Tumor-Cell-Analysis-Project

June 7, 2024

————————Tumor-Cell-Analysis-Project————————-

I will check if there are any missing values. And I will perform any necessary data imputation on the data set.

Turns out there was one missing value in the column of the second feature which is labeled '10.38'. This value has been replaced with the mean of the column, ensuring that we don't lose data by dropping the row. This should not affect the accuracy too much since the values aren't very wide spread in this column.

```
In [1]: import pandas as pd
        import numpy as np
        import matplotlib.pyplot as plt

        df = pd.read_csv('/public/bmort/python/tumor_cells.csv')
```

```
In [3]: df
```

Out[3]:

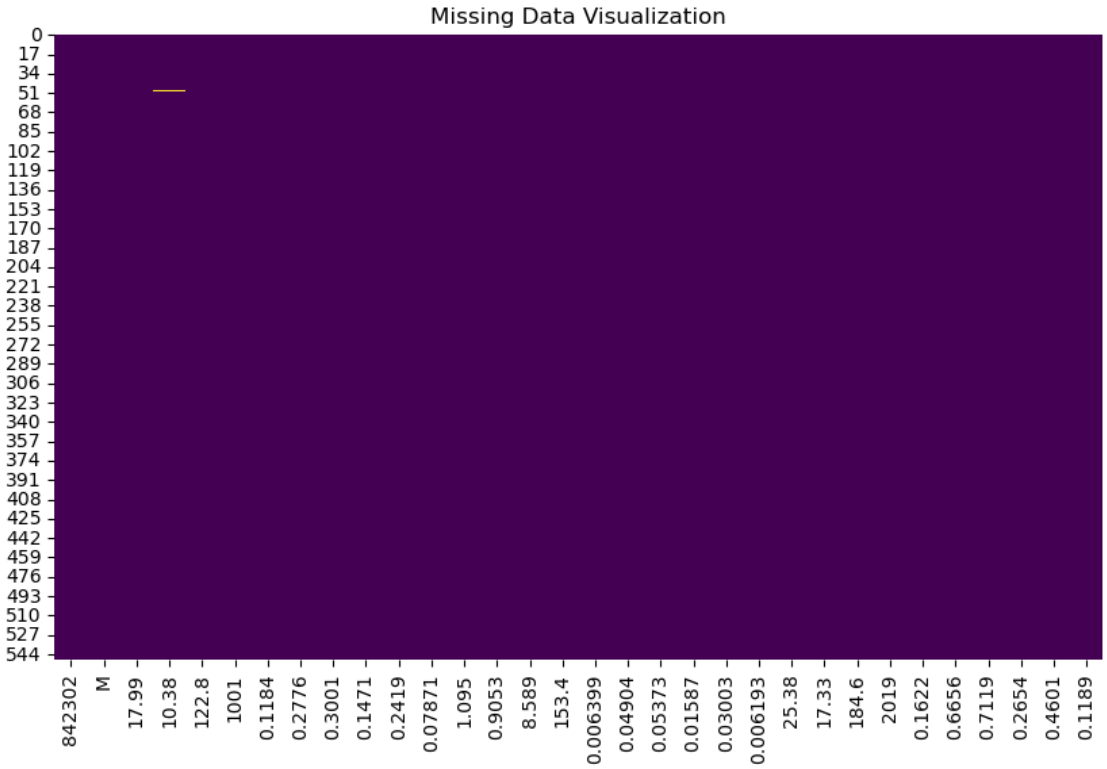
	842302	M	17.99	10.38	122.8	1001	0.1184	0.2776	0.3001	\
0	842517	M	20.570	17.77	132.90	1326.0	0.08474	0.07864	0.08690	
1	84300903	M	19.690	21.25	130.00	1203.0	0.10960	0.15990	0.19740	
2	84348301	M	11.420	20.38	77.58	386.1	0.14250	0.28390	0.24140	
3	84358402	M	20.290	14.34	135.10	1297.0	0.10030	0.13280	0.19800	
4	843786	M	12.450	15.70	82.57	477.1	0.12780	0.17000	0.15780	
..	...	..	...	...	...	...	...	...	...	
544	922576	B	13.620	23.23	87.19	573.2	0.09246	0.06747	0.02974	
545	922577	B	10.320	16.35	65.31	324.9	0.09434	0.04994	0.01012	
546	922840	B	10.260	16.58	65.85	320.8	0.08877	0.08066	0.04358	
547	923169	B	9.683	19.34	61.05	285.7	0.08491	0.05030	0.02337	
548	923465	B	10.820	24.21	68.89	361.6	0.08192	0.06602	0.01548	

	0.1471	...	25.38	17.33	184.6	2019	0.1622	0.6656	0.7119	\
0	0.070170	...	24.99	23.41	158.80	1956.0	0.1238	0.18660	0.24160	
1	0.127900	...	23.57	25.53	152.50	1709.0	0.1444	0.42450	0.45040	
2	0.105200	...	14.91	26.50	98.87	567.7	0.2098	0.86630	0.68690	
3	0.104300	...	22.54	16.67	152.20	1575.0	0.1374	0.20500	0.40000	
4	0.080890	...	15.47	23.75	103.40	741.6	0.1791	0.52490	0.53550	
..	...	...	...	...	...	...	...	...	...	
544	0.024430	...	15.35	29.09	97.58	729.8	0.1216	0.15170	0.10490	
545	0.005495	...	11.25	21.77	71.12	384.9	0.1285	0.08842	0.04384	

```
546  0.024380  ...  10.83  22.04   71.08   357.4  0.1461  0.22460  0.17830
547  0.009615  ...  10.93  25.59   69.10   364.2  0.1199  0.09546  0.09350
548  0.008160  ...  13.03  31.45   83.90   505.6  0.1204  0.16330  0.06194

      0.2654  0.4601   0.1189
0     0.18600  0.2750  0.08902
1     0.24300  0.3613  0.08758
2     0.25750  0.6638  0.17300
3     0.16250  0.2364  0.07678
4     0.17410  0.3985  0.12440
..        ...     ...      ...
544   0.07174  0.2642  0.06953
545   0.02381  0.2681  0.07399
546   0.08333  0.2691  0.09479
547   0.03846  0.2552  0.07920
548   0.03264  0.3059  0.07626

[549 rows x 32 columns]
```

In [5]:
```
df.to_csv('DATAFORTUMORCELLS.csv', index=False)
```

In [6]:
```
import seaborn as sns
plt.figure(figsize=(10,6))
sns.heatmap(df.isnull(), cbar=False, cmap='viridis')
plt.title('Missing Data Visualization')
plt.show()
```



```
In [129]: df['10.38'].isnull().sum()

Out[129]: 1

In [130]: df.isnull().sum()

Out[130]: 842302      0
          M           0
          17.99       0
          10.38       1
          122.8       0
          1001        0
          0.1184      0
          0.2776      0
          0.3001      0
          0.1471      0
          0.2419      0
          0.07871     0
          1.095       0
          0.9053      0
          8.589       0
          153.4       0
          0.006399    0
          0.04904     0
          0.05373     0
          0.01587     0
          0.03003     0
          0.006193    0
          25.38       0
          17.33       0
          184.6       0
          2019        0
          0.1622      0
          0.6656      0
          0.7119      0
          0.2654      0
          0.4601      0
          0.1189      0
          dtype: int64

In [131]: df['10.38'].fillna(value=df['10.38'].mean(), inplace=True)

In [132]: df['10.38'].isnull().sum()

Out[132]: 0
```

i) How do the ranges of the values in the columns compare?

answer:

It appears the differences between the min and max of the columns are mostly within the 10^(-1) range for the columns, with a few being in 10^0, 10^1 and 10^2 magnitude values. However it also appears that the ID column '842302' ranges all the way in the 10^8 magnitude.

ii) Does each column of data have similar magnitudes and ranges? Are there any outliers?

answer:

The values are relatively similar in most of the columns, bing small decimals around 0.20. Some feature columns are the low tens, and one feature column '0.1184' which is the 4th feature seems to have values around 10^3, while the column '842302' which is the id column seems to have values around 10^7.

To find outliers, I have found plotted boxplots of each feature to realize that many values are in fact ouliers, however I have decided to only work on removing rows where features are equivalent to many times the mean that I have determined visually to be the following values which are considered extreme outliers:

Feature 2 > 37
Feature 5 > 1e6
Feature 11 > 2.4
Feature 12 > 4.5
Feature 13 > 15
Feature 14 > 500
Feature 15 > 0.03
Feature 17 > 0.28
Feature 18 > 0.05
Feature 19 > 0.07
Feature 20 > 0.015
Feature 24 > 4000
Feature 29 > 0.6
Feature 30 > 0.16

iii) I will perform any necessary modifications on the data set and document your changes and explanations.

modification 1: It appears that the columns labels is actually a row of data, so I will be replacing the labels with the information I know which is the 'ID' column and the 'Diagnosis' column that denotes malignance or benignness, and the rest will be numbered features such as feature 1, feature 2, etc.

modification 2: The outliers outlined above came out to the following rows [238,249,211,460,191,212,67,151,77,70,175,289,2,8], which I ended up dropping entirely, losing 14 rows of data. The reason I chose to remove these outliers were for the following reasons. First of all, because many of the rows that had extreme outliers are shared between different outliers, so we wouldn't have to remove many rows. And secondly because there weren't many extreme outliers such that a significant part of the data would have to be manipulated, which wouldn't be ideal for machine learning since a large amount of accurate data would be ideal.

```
In [133]: labels = df.columns.tolist()
          labels
          def convert_numeric(data):
              converted_data = []
              for item in data:
```

```
                try:
                    converted_data.append(int(item))
                except ValueError:
                    try:
                        converted_data.append(float(item))
                    except ValueError:
                        converted_data.append(item)
            return converted_data

        converted_list = convert_numeric(labels)
```

In [134]:
```
df_spare = df
```

In [135]:
```
df_spare.loc[549] = converted_list
```

In [136]:
```
df_spare.loc[549] # finally we have appended a new row that is the values in the lab
#end of modification 1
```

Out[136]:

842302	842302
M	M
17.99	17.99
10.38	10.38
122.8	122.8
1001	1001.0
0.1184	0.1184
0.2776	0.2776
0.3001	0.3001
0.1471	0.1471
0.2419	0.2419
0.07871	0.07871
1.095	1.095
0.9053	0.9053
8.589	8.589
153.4	153.4
0.006399	0.006399
0.04904	0.04904
0.05373	0.05373
0.01587	0.01587
0.03003	0.03003
0.006193	0.006193
25.38	25.38
17.33	17.33
184.6	184.6
2019	2019.0
0.1622	0.1622
0.6656	0.6656
0.7119	0.7119
0.2654	0.2654
0.4601	0.4601

```
          0.1189        0.1189
          Name: 549, dtype: object
```

```
In [137]: df_spare.columns = ['ID', 'Diagnosis', 'Feature 1', 'Feature 2','Feature 3','Feature
```

```
In [138]: df_spare.head()
```

Out[138]:

	ID	Diagnosis	Feature 1	Feature 2	Feature 3	Feature 4	Feature 5	\
0	842517	M	20.57	17.77	132.90	1326.0	0.08474	
1	84300903	M	19.69	21.25	130.00	1203.0	0.10960	
2	84348301	M	11.42	20.38	77.58	386.1	0.14250	
3	84358402	M	20.29	14.34	135.10	1297.0	0.10030	
4	843786	M	12.45	15.70	82.57	477.1	0.12780	

	Feature 6	Feature 7	Feature 8	...	Feature 21	Feature 22	Feature 23	\
0	0.07864	0.0869	0.07017	...	24.99	23.41	158.80	
1	0.15990	0.1974	0.12790	...	23.57	25.53	152.50	
2	0.28390	0.2414	0.10520	...	14.91	26.50	98.87	
3	0.13280	0.1980	0.10430	...	22.54	16.67	152.20	
4	0.17000	0.1578	0.08089	...	15.47	23.75	103.40	

	Feature 24	Feature 25	Feature 26	Feature 27	Feature 28	Feature 29	\
0	1956.0	0.1238	0.1866	0.2416	0.1860	0.2750	
1	1709.0	0.1444	0.4245	0.4504	0.2430	0.3613	
2	567.7	0.2098	0.8663	0.6869	0.2575	0.6638	
3	1575.0	0.1374	0.2050	0.4000	0.1625	0.2364	
4	741.6	0.1791	0.5249	0.5355	0.1741	0.3985	

