

* The solution to the theoretical questions (questions 1 to 7 in the first part of the assignment) are sent in the “report” folder and is named “9531307_TinaGholami_Solutions of theory questions”.

A)

(name of the files: A.py and A2.py)

I read the file and showed it by two different methods: one in Python with no other libraries (A2.py) and two, with Pandas library (A.py). But The second method is easier and nicer when displayed.

1st method (A2.py):

```
import csv

with open ("data.csv", newline = '') as csvfile:
    spamreader = csv.reader(csvfile, delimiter = ' ', quotechar = '|')
    for row in spamreader:
        print(' '.join(row))
```

And the output:

```
CA: Command Prompt

C:\Users\NASA\proo\dm>python A.py
id,sex,birth_year,country,region,infection_reason,infected_by,confirmed_date,state
1,female,1984,China,filtered at airport,visit to Wuhan,,1/20/2020,released
2,male,1964,Korea,filtered at airport,visit to Wuhan,,1/24/2020,released
3,male,1966,Korea,capital area,visit to Wuhan,,1/26/2020,released
4,male,1964,Korea,capital area,visit to Wuhan,,1/27/2020,released
5,male,1987,Korea,capital area,visit to Wuhan,,1/30/2020,released
6,male,1964,Korea,capital area,contact with patient,3,1/30/2020,released
7,male,1991,Korea,capital area,visit to Wuhan,,1/30/2020,released
8,female,1957,Korea,Jeollabuk-do,visit to Wuhan,,1/31/2020,released
9,female,1992,Korea,capital area,contact with patient,5,1/31/2020,released
10,female,1966,Korea,capital area,contact with patient,6,1/31/2020,released
11,male,1995,Korea,capital area,contact with patient,6,1/31/2020,released
12,male,1971,China,capital area,contact with patient in Japan,,2/1/2020,released
13,male,1992,Korea,filtered at airport,residence in Wuhan,,2/2/2020,released
14,female,1980,China,capital area,contact with patient,12,2/2/2020,released
15,male,1977,Korea,capital area,contact with patient,4,2/2/2020,released
16,female,1977,Korea,Gwangju,visit to Thailand,,2/4/2020,released
17,male,1982,Korea,capital area,contact with patient in Singapore,,2/5/2020,released
18,female,1999,Korea,Gwangju,contact with patient,16,2/5/2020,released
19,male,1983,Korea,capital area,contact with patient in Singapore,,2/5/2020,released
20,female,1978,Korea,capital area,contact with patient,15,2/5/2020,released
21,female,1960,Korea,capital area,contact with patient,6,2/5/2020,released
```

Second method (A.py):

```
import pandas as pd

df = pd.read_csv("data.csv") #data frame #read the .csv file

with pd.option_context('display.max_rows', None, 'display.max_columns', None, 'display.width', None): #method number 3 (please enlarge your command window to see the whole dataframe in alignment)
    print(df)
```

