1913 126.7985
                                                                                     0
                                                                                           NaN
                                               14
                                         8.9638e-
         3 -221.4325 285.7197 337.1167
                                                   -337.1167 414.1913 126.7985
                                                                                     0
                                                                                           NaN
                                              14
                                         8.9638e-
            -27.1521 194.2803 337.1167
                                                   -337.1167 414.1913 126.7985
                                                                                     0
                                                                                           NaN
                                               14
```



```
# Plot the I chart
plt.title('I chart')
plt.plot(df_res['I'], color='b', linestyle='--', marker='o')
plt.plot(df_res['I'], color='b', linestyle='--', marker='o')
plt.plot(df_res['I_UCL'], color='r')
plt.plot(df_res['I_CL'], color='g')
plt.plot(df_res['I_LCL'], color='r')
plt.ylabel('Individual Value')
plt.xlabel('Sample number')
# add the values of the control limits on the right side of the plot
# print the first value of the column I_UCL
plt.text(len(df_res)+.5, df_res['I_UCL'].iloc[0],
        'UCL = {:.2f}'.format(df_res['I_UCL'].iloc[0]),
        verticalalignment='center')
plt.text(len(df_res)+.5, df_res['I_CL'].iloc[0],
        'CL = {:.2f}'.format(df_res['I_CL'].iloc[0]),
        verticalalignment='center')
plt.text(len(df_res)+.5, df_res['I_LCL'].iloc[0],
        'LCL = {:.2f}'.format(df_res['I_LCL'].iloc[0]),
        verticalalignment='center')
# highlight the points that violate the alarm rules
plt.plot(df_res['I_TEST1'], linestyle='none', marker='s',
        color='r', markersize=10)
plt.show()
```



```
plt.title('MR chart')
plt.plot(df_res['MR'], color='b', linestyle='--', marker='o')
plt.plot(df_res['MR_UCL'], color='r')
plt.plot(df_res['MR_CL'], color='g')
plt.plot(df_res['MR_LCL'], color='r')
plt.ylabel('Moving Range')
plt.xlabel('Sample number')
# add the values of the control limits on the right side of the plot
plt.text(len(df_res)+.5, df_res['MR_UCL'].iloc[0], \
         'UCL = {:.2f}'.format(df_res['MR_UCL'].iloc[0]),
         verticalalignment='center')
plt.text(len(df_res)+.5, df_res['MR_CL'].iloc[0],
        'CL = {:.2f}'.format(df_res['MR_CL'].iloc[0]),
        verticalalignment='center')
plt.text(len(df_res)+.5, df_res['MR_LCL'].iloc[0],
        'LCL = {:.2f}'.format(df_res['MR_LCL'].iloc[0]),
        verticalalignment='center')
# highlight the points that violate the alarm rules
plt.plot(df res['MR TEST1'], linestyle='none', marker='s',
        color='r', markersize=10)
plt.show()
```



Now assume we found an assignable cause for the OOC observation 8.

We need to redesign the control charts by inserting a DUMMY VARIABLE such that:

- dummy = 0 for $t \neq 8$
- dummy = 1 for t = 8

```
In [ ]: # Create the dummy variable X
data['dummy'] = np.where((data['t'] == 8), 1, 0)
data.head()
```

```
Out[]:
           time
                  MR t dummy
        0
            600
                 NaN 1
                              0
            480
                120.0 2
            540
                              0
                 60.0 3
            240 300.0 4
            420
               180.0 5
                              0
```

```
In []: # Fit a model
x = data[['t', 'dummy']]
x = sm.add_constant(x)
y = data['time']
model2 = sm.OLS(y,x).fit()
qda.summary(model2)
```

```
time = +491.459 const -13.138 t +303.648 dummy
```

COEFFICIENTS

```
Term Coef SE Coef T-Value P-Value const 491.4591 40.4001 12.1648 1.6827e-11 t -13.1384 2.5785 -5.0953 3.6839e-05 dummy 303.6483 100.5632 3.0195 6.1044e-03
```

MODEL SUMMARY

S R-sq R-sq(adj) 97.5439 0.6376 0.6061

ANALYSIS OF VARIANCE

```
        Source
        DF
        Adj SS
        Adj MS
        F-Value
        P-Value

        Regression
        2.0
        3.8499e+05
        1.9250e+05
        20.2313
        8.5294e-06

        const
        1.0
        1.4080e+06
        1.4080e+06
        147.9824
        1.6827e-11