	Feature 30
0	0.08902
1	0.08758
2	0.17300
3	0.07678
4	0.12440

[5 rows x 32 columns]

```
In [139]: range_df = df.describe().loc['max'] - df.describe().loc['min']
          print(range_df)
```

```
ID             9.113118e+08
Feature 1      2.112900e+01
Feature 2      2.957000e+01
Feature 3      1.447100e+02
Feature 4      2.357500e+03
Feature 5      1.007000e+06
Feature 6      3.260200e-01
Feature 7      4.268000e-01
Feature 8      2.012000e-01
```

```
Feature 9     1.873000e-01
Feature 10    4.748000e-02
Feature 11    2.761500e+00
Feature 12    4.524800e+00
Feature 13    2.122300e+01
Feature 14    5.353980e+02
Feature 15    2.941700e-02
Feature 16    1.331480e-01
Feature 17    3.960000e-01
Feature 18    5.279000e-02
Feature 19    7.106800e-02
Feature 20    2.894520e-02
Feature 21    2.811000e+01
Feature 22    3.752000e+01
Feature 23    2.007900e+02
Feature 24    4.068800e+03
Feature 25    1.514300e-01
Feature 26    1.030710e+00
Feature 27    1.252000e+00
Feature 28    2.910000e-01
Feature 29    5.073000e-01
Feature 30    1.524600e-01
dtype: float64
```

```
In [140]: df[['Feature 1', 'Feature 2','Feature 3','Feature 4','Feature 5','Feature 6','Feature
```

Out[140]:

	Feature 1	Feature 2	Feature 3	Feature 4	Feature 5
count	550.000000	550.000000	550.000000	550.000000	5.500000e+02
mean	14.140805	19.059209	92.052691	655.540727	1.831005e+03
std	3.496656	4.150726	24.087190	350.132761	4.293862e+04
min	6.981000	9.710000	43.790000	143.500000	6.251000e-02
25%	11.740000	16.070000	75.467500	423.075000	8.663500e-02
50%	13.390000	18.690000	86.415000	552.050000	9.595500e-02
75%	15.780000	21.540000	104.025000	782.675000	1.054000e-01
max	28.110000	39.280000	188.500000	2501.000000	1.007000e+06

	Feature 6	Feature 7	Feature 8	Feature 9	Feature 10	Feature 11
count	550.000000	550.000000	550.000000	550.000000	550.000000	550.000000
mean	0.104418	0.088416	0.048941	0.181533	0.062839	0.404212
std	0.052316	0.078490	0.038336	0.027259	0.007118	0.277486
min	0.019380	0.000000	0.000000	0.116700	0.049960	0.111500
25%	0.065525	0.029600	0.020413	0.162250	0.057800	0.231925
50%	0.093125	0.061545	0.033600	0.179850	0.061580	0.325000
75%	0.130475	0.130350	0.073910	0.195700	0.066195	0.478375
max	0.345400	0.426800	0.201200	0.304000	0.097440	2.873000

	Feature 12	Feature 13	Feature 14	Feature 15

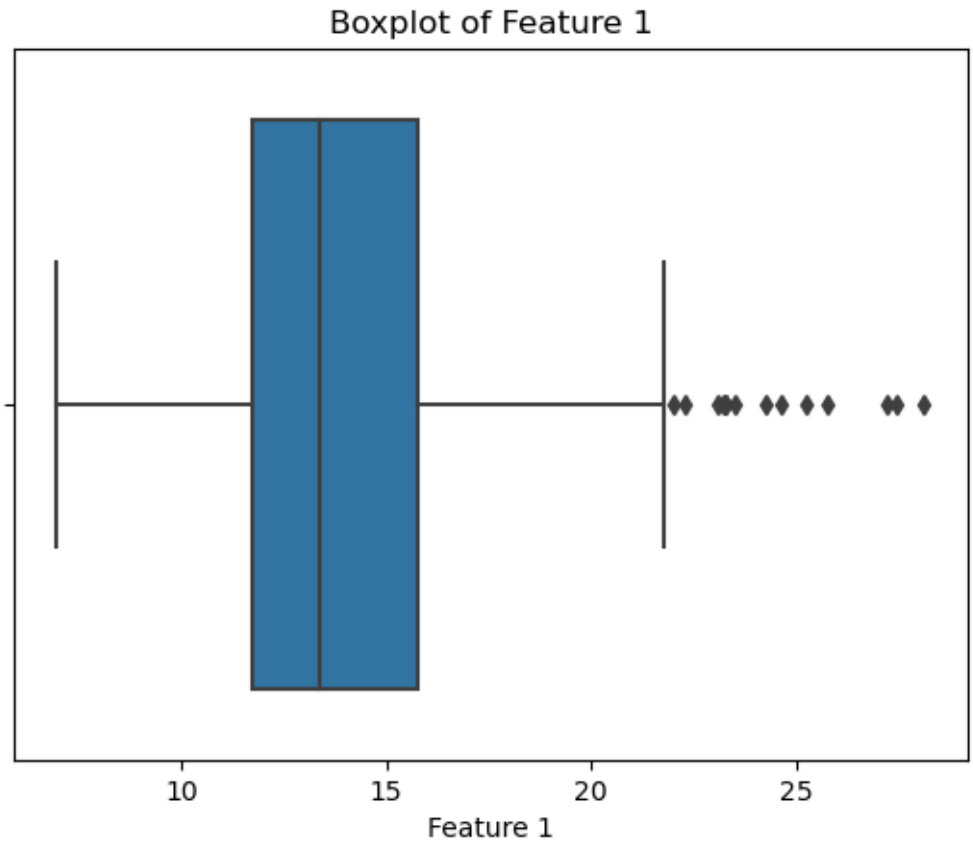
```
count  550.000000  550.000000  550.000000  550.000000
mean     1.196925    2.854629   40.285796    0.007008
std      0.532101    2.018917   45.643100    0.003009
min      0.360200    0.757000    6.802000    0.001713
25%      0.828050    1.598250   17.852500    0.005139
50%      1.078500    2.288000   24.650000    0.006302
75%      1.464250    3.325500   45.132500    0.008079
max      4.885000   21.980000  542.200000    0.031130
```

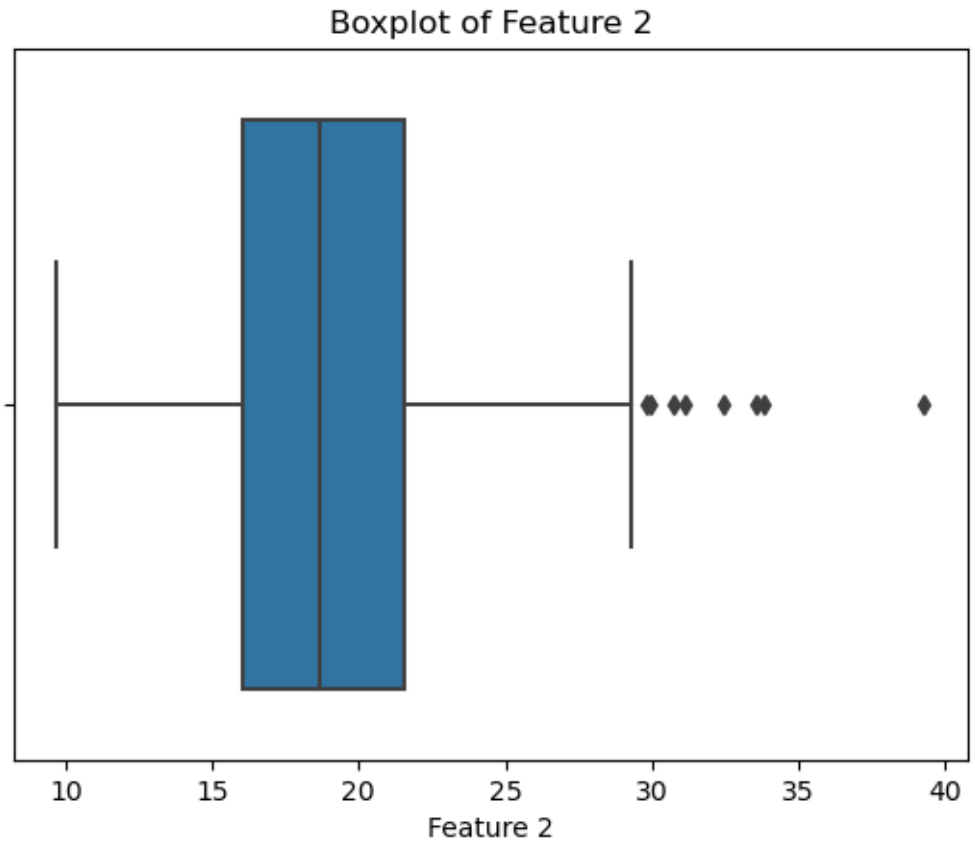
In [141]:
```
df[['Feature 16','Feature 17','Feature 18','Feature 19','Feature 20','Feature 21','F
```

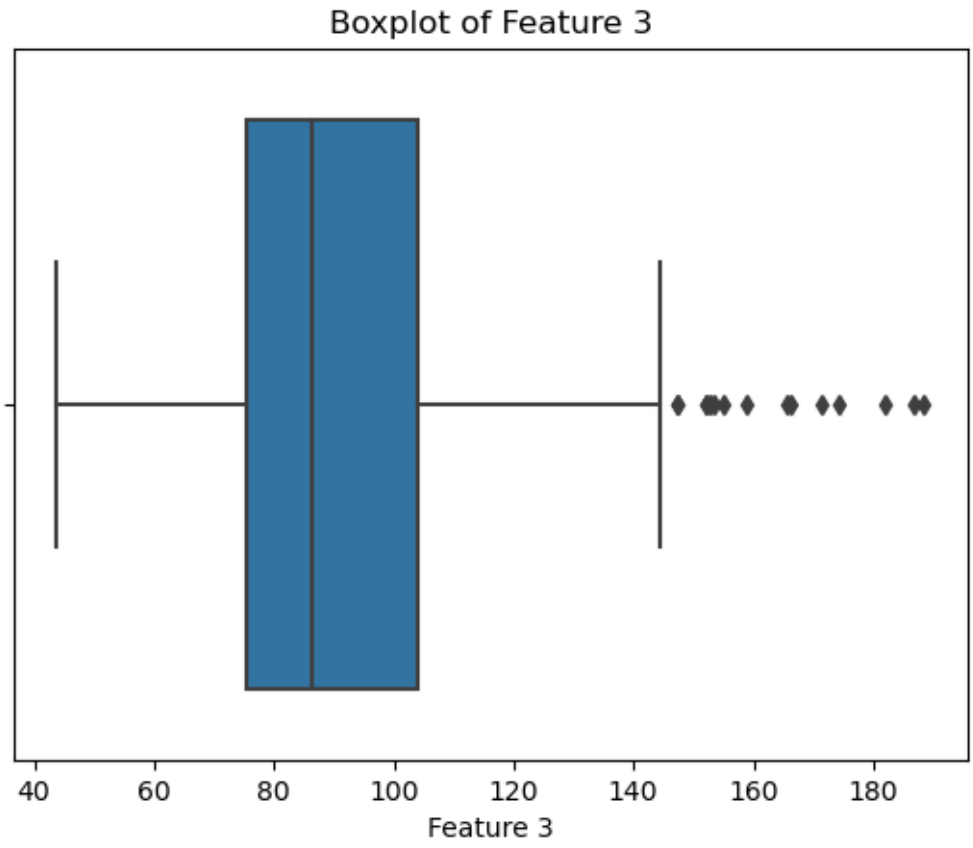
Out[141]:

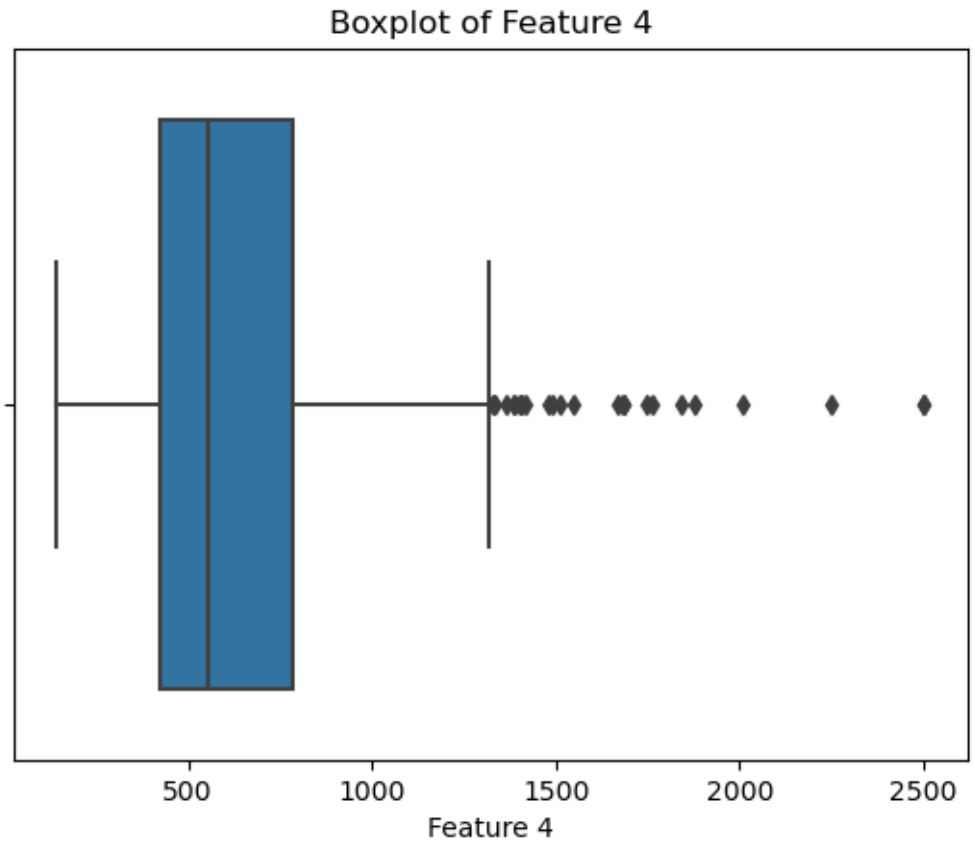
```
       Feature 16  Feature 17  Feature 18  Feature 19  Feature 20  Feature 21  \
count  550.000000  550.000000  550.000000  550.000000  550.000000  550.000000
mean     0.025423    0.031751    0.011794    0.020499    0.003790   16.297451
std      0.018007    0.030296    0.006111    0.008317    0.002678    4.809329
min      0.002252    0.000000    0.000000    0.007882    0.000895    7.930000
25%      0.013097    0.015100    0.007681    0.015023    0.002225   13.060000
50%      0.020165    0.025735    0.010905    0.018700    0.003131   14.975000
75%      0.032372    0.040852    0.014605    0.023365    0.004488   18.782500
max      0.135400    0.396000    0.052790    0.078950    0.029840   36.040000

       Feature 22  Feature 23   Feature 24  Feature 25  Feature 26  \
count  550.000000  550.000000   550.000000  550.000000  550.000000
mean    25.439691  107.405582   882.948364    0.132768    0.254555
std      6.027639   33.341975   568.917761    0.022858    0.154603
min     12.020000   50.410000   185.200000    0.071170    0.027290
25%     20.930000   84.465000   516.825000    0.117125    0.147900
50%     25.215000   97.745000   687.100000    0.131600    0.215700
75%     29.257500  125.075000  1080.500000    0.146400    0.341175
max     49.540000  251.200000  4254.000000    0.222600    1.058000

       Feature 27  Feature 28  Feature 29  Feature 30
count  550.000000  550.000000  550.000000  550.000000
mean     0.271628    0.115063    0.291221    0.084052
std      0.203799    0.064801    0.061544    0.017979
min      0.000000    0.000000    0.156500    0.055040
25%      0.116725    0.065280    0.252225    0.071857
50%      0.227450    0.100550    0.282700    0.080090
75%      0.384700    0.161375    0.318700    0.092105
max      1.252000    0.291000    0.663800    0.207500
```

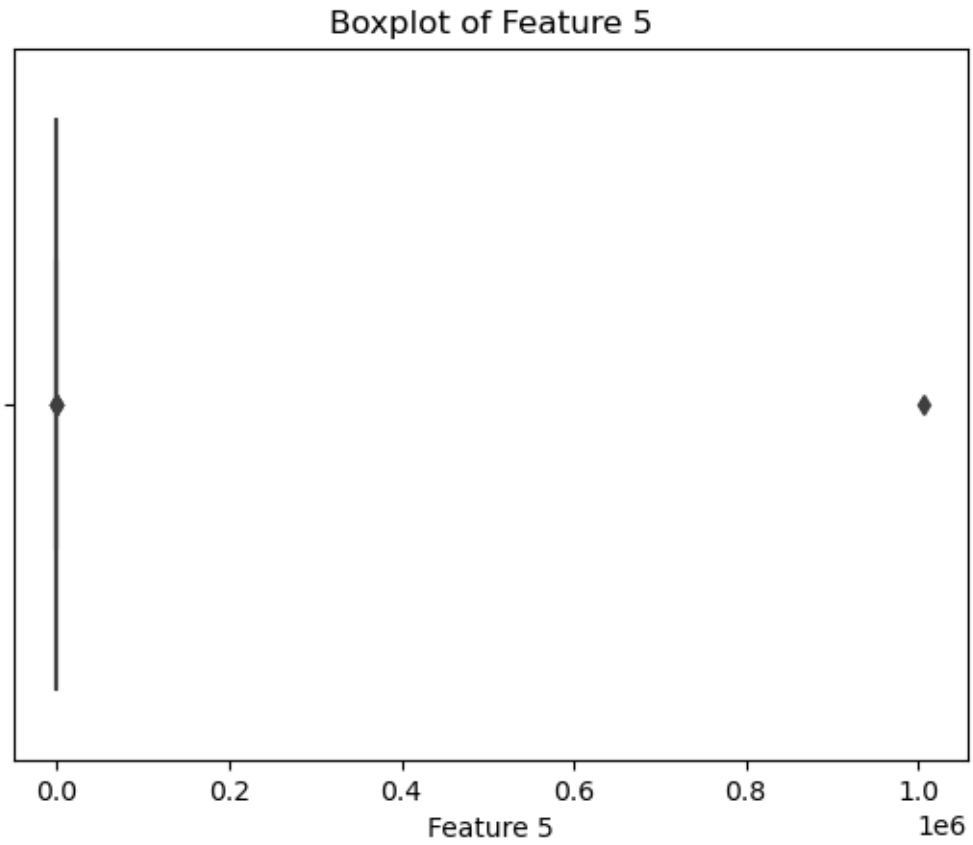
In [142]:
```
for i in range(1,31):
    sns.boxplot(x=df[f'Feature {i}'])
    plt.title('Boxplot of Feature {}'.format(i))
    plt.show()
```