And the output:

```
C:\Users\NASA\proo\dm>python A2.py
   id  sex  birth_year country      region      infection_reason  infected_by  confirmed_date  state
0    1  female    1984.0   China  filtered at airport      visit to Wuhan         NaN    1/20/2020  released
1    2    male    1964.0   Korea  filtered at airport      visit to Wuhan         NaN    1/24/2020  released
2    3    male    1966.0   Korea    capital area      visit to Wuhan         NaN    1/26/2020  released
3    4    male    1964.0   Korea    capital area      visit to Wuhan         NaN    1/27/2020  released
4    5    male    1987.0   Korea    capital area      visit to Wuhan         NaN    1/30/2020  released
5    6    male    1964.0   Korea    capital area  contact with patient         3.0    1/30/2020  released
6    7    male    1991.0   Korea    capital area      visit to Wuhan         NaN    1/30/2020  released
7    8  female    1957.0   Korea  Jeollabuk-do      visit to Wuhan         NaN    1/31/2020  released
8    9  female    1992.0   Korea    capital area  contact with patient         5.0    1/31/2020  released
9   10  female    1966.0   Korea    capital area  contact with patient         6.0    1/31/2020  released
10  11    male    1995.0   Korea    capital area  contact with patient         6.0    1/31/2020  released
11  12    male    1971.0   China    capital area  contact with patient in Japan         NaN    2/1/2020  released
12  13    male    1992.0   Korea  filtered at airport      residence in Wuhan         NaN    2/2/2020  released
13  14  female    1980.0   China    capital area  contact with patient        12.0    2/2/2020  released
14  15    male    1977.0   Korea    capital area  contact with patient         4.0    2/2/2020  released
15  16  female    1977.0   Korea      Gwangju      visit to Thailand         NaN    2/4/2020  released
16  17    male    1982.0   Korea    capital area  contact with patient in Singapore         NaN    2/5/2020  released
17  18  female    1999.0   Korea      Gwangju  contact with patient        16.0    2/5/2020  released
18  19    male    1983.0   Korea    capital area  contact with patient in Singapore         NaN    2/5/2020  released
19  20  female    1978.0   Korea    capital area  contact with patient        15.0    2/5/2020  released
20  21  female    1960.0   Korea    capital area  contact with patient         6.0    2/5/2020  released
21  22    male    1973.0   Korea      Gwangju  contact with patient        16.0    2/6/2020  released
22  23  female    1962.0   China    capital area      visit to Wuhan         NaN    2/6/2020  released
23  24    male    1992.0   Korea  filtered at airport      residence in Wuhan         NaN    2/6/2020  released
24  25  female    1946.0   Korea    capital area  contact with patient        27.0    2/9/2020  isolated
25  26    male    1968.0   Korea    capital area  contact with patient        27.0    2/9/2020  isolated
26  27  female    1982.0   China    capital area      visit to China         NaN    2/9/2020  isolated
27  28  female    1989.0   China    capital area  contact with patient         3.0    2/10/2020  released
28  29    male    1938.0   Korea    capital area  contact with patient        83.0    2/16/2020  isolated
29  30  female    1952.0   Korea    capital area  contact with patient        29.0    2/16/2020  isolated
30  31  female    1959.0   Korea      Daegu         NaN         NaN    2/18/2020  isolated
31  32  female    2009.0   Korea    capital area  contact with patient        20.0    2/18/2020  released
```

So by now, I have read the csv (comma separated values) file and showed it in my command prompt as a table. The second method is the one I chose for the next parts of the question.

B)

(The name of the file: B.py)

```
import pandas as pd

df = pd.read_csv("data.csv") #Reading the data frame fro a .csv file

print("The size of the data is:")
print(df.size)

print("\nThe dimention of the table is:")
print(df.shape)

print ("\nThe names of the columns are:") #printing the names of the columns
for col in df.columns:
    print(col)
```

Ant the output:

```
C:\Users\NASA\proo\dm>python B.py
The size of the data is:
1584

The dimention of the table is:
(176, 9)

The names of the columns are:
id
sex
birth_year
country
region
infection_reason
infected_by
confirmed_date
state
```

The data is separated into 9 columns and 176 rows. The data is of all strings, integers and float.

C)

(The name of the file: C.py)

I used Pandas in-built methods to calculate mean, max and standard deviation of birth_year column of the data.

```
import pandas as pd

df = pd.read_csv("data.csv") #Reading the data frame fro a .csv file

print("The max of the birth years is:")
print(df['birth_year'].max())

print("\nThe mean of the birth years is:")
print(df['birth_year'].mean())

print("\nThe std of the birth year is:")
print(df['birth_year'].std())
```

And the output:

```
C:\Users\NASA\proo\dm>python C.py
The max of the birth years is:
2009.0

The mean of the birth years is:
1973.3855421686746

The std of the birth year is:
17.032824869574775
```

And if we want the output to be shown in a table, we should:

```
import pandas as pd

df = pd.read_csv("data.csv") #Reading the data frame fro a .csv file

output = pd.DataFrame([df['birth_year'].max(), df['birth_year'].mean(), df['birth_year'].std()], ['max', 'mean', 'std']) # To show output in a table
print(output)
```

And the output:

```
C:\Users\NASA\proo\dm>python c.py
      0
max    2009.000000
mean   1973.385542
std     17.032825
```

D)

(The name of the file: D.py)

I chose the “region” column:

```
import pandas as pd

df = pd.read_csv("data.csv") #Reading the data frame fro a .csv file

print("The number of fields in the 'region' column is:")
print(df['region'].count())
```

And the output:

```
C:\Users\NASA\proo\dm>python D.py
The number of fields in the 'region' column is:
166
```

There are 166 fields in the “region” column.