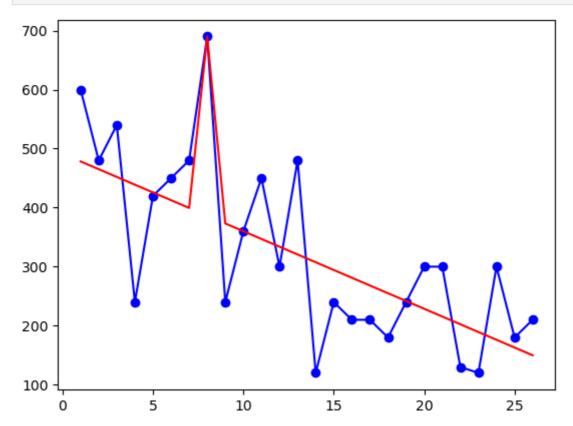
        t
        1.0
        2.4702e+05
        2.4702e+05
        25.9620
        3.6839e-05

        dummy
        1.0
        8.6749e+04
        8.6749e+04
        9.1172
        6.1044e-03

        Error
        23.0
        2.1884e+05
        9.5148e+03
        NaN
        NaN

        Total
        25.0
        6.0383e+05
        NaN
        NaN
        NaN
```

```
In [ ]: plt.plot(data['t'], data['time'], color='b', linestyle='-', marker='o')
   plt.plot(data['t'], model2.fittedvalues, color='r')
   plt.show()
```



Now that we have a trend model, we can check if the assumptions on the residuals are met (randomness and normality).

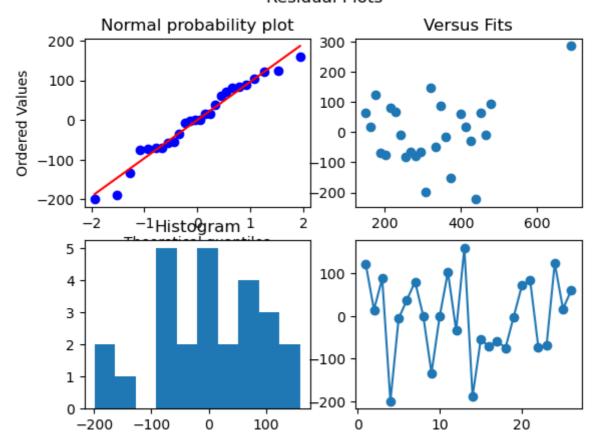
```
In [ ]: fig, axs = plt.subplots(2, 2)
fig.suptitle('Residual Plots')
```

```
stats.probplot(model2.resid, dist="norm", plot=axs[0,0])
axs[0,0].set_title('Normal probability plot')
axs[0,1].scatter(model2.fittedvalues, model.resid)
axs[0,1].set_title('Versus Fits')
axs[1,0].hist(model2.resid)
axs[1,0].set_title('Histogram')
axs[1,1].plot(np.arange(1, len(model2.resid)+1), model2.resid, 'o-')

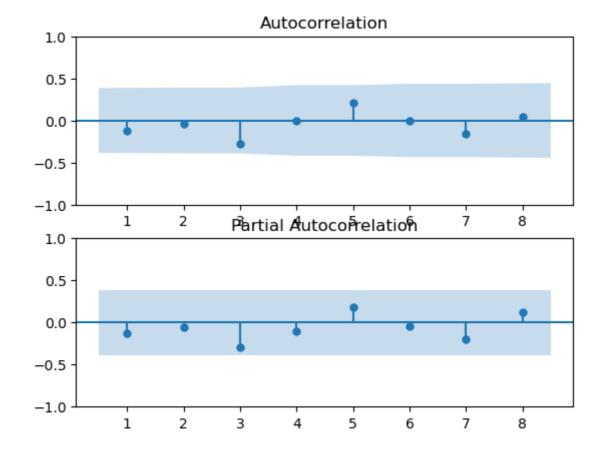
_, pval_SW_res = stats.shapiro(model2.resid)
print('Shapiro-Wilk test p-value on the residuals = %.3f' % pval_SW_res)
```

Shapiro-Wilk test p-value on the residuals = 0.530

Residual Plots



Runs test p-value on the residuals = 0.230



Build a new SCC control chart on the residuals of the new trend model.

```
In [ ]: # Make a new dataframe for the new residuals
    df_res2 = pd.DataFrame({'res2': model2.resid})

# Create the IMR chart
    df_res2 = qda.ControlCharts.IMR(df_res2, 'res2')
```

I-MR charts of res2