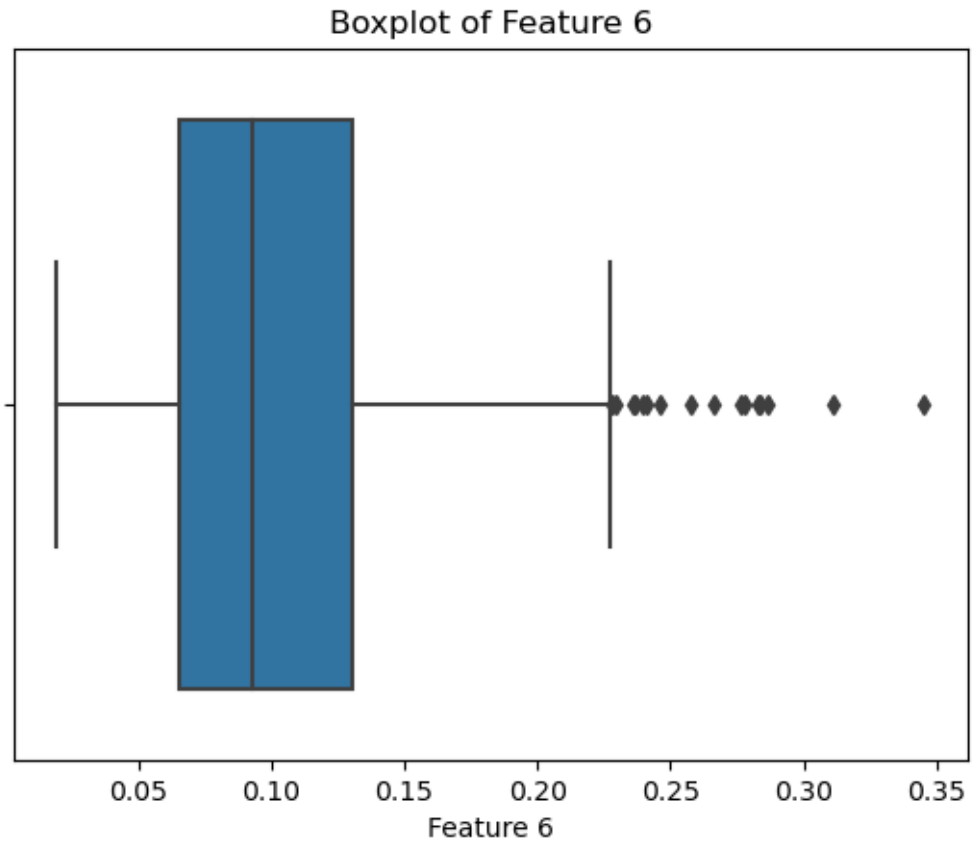

Boxplot of Feature 1
10
15
20
25
Feature 1

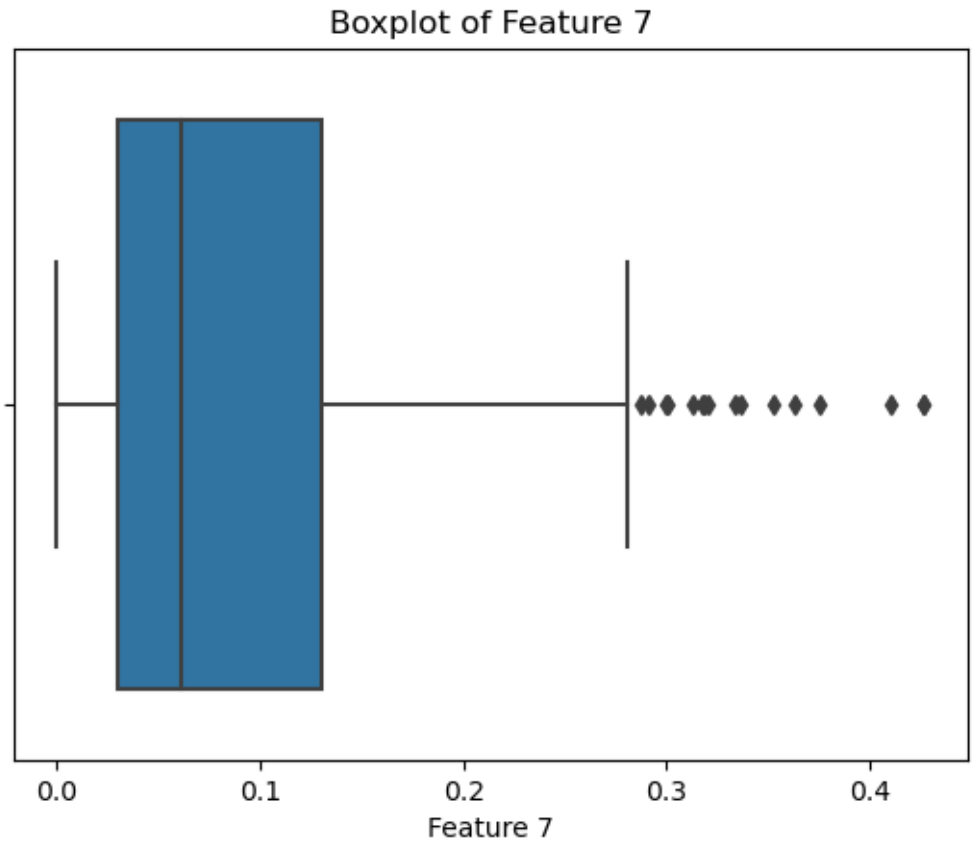

Boxplot of Feature 2
10
15
20
25
30
35
40
Feature 2

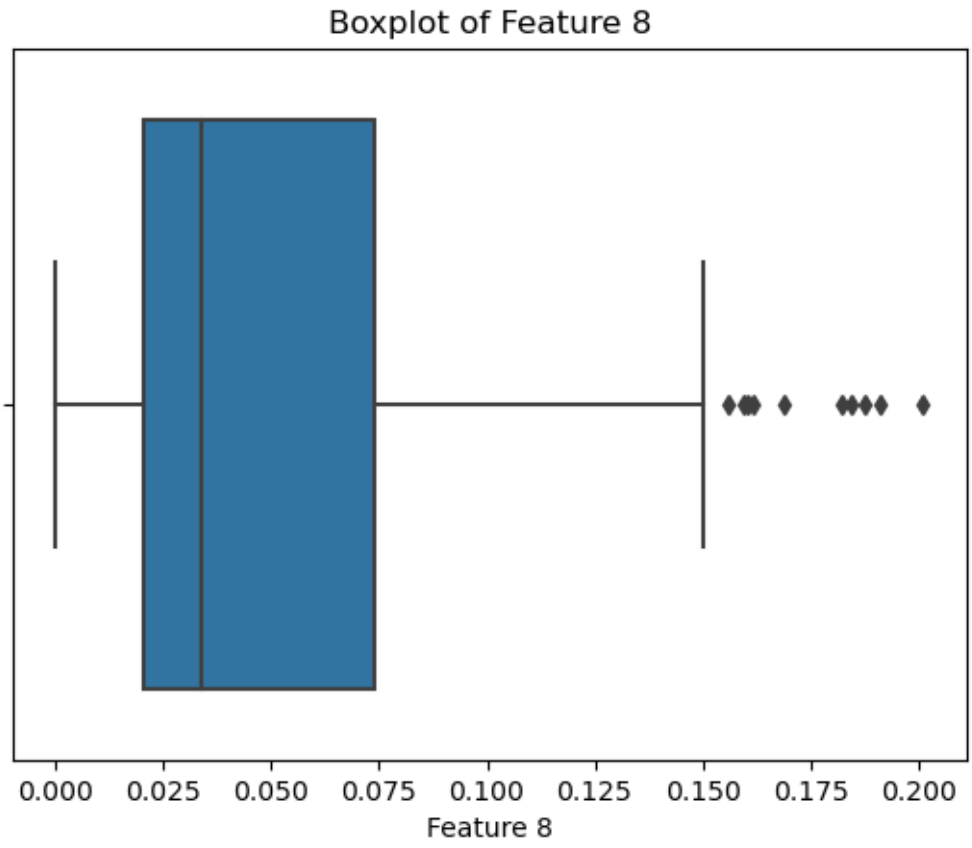

Boxplot of Feature 3
40
60
80
100
120
140
160
180
Feature 3

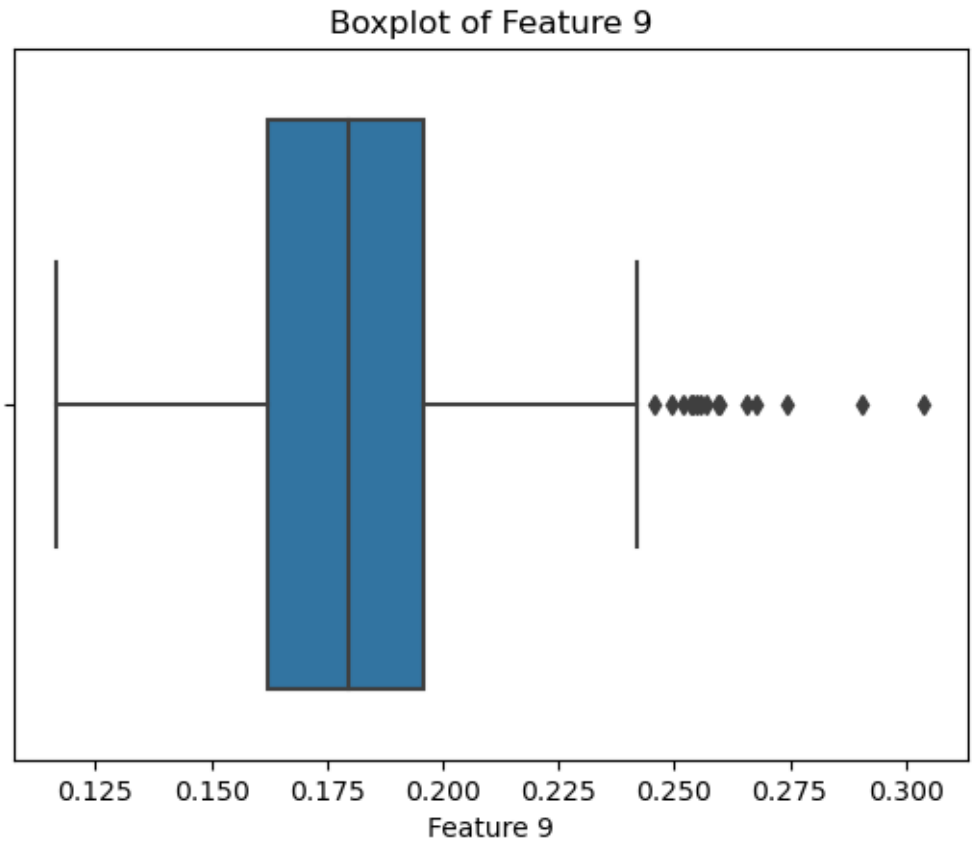

Boxplot of Feature 4
500
1000
1500
2000
2500
Feature 4

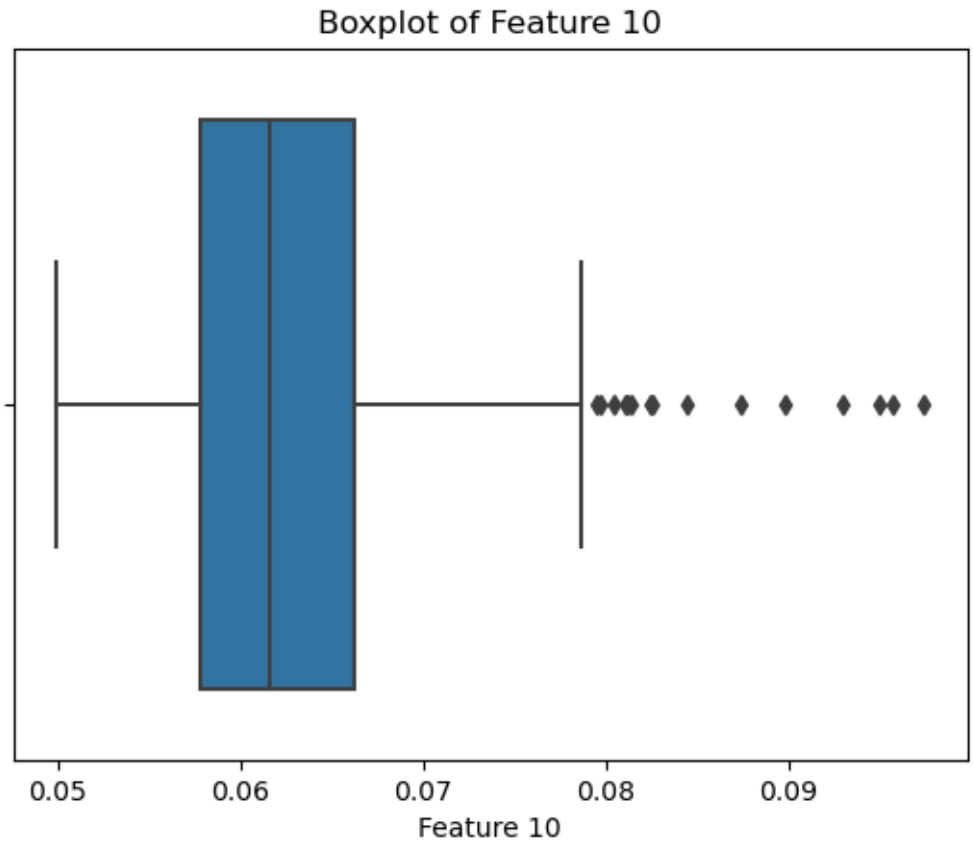

Boxplot of Feature 5
0.0
0.2
0.4
0.6
0.8
1.0
Feature 5
1e6

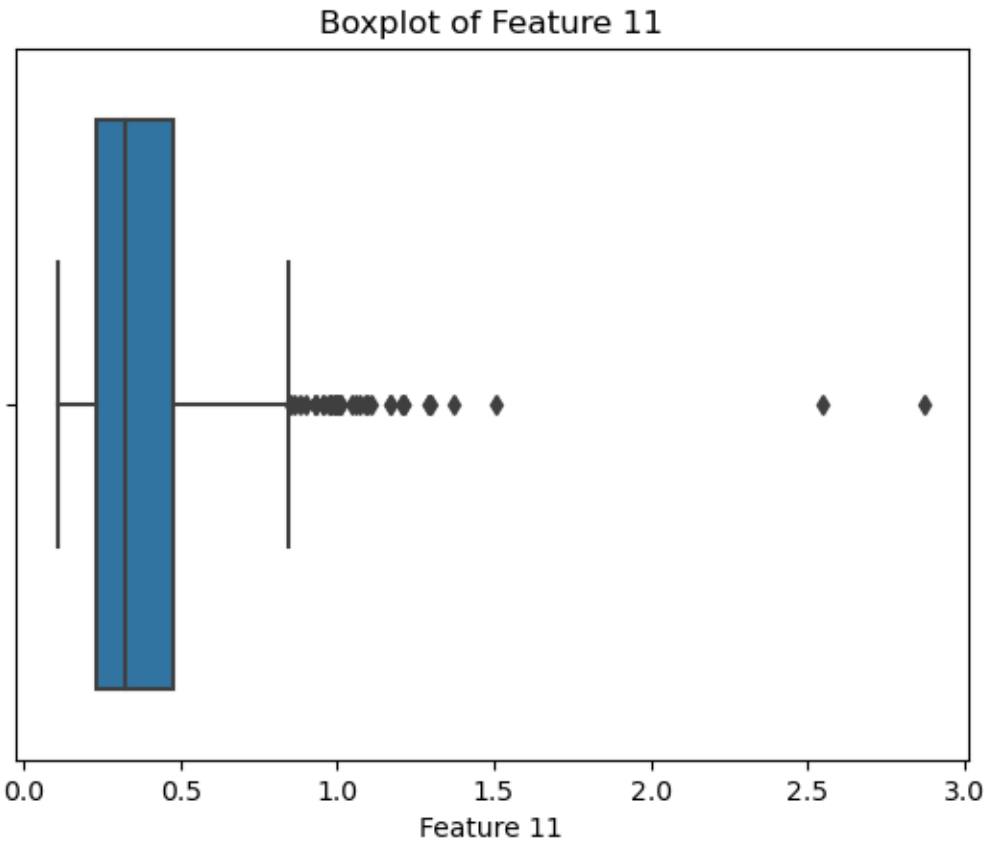

Boxplot of Feature 6
0.05
0.10
0.15
0.20
0.25
0.30
0.35
Feature 6

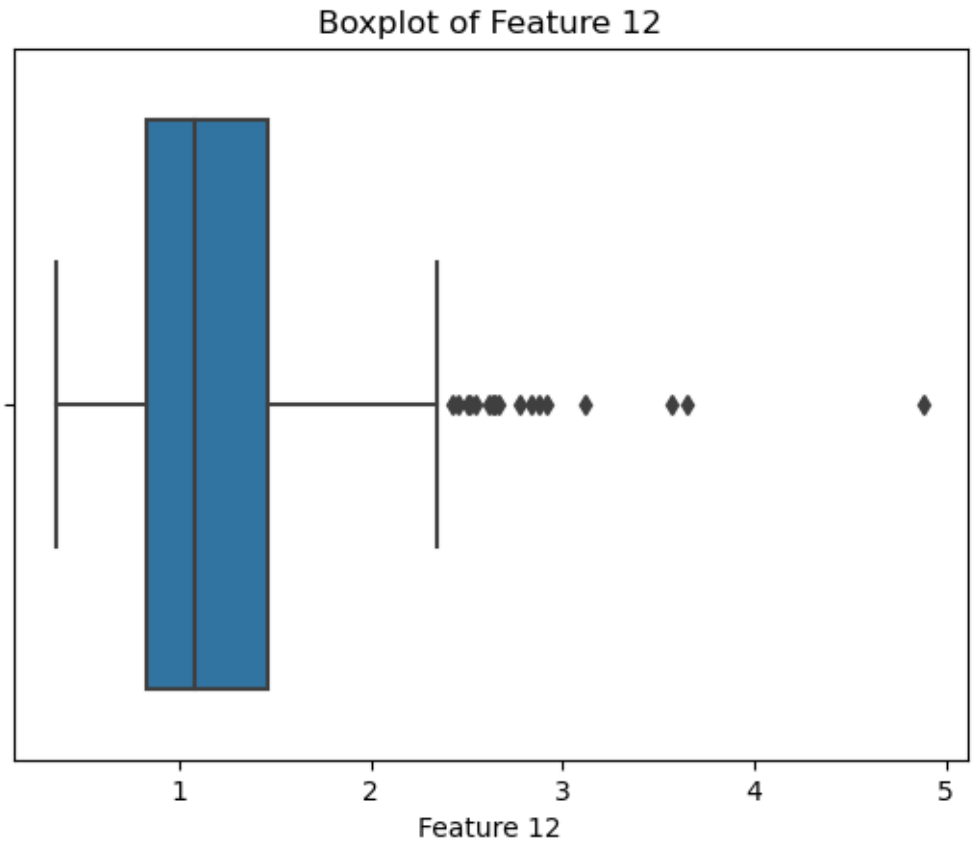

Boxplot of Feature 7
0.0
0.1
0.2
0.3
0.4
Feature 7

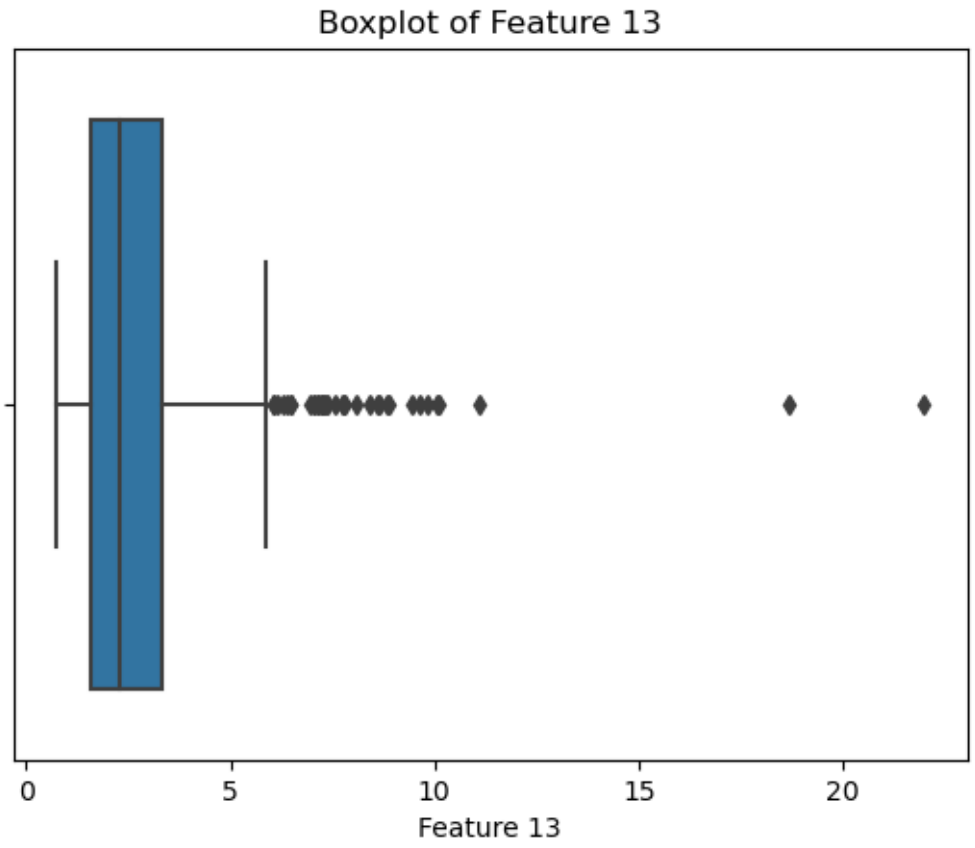

Boxplot of Feature 8
0.000
0.025
0.050
0.075
0.100
0.125
0.150
0.175
0.200
Feature 8