E)

(The name of the files: E.py and E2.py)

I checked the null values in data by “isna” method, which outputs a table with “False” or “True”, based on the availability of Null values. And we see in the output that there ARE null values as “NaN”s in the data frame. Then, I checked 10 solutions to handle the null values in file “E2.py”, but eventually, I chose “method 6”: interpolation and “method 10”: deleting specific rows in file “E.py”. The “E2.py” code, involves all the methods I tried to handle these null values and the “E.py” is the final solutions I chose. But here, for the sake of being concise, I only put the “E.py” code and its output.

```
import pandas as pd

df = pd.read_csv("data.csv") #Reading the data frame fro a .csv file
with pd.option_context('display.max_rows', None, 'display.max_columns', None, 'display.width', None):
    print(pd.isna(df))

print("\n")
#First, I use interpolate method to estimate numerical missing values, then I use dropna method to delete string missing values.
df_interp = df.interpolate(method = 'linear', limit_direction = 'forward') #The interpolate method

df_drop = df_interp.dropna(axis = 0, how = 'any') #The dropna method
with pd.option_context('display.max_rows', None, 'display.max_columns', None, 'display.width', None): #Droopping the rows that contain NaN
    print(df_drop)

print("\nOld data frame length:", len(df))
print("New data frame length:", len(df_drop))
print("Number of rows with at least 1 NaN value: ", (len(df) - len(df_drop)))
```


And the outputs:

```
C:\Users\NASA\proo\dm>python E2.py
```

	id	sex	birth_year	country	region	infection_reason	infected_by	confirmed_date	state
0	False	False	False	False	False	False	True	False	False
1	False	False	False	False	False	False	True	False	False
2	False	False	False	False	False	False	True	False	False
3	False	False	False	False	False	False	True	False	False
4	False	False	False	False	False	False	True	False	False
5	False	False	False	False	False	False	False	False	False
6	False	False	False	False	False	False	True	False	False
7	False	False	False	False	False	False	True	False	False
8	False	False	False	False	False	False	False	False	False
9	False	False	False	False	False	False	False	False	False
10	False	False	False	False	False	False	False	False	False
11	False	False	False	False	False	False	True	False	False
12	False	False	False	False	False	False	True	False	False
13	False	False	False	False	False	False	False	False	False
14	False	False	False	False	False	False	False	False	False
15	False	False	False	False	False	False	True	False	False
16	False	False	False	False	False	False	True	False	False
17	False	False	False	False	False	False	False	False	False
18	False	False	False	False	False	False	True	False	False
19	False	False	False	False	False	False	False	False	False
20	False	False	False	False	False	False	False	False	False

“Isna” Method to detect whether there are Null values in the dataset, and the “True”s indicate that there are.