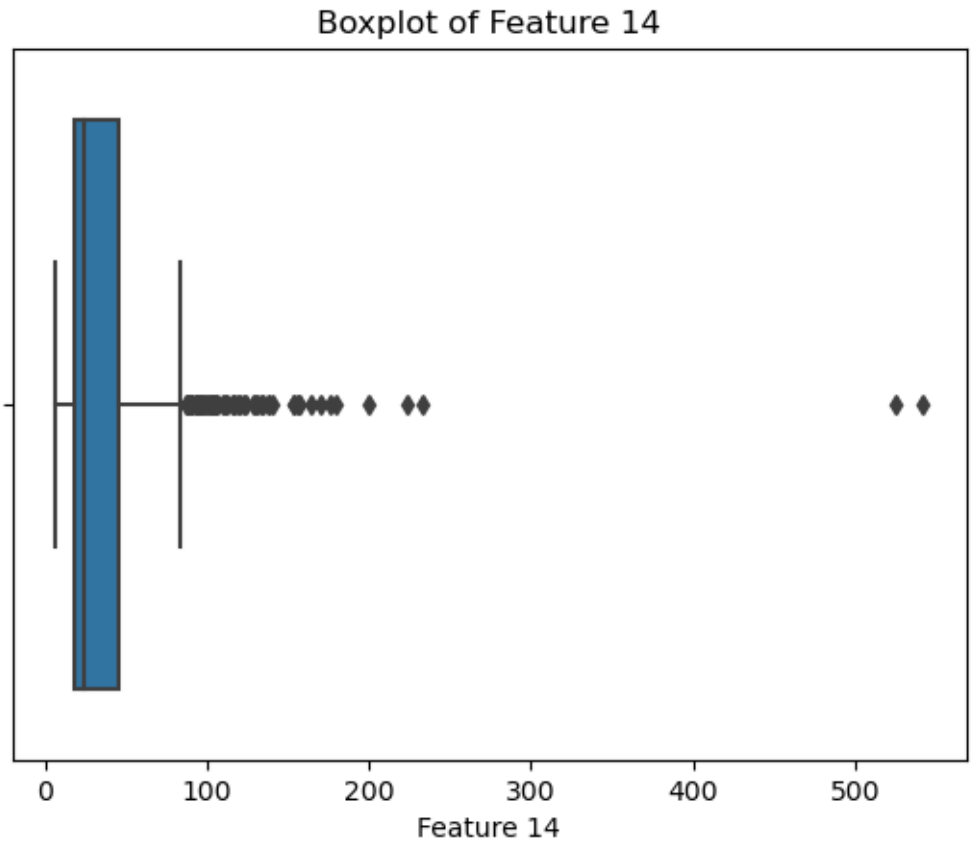

Boxplot of Feature 9
0.125
0.150
0.175
0.200
0.225
0.250
0.275
0.300
Feature 9

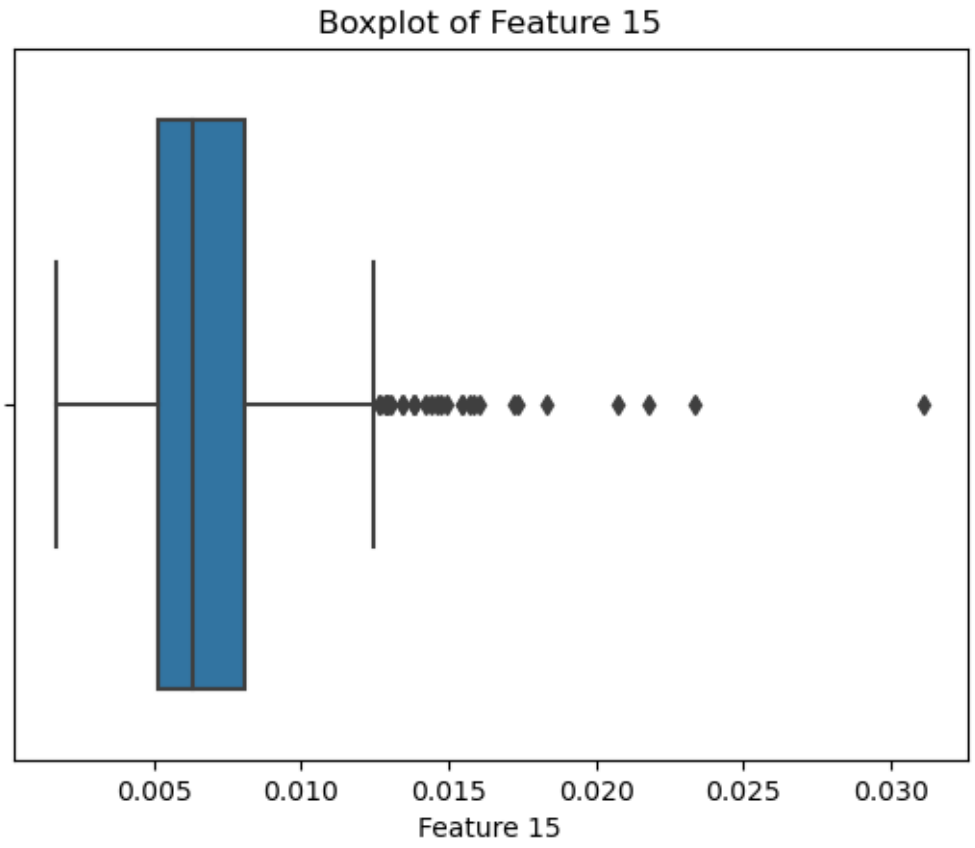

Boxplot of Feature 10
0.05
0.06
0.07
0.08
0.09
Feature 10

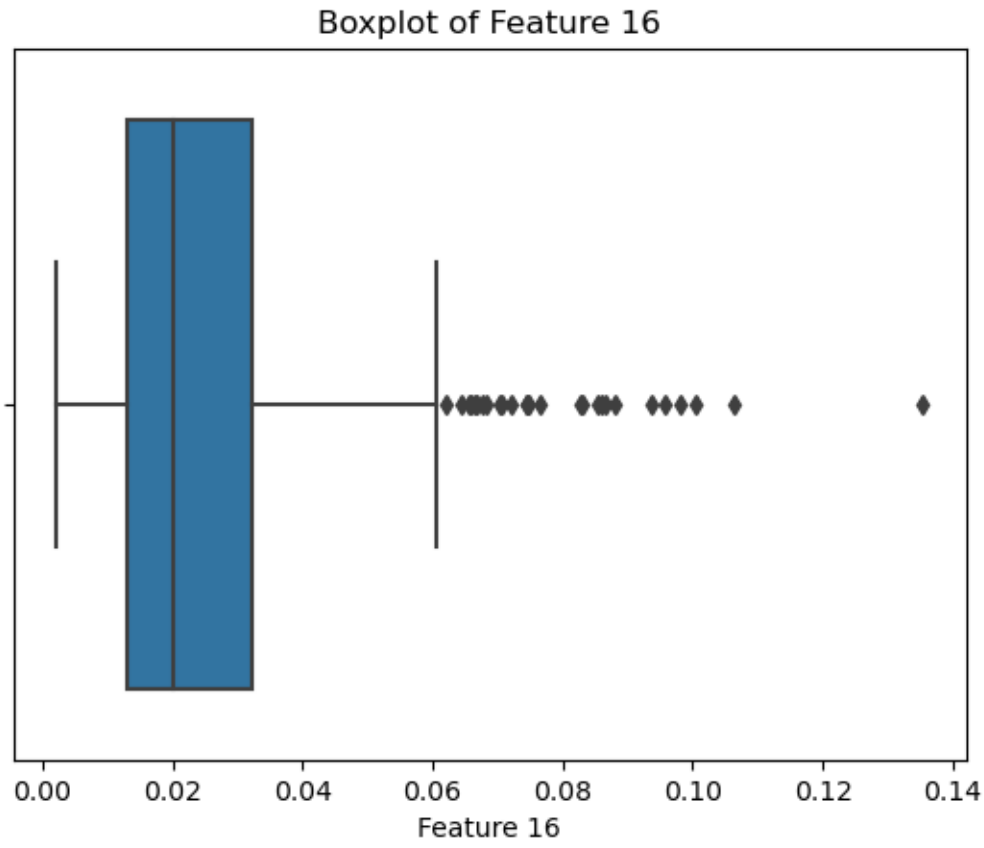

Boxplot of Feature 11
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Feature 11

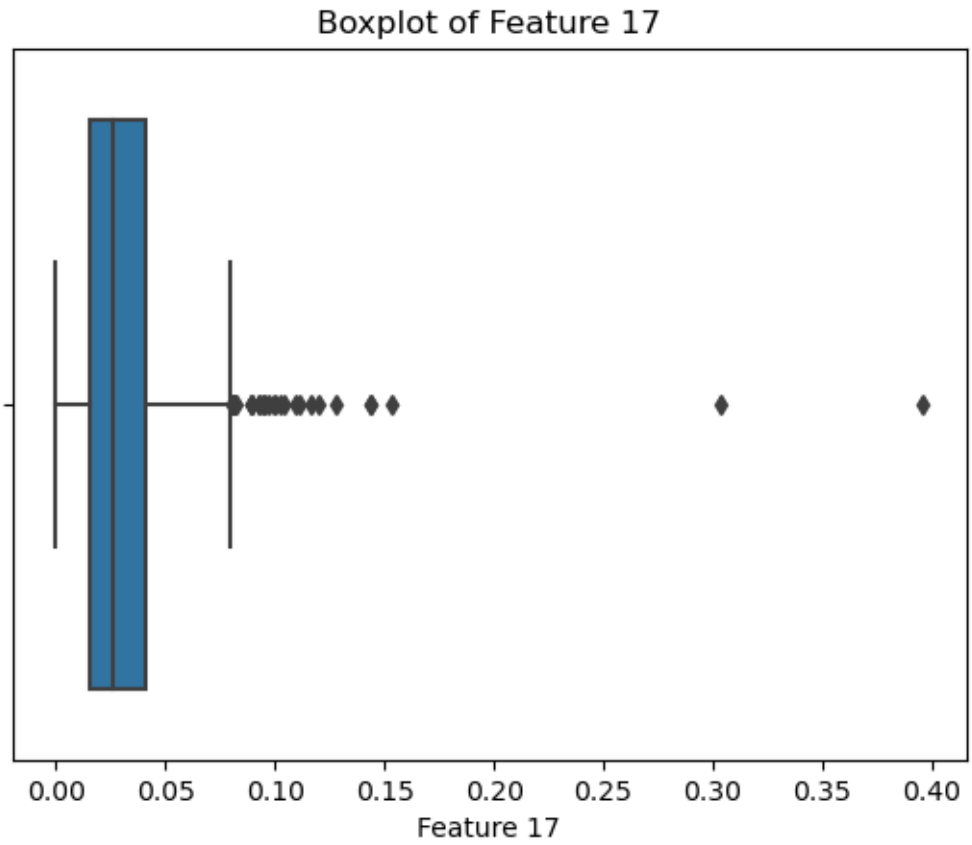

Boxplot of Feature 12
1
2
3
4
5
Feature 12

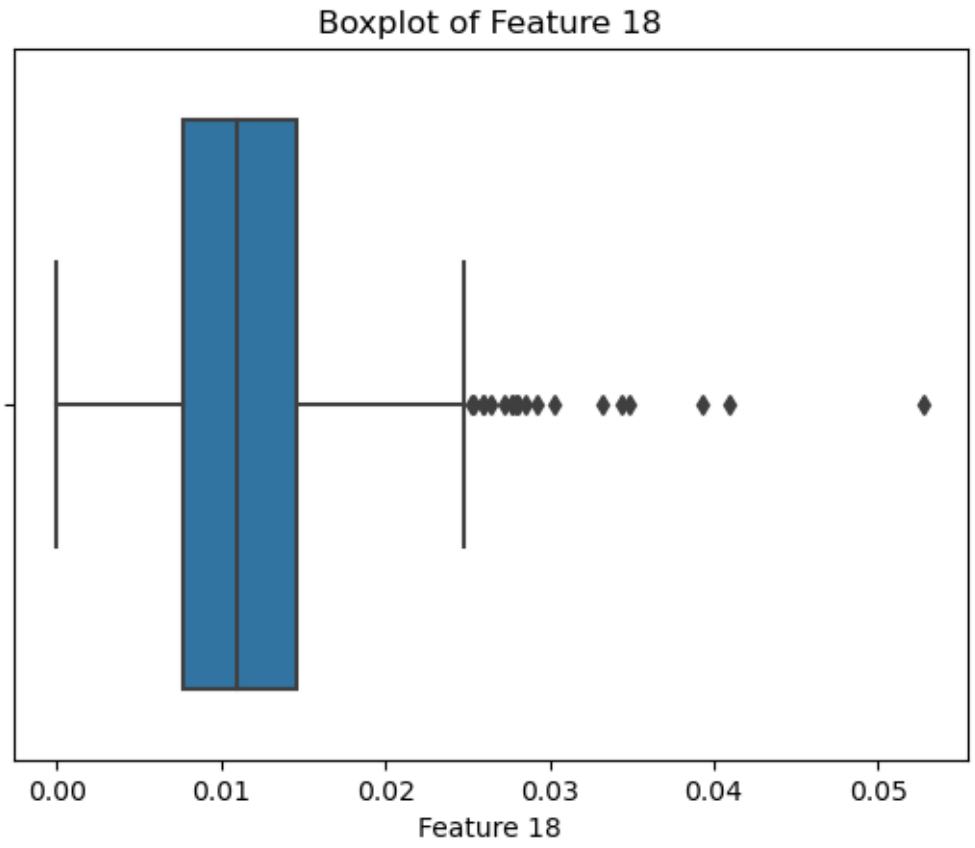

Boxplot of Feature 13
0
5
10
15
20
Feature 13

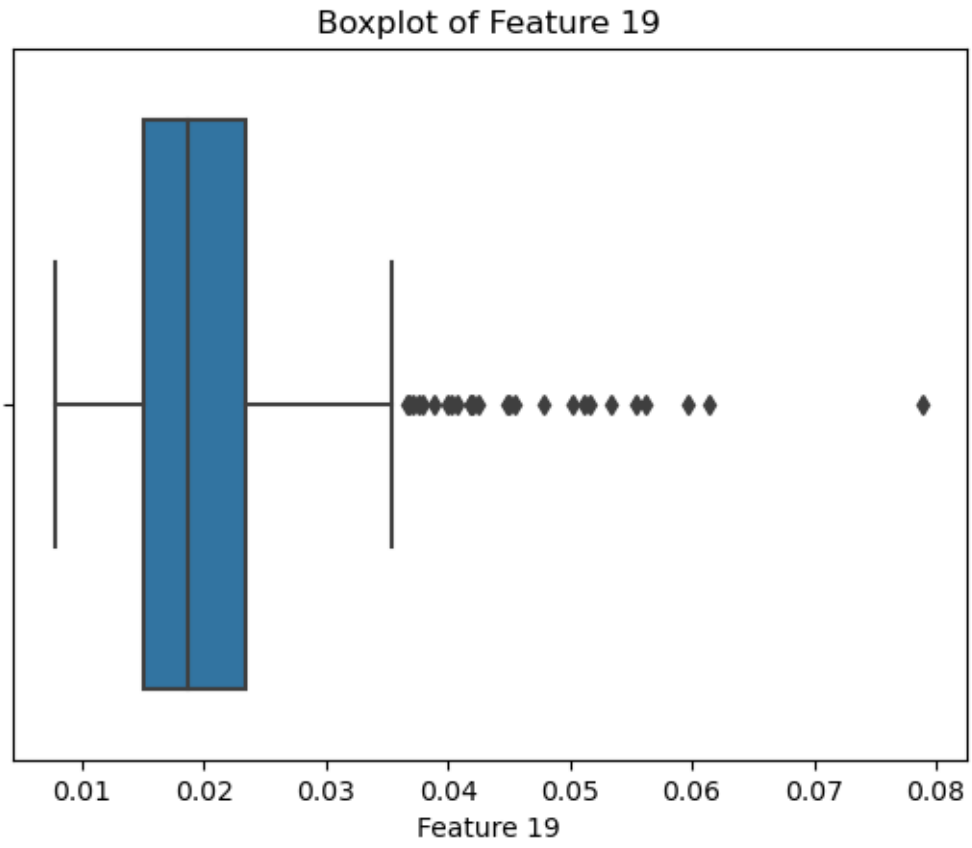

Boxplot of Feature 14
0
100
200
300
400
500
Feature 14

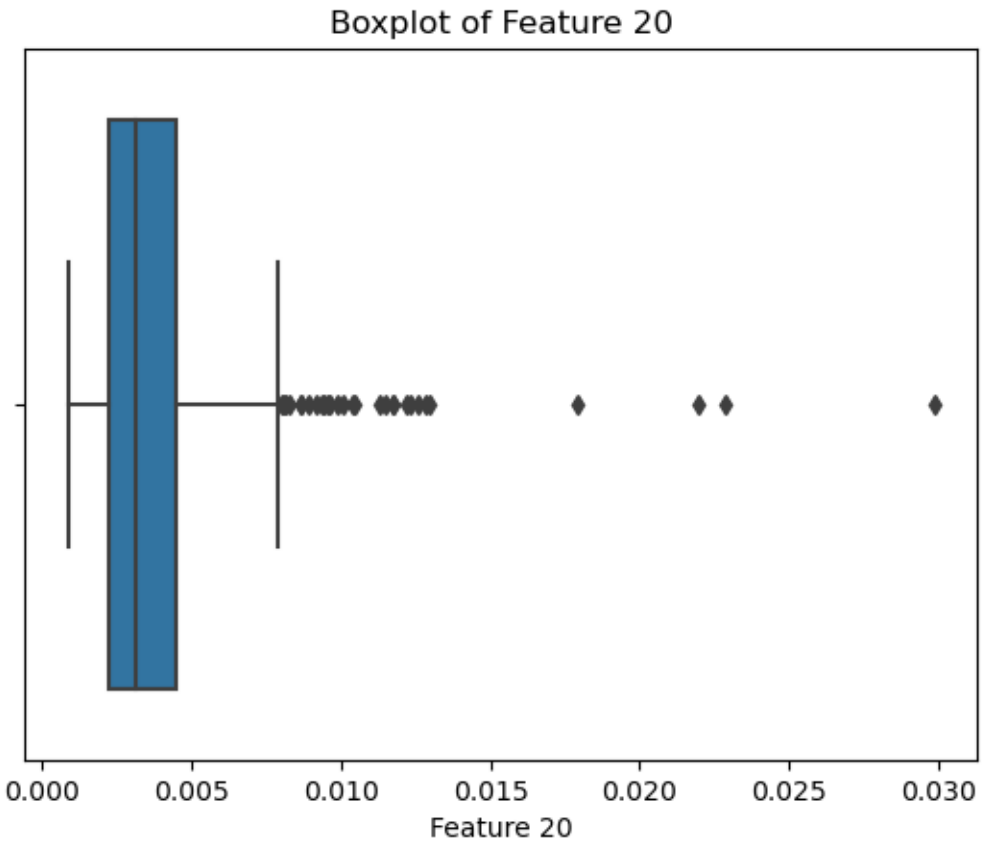

Boxplot of Feature 15
0.005
0.010
0.015
0.020
0.025
0.030
Feature 15

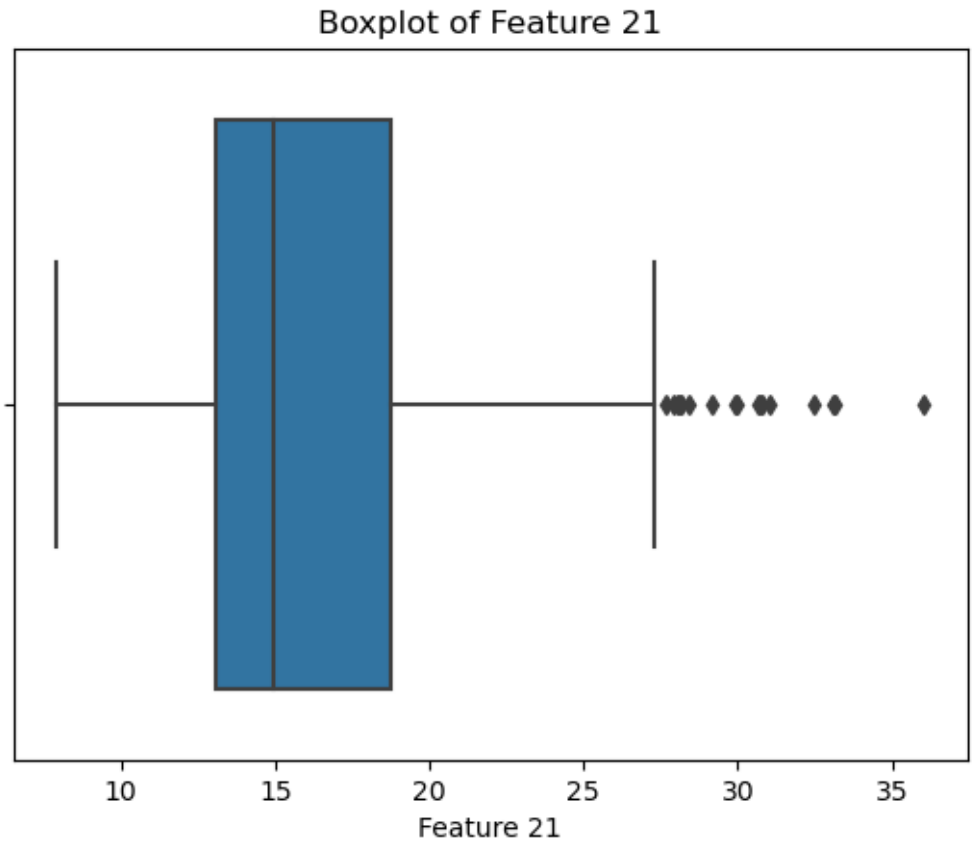

Boxplot of Feature 16
0.00
0.02
0.04
0.06
0.08
0.10
0.12
0.14
Feature 16

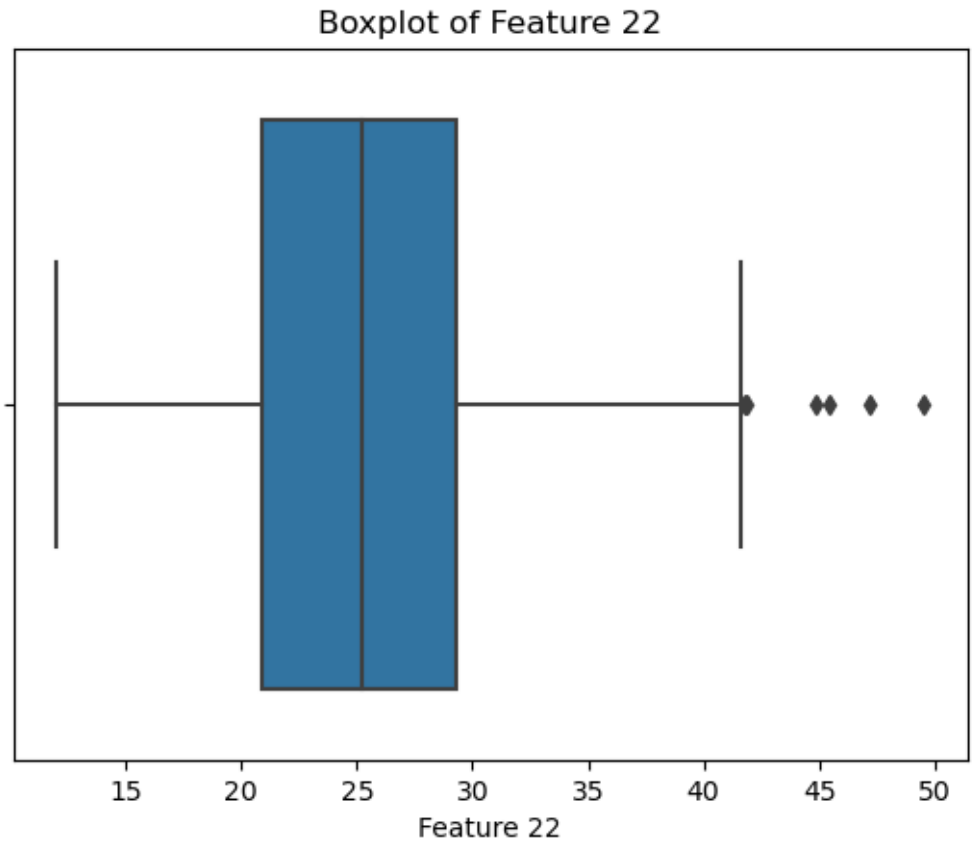

Boxplot of Feature 17
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
0.40
Feature 17