	id	sex	birth_year	country	region	infection_reason	infected_by	confirmed_date	state
5	6	male	1964.000000	Korea	capital area	contact with patient	3.000000	1/30/2020	released
6	7	male	1991.000000	Korea	capital area	visit to Wuhan	3.666667	1/30/2020	released
7	8	female	1957.000000	Korea	Jeollabuk-do	visit to Wuhan	4.333333	1/31/2020	released
8	9	female	1992.000000	Korea	capital area	contact with patient	5.000000	1/31/2020	released
9	10	female	1966.000000	Korea	capital area	contact with patient	6.000000	1/31/2020	released
10	11	male	1995.000000	Korea	capital area	contact with patient	6.000000	1/31/2020	released
11	12	male	1971.000000	China	capital area	contact with patient in Japan	8.000000	2/1/2020	released
12	13	male	1992.000000	Korea	filtered at airport	residence in Wuhan	10.000000	2/2/2020	released
13	14	female	1980.000000	China	capital area	contact with patient	12.000000	2/2/2020	released
14	15	male	1977.000000	Korea	capital area	contact with patient	4.000000	2/2/2020	released
15	16	female	1977.000000	Korea	Gwangju	visit to Thailand	8.000000	2/4/2020	released
16	17	male	1982.000000	Korea	capital area	contact with patient in Singapore	12.000000	2/5/2020	released
17	18	female	1999.000000	Korea	Gwangju	contact with patient	16.000000	2/5/2020	released
18	19	male	1983.000000	Korea	capital area	contact with patient in Singapore	15.500000	2/5/2020	released
19	20	female	1978.000000	Korea	capital area	contact with patient	15.000000	2/5/2020	released
20	21	female	1960.000000	Korea	capital area	contact with patient	6.000000	2/5/2020	released
21	22	male	1973.000000	Korea	Gwangju	contact with patient	16.000000	2/6/2020	released
22	23	female	1962.000000	China	capital area	visit to Wuhan	19.666667	2/6/2020	released
23	24	male	1992.000000	Korea	filtered at airport	residence in Wuhan	23.333333	2/6/2020	released
24	25	female	1946.000000	Korea	capital area	contact with patient	27.000000	2/9/2020	isolated
25	26	male	1968.000000	Korea	capital area	contact with patient	27.000000	2/9/2020	isolated
26	27	female	1982.000000	China	capital area	visit to China	15.000000	2/9/2020	isolated
27	28	female	1989.000000	China	capital area	contact with patient	3.000000	2/10/2020	released
28	29	male	1938.000000	Korea	capital area	contact with patient	83.000000	2/16/2020	isolated
29	30	female	1952.000000	Korea	capital area	contact with patient	29.000000	2/16/2020	isolated
31	32	female	2009.000000	Korea	capital area	contact with patient	20.000000	2/18/2020	released
32	33	female	1980.000000	Korea	Daegu	contact with patient	31.000000	2/18/2020	isolated

Filtered data, which does not contain Null values

```
Old data frame length: 176
New data frame length: 90
Number of rows with at least 1 NaN value: 86
```

Simple calculations to show how many rows have been deleted in the process

F)

(The name of the file: F.py)