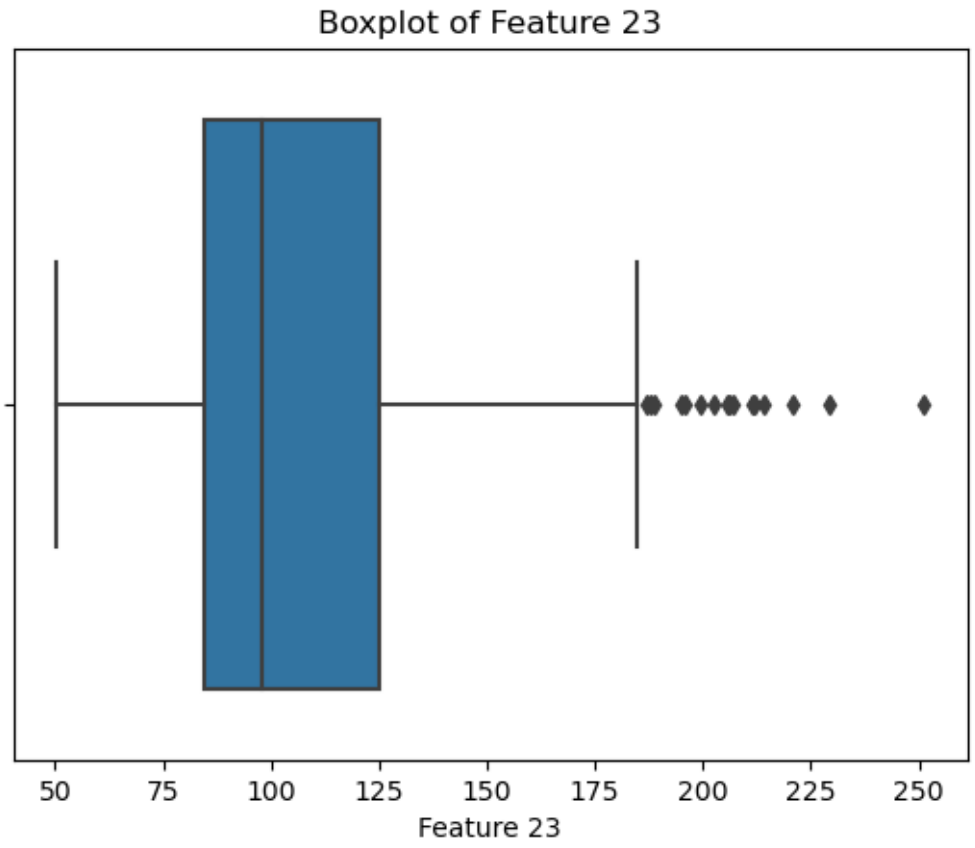

Boxplot of Feature 18
0.00
0.01
0.02
0.03
0.04
0.05
Feature 18

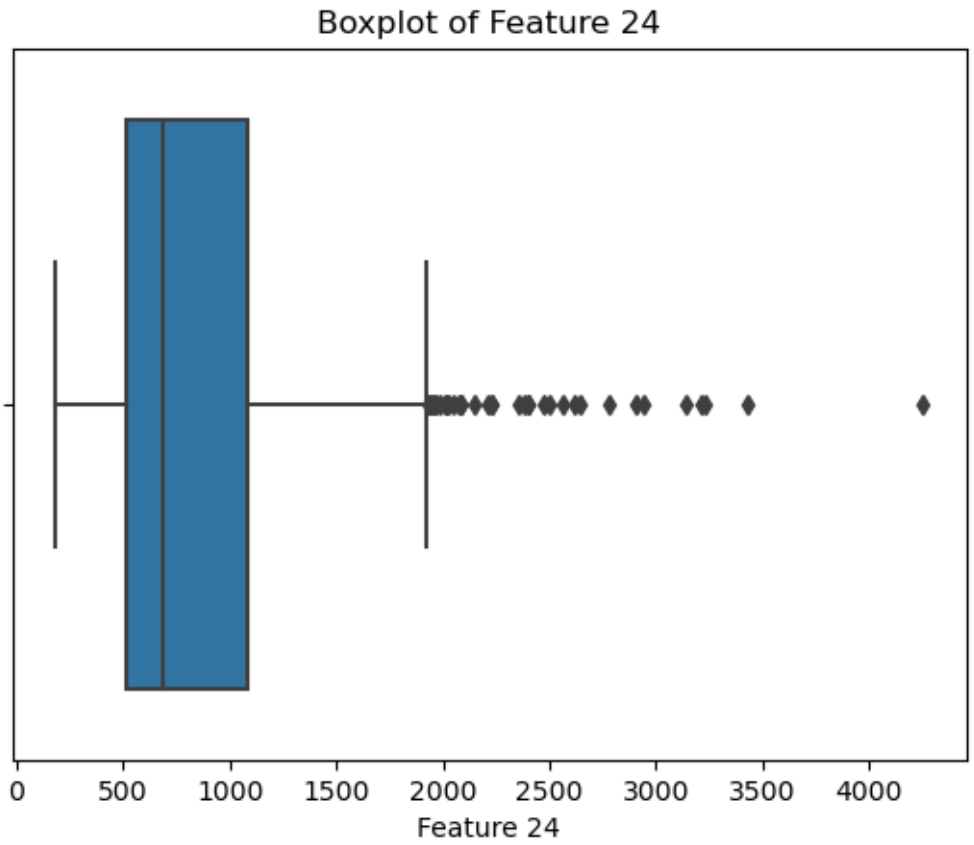

Boxplot of Feature 19
0.01
0.02
0.03
0.04
0.05
0.06
0.07
0.08
Feature 19

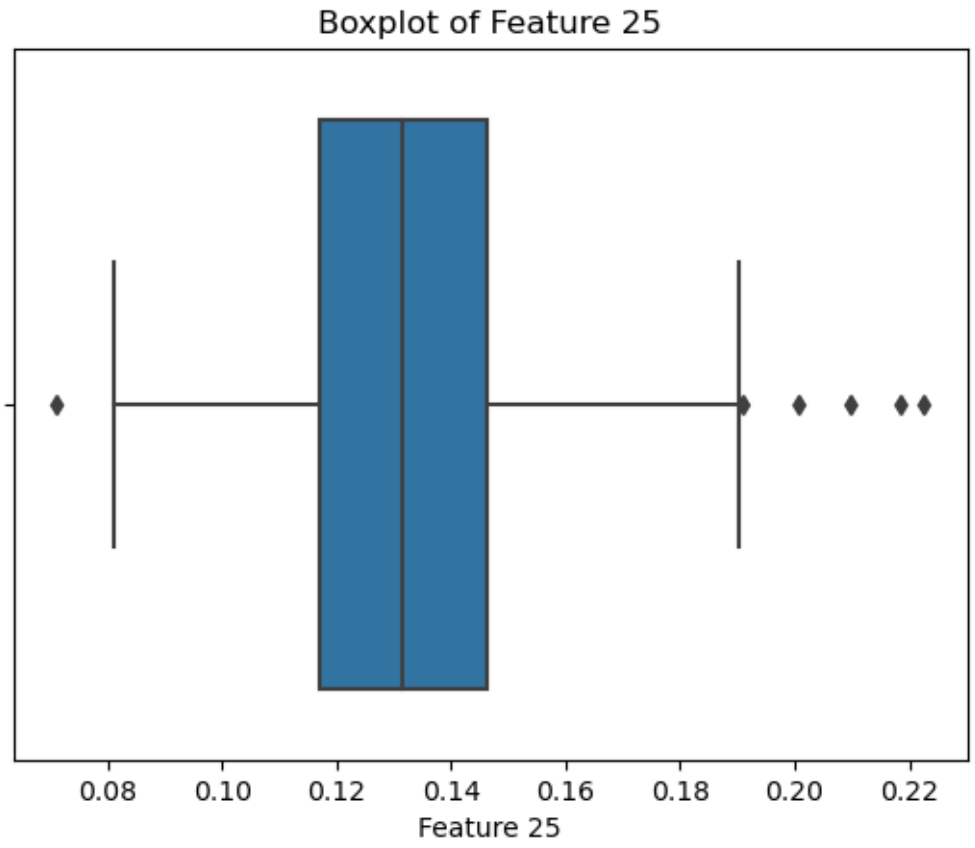

Boxplot of Feature 20
0.000
0.005
0.010
0.015
0.020
0.025
0.030
Feature 20

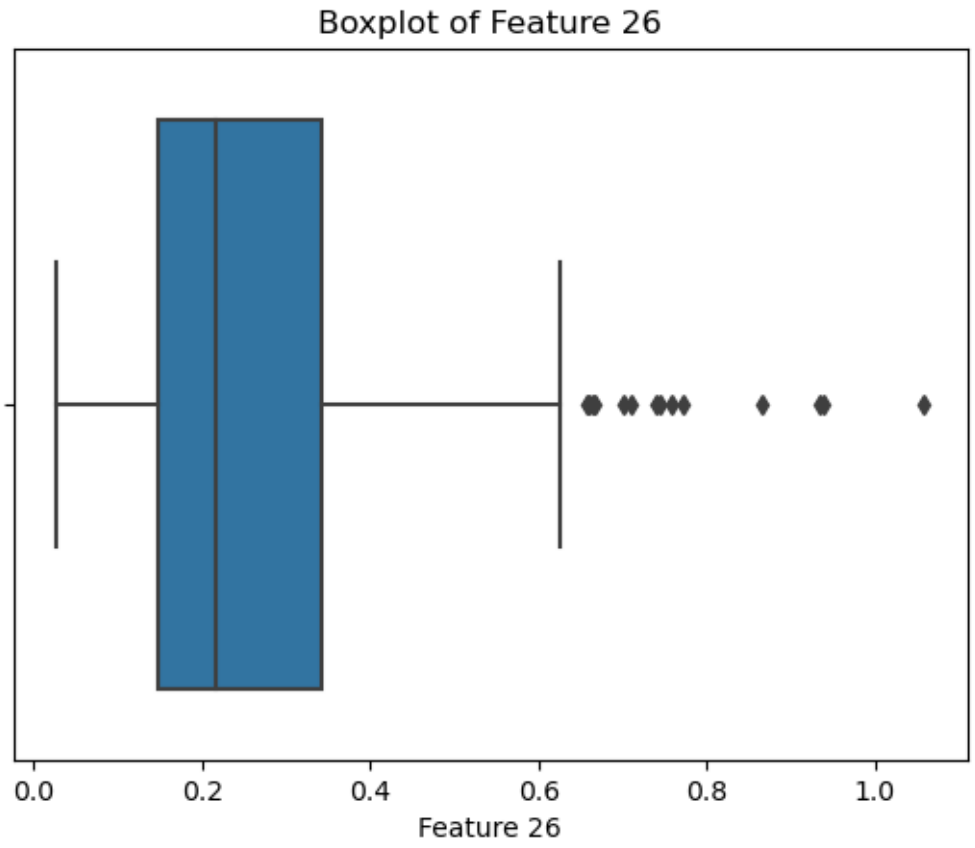

Boxplot of Feature 21
10
15
20
25
30
35
Feature 21

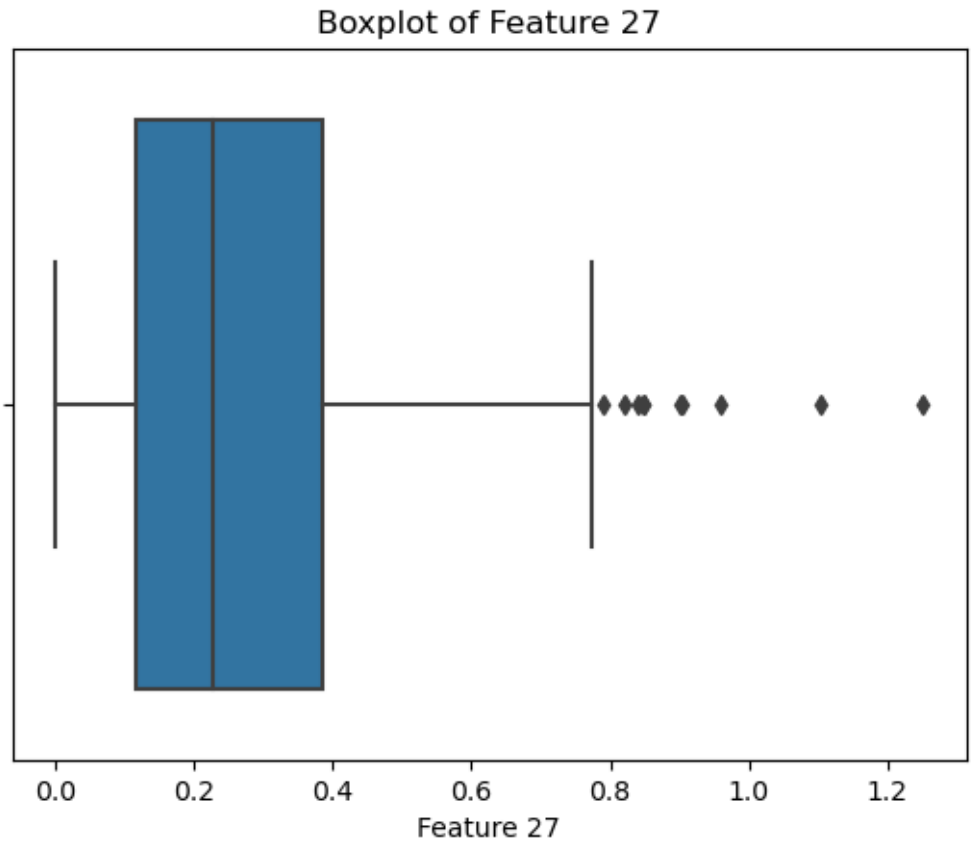

Boxplot of Feature 22
15
20
25
30
35
40
45
50
Feature 22

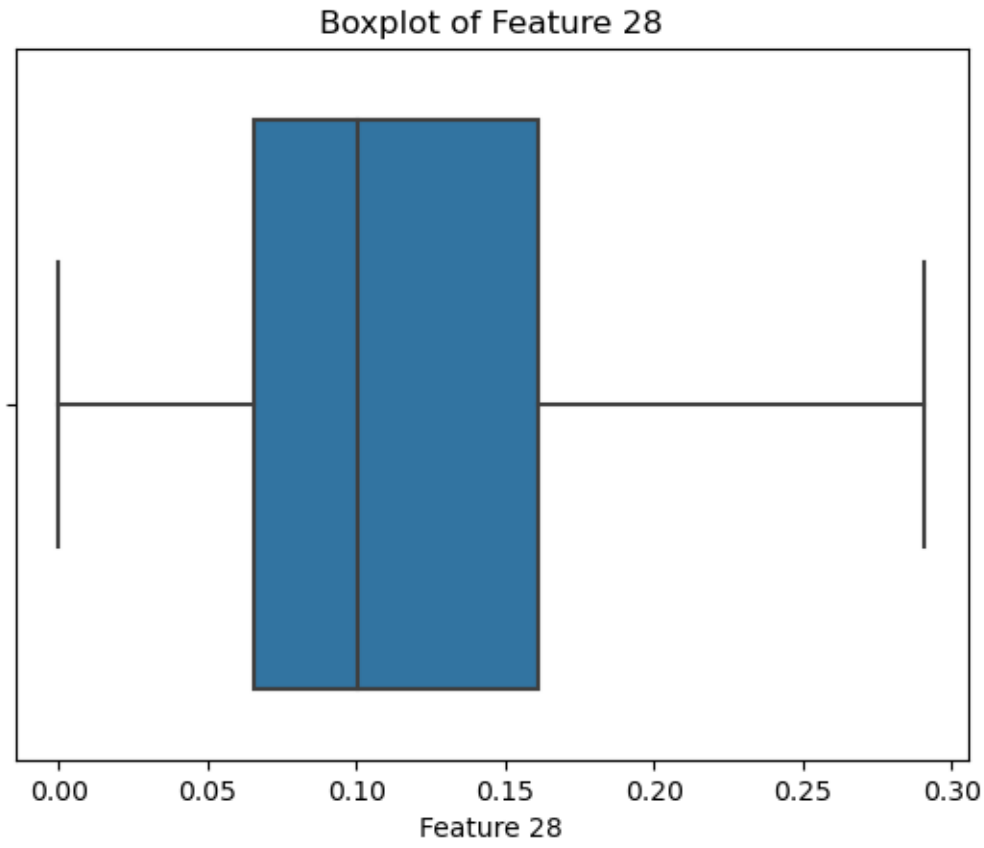

Boxplot of Feature 23
50
75
100
125
150
175
200
225
250
Feature 23

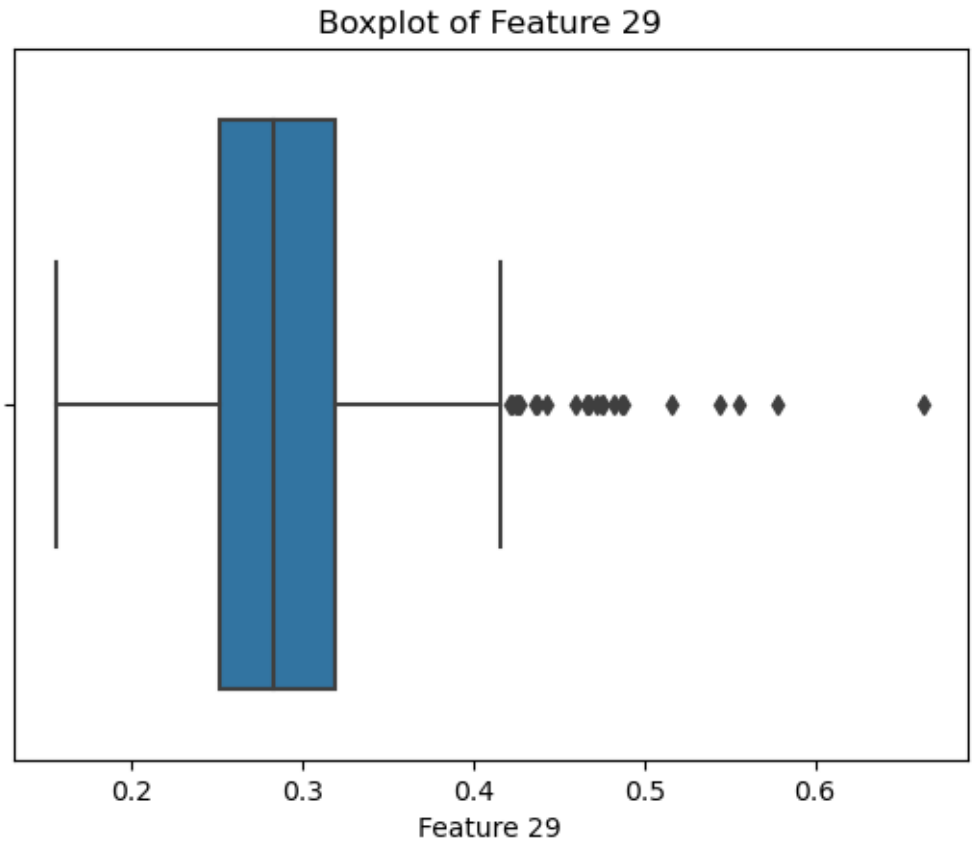

Boxplot of Feature 24
0
500
1000
1500
2000
2500
3000
3500
4000
Feature 24

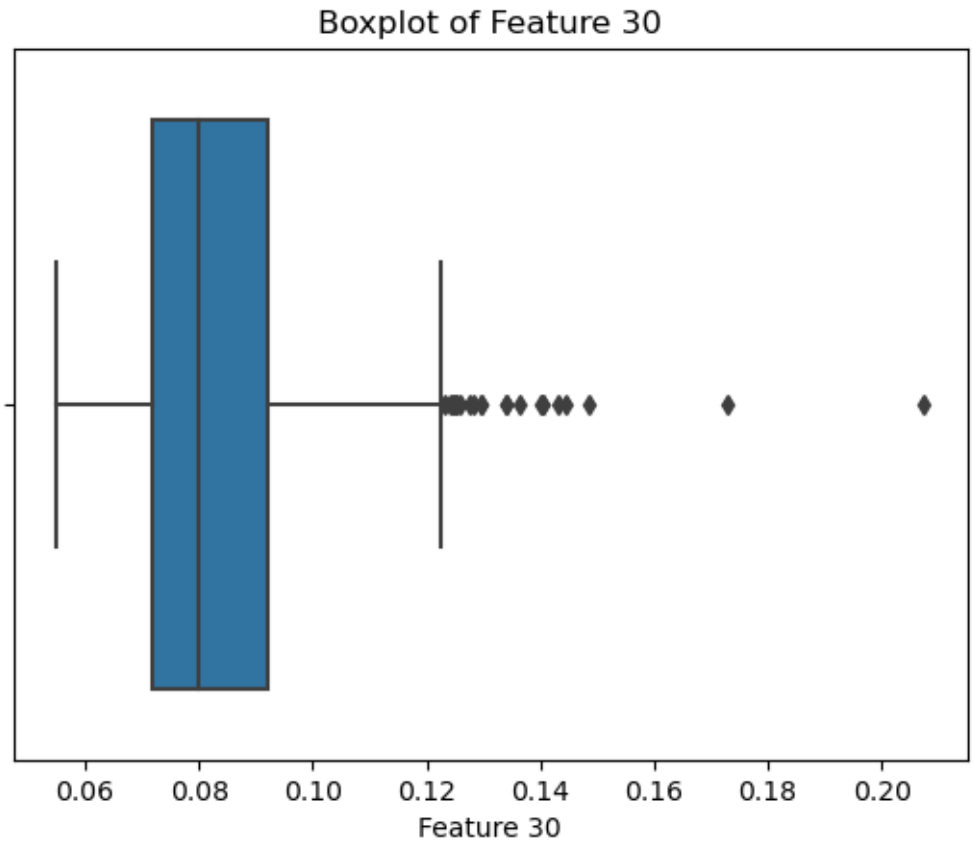

Boxplot of Feature 25
0.08
0.10
0.12
0.14
0.16
0.18
0.20
0.22
Feature 25


Boxplot of Feature 26
0.0
0.2
0.4
0.6
0.8
1.0
Feature 26


Boxplot of Feature 27
0.0
0.2
0.4
0.6
0.8
1.0
1.2
Feature 27


Boxplot of Feature 28
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Feature 28


Boxplot of Feature 29
0.2
0.3
0.4
0.5
0.6
Feature 29



We can see in these boxplots that some of the features need some cleaning, as they are extreme outliers that will negatively impact the accuracy of our analysis, these extreme outliers include the following that are a couple times or many times the value of the mean:

Feature 2 > 37
Feature 5 > 1e6
Feature 11 > 2.4
Feature 12 > 4.5
Feature 13 > 15
Feature 14 > 500
Feature 15 > 0.03
Feature 17 > 0.28
Feature 18 > 0.05
Feature 19 > 0.07
Feature 20 > 0.015
Feature 24 > 4000
Feature 29 > 0.6
Feature 30 > 0.16
Now lets work on removing these

```
In [143]: df[df['Feature 2'] > 37]
```

```
Out[143]:            ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  \
          238  88330202         M      17.46      39.28      113.4      920.6

               Feature 5  Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  \
          238    0.09812     0.1298     0.1417    0.08811  ...       22.51       44.87

               Feature 23  Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  \
          238       141.2      1408.0      0.1365      0.3735      0.3241      0.2066

               Feature 29  Feature 30
          238      0.2853     0.08496

          [1 rows x 32 columns]

In [144]: df[df['Feature 5'] > 10000]

Out[144]:          ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  Feature 5  \
          249  884948         M      20.94      23.56      138.9     1364.0  1007000.0

               Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  Feature 23  \