I used three different visualization methods on “birth_year” column: Histogram, Boxplot, and Scatterplot.

```
import pandas as pd
from matplotlib import pyplot

df = pd.read_csv("data.csv") #Reading the data frame fro a .csv file

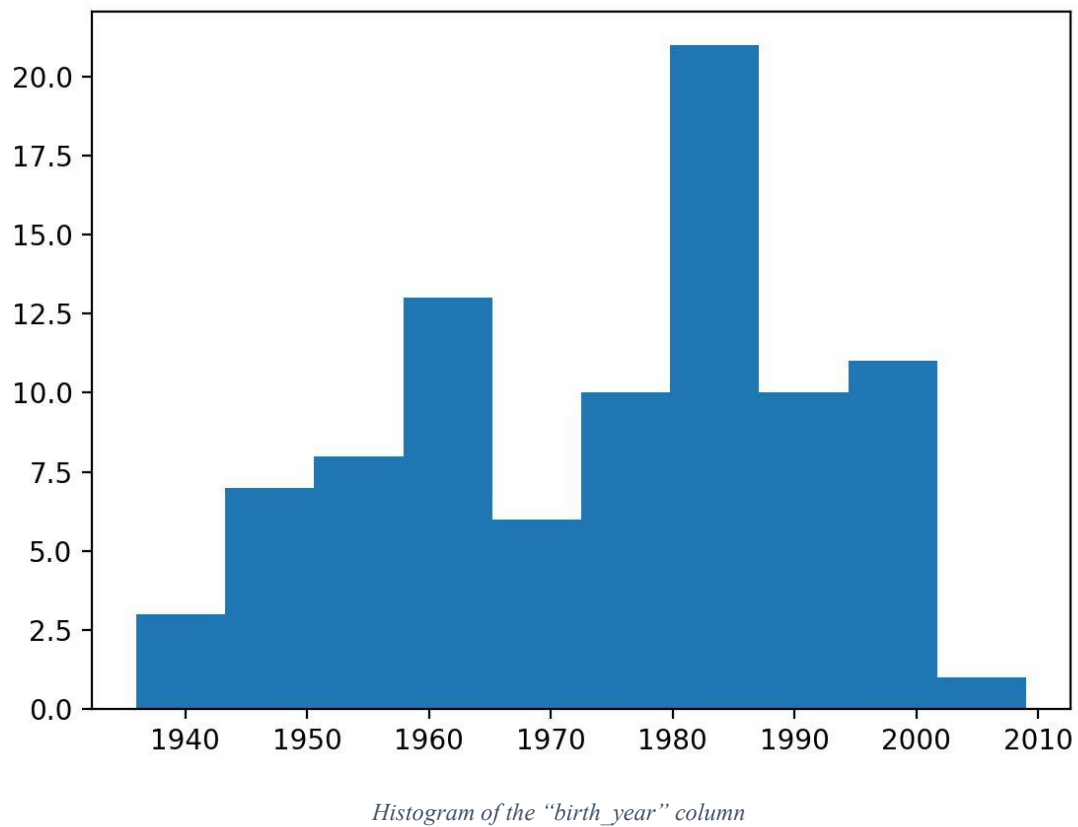
#First, I use interpolate method to estimate numerical missing values, then I use
dropna method to delete string missing values.
df_interp = df.interpolate(method = 'linear', limit_direction = 'forward') #The i
nterpolate method
df_drop = df_interp.dropna(axis = 0, how = 'any') #The dropna method
df_new = df_drop #Therefore, our data frame from now on is "df_new".

pyplot.figure(); #Histogram Plotiing
pyplot.hist(df_new['birth_year'])
pyplot.show()
pyplot.savefig('histogram.png')

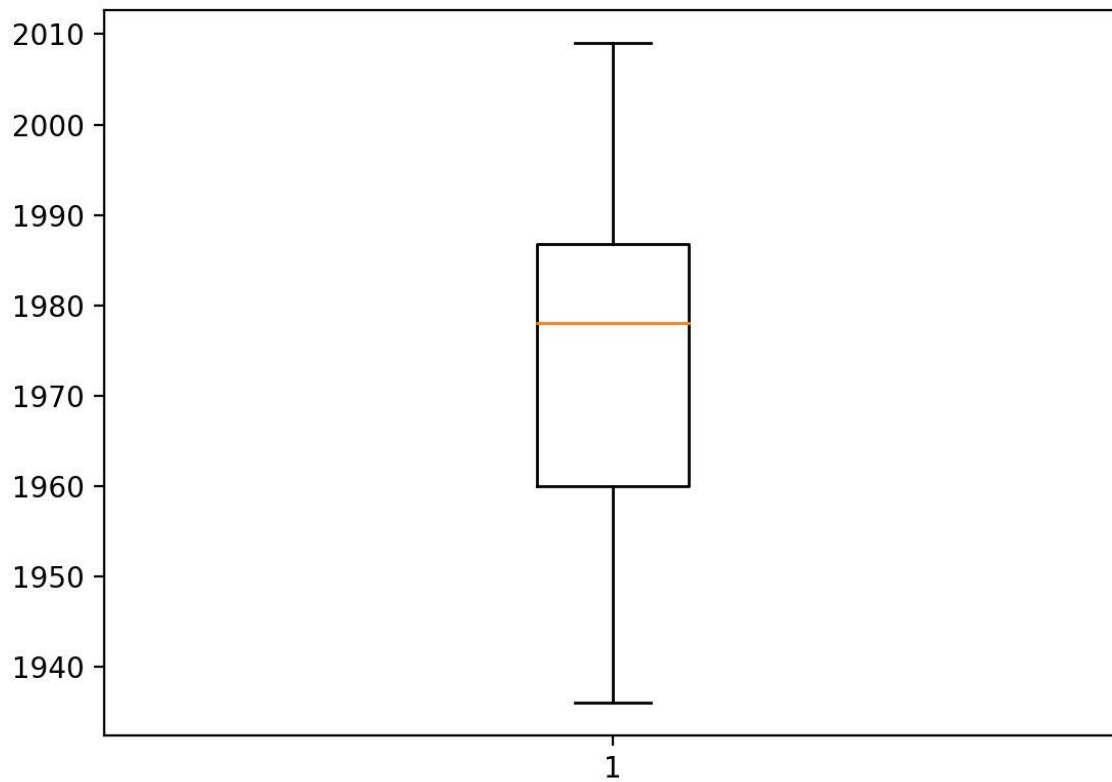
pyplot.figure(); #Boxplot Plotiing
pyplot.boxplot(df_new['birth_year'])
pyplot.show()
pyplot.savefig('boxplot.png')

pyplot.figure(); #Scatter Plotiing
pyplot.scatter(df_new['state'], df_new['birth_year'])
pyplot.show()
pyplot.savefig('scatter.png')
```


And the outputs:



As we can see, the distribution of "birth_year" is the highest in the sixth bin, between the years 1980 and 1990. So most of the patients were between 40 and 50 years old.



Boxplot of the "birth_year" column

The mean of the data is in the square box, which has occurred between the years 1980 and 1970.



Scatterplot of the "birth_year" column

The scatterplot shows the data for “released” and “isolated” patients, based on the number of the incidents detected. And as we can see, the patients who were “released” are more scattered and sparse. Therefore, the probability of the existence of outlier for “released” patients is higher.

G)

(The name of the file: G.py and G2.py)

the ways to identify an outlier:

- Data point that falls outside of 3 standard deviations. we can use a z-score and if the z-score falls outside of 2 standard-deviation = the z-score method
- Data point that falls outside of 1.5 times of an interquartile range above the 3rd quartile and below the 1st quartile = IQR interquartile method
- using scatter plots

The reason for an outlier to exists in a dataset:

- Variability in the data
- An experimental measurement error

The impacts of the outlier:

Causing serious issues for statistical analysis, such as:

- Skew the data
- Significant impact on mean (**so, this shows it is better not to use mean method in detecting missing values in part (E), since we have outliers in the data and these outliers can significantly change the mean.)
- Significant impact on the standard deviation

a) Z-score method (file G.py):

To check if there is outlier in the data, I showed the presence of outlier in three numerical columns “infected_by”, “birth_year”, and “id” and only the “infected_by” column contained outlier based on the “z-score” method that I used. I also used the scatterplot, but it is not precise to say that some data points are outliers based on the scatterplot since there was not very distinct data points to make one doubt of the presence of outliers and also the numerical methods such as z-score and IQR are more precise.

1) For the “infected_by” column

```
import pandas as pd
from matplotlib import pyplot
import numpy as np

df = pd.read_csv("data.csv") #Reading the data frame fro a .csv file

#First, I use interpolate method to estimate numerical missing values, then I use
dropna method to delete string missing values.
df_interp = df.interpolate(method = 'linear', limit_direction = 'forward') #The i
nterpolate method
df_drop = df_interp.dropna(axis = 0, how = 'any') #The dropna method
df_new = df_drop #Therefore, our data frame from now on is "df_new".
df_new_column = df_new['infected_by']
# df_new_column = df_new['birth_year']
# df_new_column = df_new['id']

#Method 1: Using scatterplot to detect outliers:
pyplot.figure() #Scatter Plotiing
pyplot.scatter(df_new['state'], df_new['birth_year'])
pyplot.show()

#Method 2: Using Z-score to detect outliers:
outliers = []

def detect_outlier(data):

    threshold = 3
    mean_data = np.mean(data)
    std_data = np.std(data)

    for item in data:
        z_score = (item - mean_data) / std_data
```

```

        if np.abs(z_score) > threshold:
            outliers.append(item)
        return outliers

outlier_df = detect_outlier(df_new_column)
print(outlier_df)

df_filtered = df_new.drop([162])
with pd.option_context('display.max_rows', None, 'display.max_columns', None, 'display.width', None):
    print(df_filtered)

```

As we can see above, an outlier was detected in row number 162, so I dropped this row in order to handle the outliers.

And the output:



Scatterplot for the "infected_by" column to check for outliers


```
C:\Users\NASA\proo\dm>python 6.py
[372.0]
```

	id	sex	birth_year	country	region	infection_reason	infected_by	confirmed_date	state
5	6	male	1964.000000	Korea	capital area	contact with patient	3.000000	1/30/2020	released
6	7	male	1991.000000	Korea	capital area	visit to Wuhan	3.666667	1/30/2020	released
7	8	female	1957.000000	Korea	Jeollabuk-do	visit to Wuhan	4.333333	1/31/2020	released
8	9	female	1992.000000	Korea	capital area	contact with patient	5.000000	1/31/2020	released
9	10	female	1966.000000	Korea	capital area	contact with patient	6.000000	1/31/2020	released
10	11	male	1995.000000	Korea	capital area	contact with patient	6.000000	1/31/2020	released
11	12	male	1971.000000	China	capital area	contact with patient in Japan	8.000000	2/1/2020	released
12	13	male	1992.000000	Korea	filtered at airport	residence in Wuhan	10.000000	2/2/2020	released

We notice that element [372.0] in the “infected_by” column was detected as an outlier.

And since this data belongs to row number 162, this row is deleted from the data frame after it was detected by the z-score method, below:

160	161	male	1980.000000	Korea	capital area	contact with patient	246.000000	2/23/2020	isolated
163	164	male	1997.000000	Korea	capital area	visit to Daegu	249.000000	2/23/2020	isolated
164	165	female	1985.000000	Korea	Gwangju	contact with patient	126.000000	2/23/2020	released
166	167	male	1968.000000	Korea	capital area	visit to Vietnam	138.666667	2/23/2020	isolated
168	169	female	1984.666667	Korea	Gyeongsangbuk-do	contact with patient	151.333333	2/24/2020	isolated
170	171	male	1985.000000	Korea	Gwangju	contact with patient	164.000000	2/24/2020	isolated

2) For the “birth_year” column:

We only need to un-command this line of the code:

```
df_new_column = df_new['birth_year']
```

And the outputs are:



```
C:\Users\NASA\proo\dm>python G.py
[]
```

	id	sex	birth_year	country	region	infection_reason	infected_by	confirmed_date	state
5	6	male	1964.000000	Korea	capital area	contact with patient	3.000000	1/30/2020	released
6	7	male	1991.000000	Korea	capital area	visit to Wuhan	3.666667	1/30/2020	released
7	8	female	1957.000000	Korea	Jeollabuk-do	visit to Wuhan	4.333333	1/31/2020	released
8	9	female	1992.000000	Korea	capital area	contact with patient	5.000000	1/31/2020	released
9	10	female	1966.000000	Korea	capital area	contact with patient	6.000000	1/31/2020	released
10	11	male	1995.000000	Korea	capital area	contact with patient	6.000000	1/31/2020	released
11	12	male	1971.000000	China	capital area	contact with patient in Japan	8.000000	2/1/2020	released
12	13	male	1992.000000	Korea	filtered at airport	residence in Wuhan	10.000000	2/2/2020	released
13	14	female	1990.000000	China	capital area	contact with patient	11.000000	2/2/2020	released

As we see, no outlier was detected, therefore no row will be dropped.

3) For the “id” column:

We only need to un-command this line of the code:

```
df_new_column = df_new['id']
```

And the outputs are:



```
C:\Users\NASA\proo\dm>python G.py
[]
  id  sex  birth_year  country  region  infection_reason  infected_by  confirmed_date  state
5   6  male  1964.000000  Korea    capital area  contact with patient  3.000000  1/30/2020  released
6   7  male  1991.000000  Korea    capital area  visit to Wuhan  3.666667  1/30/2020  released
7   8  female  1957.000000  Korea  Jeollabuk-do  visit to Wuhan  4.333333  1/31/2020  released
8   9  female  1992.000000  Korea    capital area  contact with patient  5.000000  1/31/2020  released
9  10  female  1966.000000  Korea    capital area  contact with patient  6.000000  1/31/2020  released
10  11  male  1995.000000  Korea    capital area  contact with patient  6.000000  1/31/2020  released
11  12  male  1971.000000  China    capital area  contact with patient in Japan  8.000000  2/1/2020  released
12  13  male  1992.000000  Korea  filtered at airport  residence in Wuhan  10.000000  2/2/2020  released
13  14  female  1980.000000  China    capital area  contact with patient  12.000000  2/2/2020  released
14  15  male  1977.000000  Korea    capital area  contact with patient  4.000000  2/2/2020  released
```

Again in here, the system does not detect any outliers in the “id” column, thus no row will be deleted.

b) IQR Interquartile method (file G2.py):

IQR tells how spread the middle values are. It can be used to tell when a value is too far from the middle. An outlier is a point which falls more than 1.5 times the interquartile range above the third quartile or below the first quartile.

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

df = pd.read_csv("data.csv") #Reading the data frame from a .csv file

#First, I use interpolate method to estimate numerical missing values, then I use
dropna method to delete string missing values.
df_interp = df.interpolate(method = 'linear', limit_direction = 'forward') #The i
nterpolate method
df_drop = df_interp.dropna(axis = 0, how = 'any') #The dropna method
df_new = df_drop #Therefore, our data frame from now on is "df_new".

q1 = df_new.quantile(0.25) #Calculating the quartiles
q3 = df_new.quantile(0.75)
iqr = q3 - q1

with pd.option_context('display.max_rows', None, 'display.max_columns', None, 'di
splay.width', None): #Showing the outliers
    print((df_new <= (q1 - 1.5 * iqr)) | (df_new >= (q3 + 1.5 * iqr)))

# df_drop = df_interp.dropna([]) #Dropping the row containing outlier
```

And the output:

```
133      False      False      False      False      False      False      False      False      False
134      False      False      False      False      False      False      False      False      False
135      False      False      False      False      False      False      False      False      False
136      False      False      False      False      False      False      False      False      False
137      False      False      False      False      False      False      False      False      False
138      False      False      False      False      False      False      False      False      False
139      False      False      False      False      False      False      False      False      False
144      False      False      False      False      False      False      False      False      False
145      False      False      False      False      False      False      False      False      False
147      False      False      False      False      False      False      False      False      False
149      False      False      False      False      False      False      False      False      False
150      False      False      False      False      False      False      False      False      False
154      False      False      False      False      False      False      False      False      False
155      False      False      False      False      False      False      False      False      False
156      False      False      False      False      False      False      False      False      False
160      False      False      False      False      False      False      False      False      False
162      False      False      False      False      False      False      False      False      False
163      False      False      False      False      False      False      False      False      False
164      False      False      False      False      False      False      False      False      False
166      False      False      False      False      False      False      False      False      False
168      False      False      False      False      False      False      False      False      False
170      False      False      False      False      False      False      False      False      False
```

Which shows that unlike Z-score method, the IQR method didn't detect any outlier. (in the Z-score method, we had an outlier in row 162 for "infected_by" column.)

c) Scatterplot method:

Just like part (F), the scatter plot for the "birth_year" data is:

1) Scatterplot for "birth_year" column:



Scatterplot for the "birth_year" data

As I guess just by looking at the histogram above, there seems to be two outliers in the "released" data, one between 1940 and 1950 and the other between 2000 to 2010.

But if we take these two points as outliers, we should consider the relative data points between those two year intervals for the "isolated" data as outliers, as well.

But should we really take any data points between years (1940 and 1950) and (2000 and 2010) as outliers? Well I think we cannot answer this question with certainty just by looking at the histogram

above. As I have mentioned in Z-score and IQR method, we'd better employ numerical methods to detect outliers, since when the data is big, like in this scenario, we should decide which data points are outliers by measuring their relative distance from the mean of all the data point we have in hand.

2) Scatterplot for “infected_by” column:



Scatterplot for the “infected_by” data

3) Scatterplot for “id” column:



Scatterplot for the “id” data