          249     0.1606     0.2712      0.131  ...       25.58        27.0       165.3

               Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  Feature 29  \
          249      2010.0      0.1211      0.3172      0.6991      0.2105      0.3126

               Feature 30
          249     0.07849

          [1 rows x 32 columns]

In [145]: df[df['Feature 11'] > 2.4]

Out[145]:             ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  \
          211    8810703         M      28.11      18.47      188.5     2499.0
          460  911296202         M      27.42      26.27      186.9     2501.0

               Feature 5  Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  \
          211     0.1142     0.1516     0.3201     0.1595  ...       28.11       18.47
          460     0.1084     0.1988     0.3635     0.1689  ...       36.04       31.37

               Feature 23  Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  \
          211       188.5      2499.0      0.1142      0.1516      0.3201      0.1595
          460       251.2      4254.0      0.1357      0.4256      0.6833      0.2625

               Feature 29  Feature 30
          211      0.1648     0.05525
          460      0.2641     0.07427

          [2 rows x 32 columns]
```

```
In [146]: df[df['Feature 12'] > 4.5]
```

```
Out[146]:          ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  Feature 5  \
          191  875099         B       9.72      18.22      60.73      288.1     0.0695

               Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  Feature 23  \
          191    0.02344        0.0        0.0  ...       9.968       20.83       62.25

               Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  Feature 29  \
          191       303.8     0.07117     0.02729         0.0         0.0      0.1909

               Feature 30
          191     0.06559

          [1 rows x 32 columns]
```

```
In [147]: df[df['Feature 13'] > 15]
```

```
Out[147]:             ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  \
          211    8810703         M      28.11      18.47      188.5     2499.0
          460  911296202         M      27.42      26.27      186.9     2501.0

               Feature 5  Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  \
          211     0.1142     0.1516     0.3201     0.1595  ...       28.11       18.47
          460     0.1084     0.1988     0.3635     0.1689  ...       36.04       31.37

               Feature 23  Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  \
          211       188.5      2499.0      0.1142      0.1516      0.3201      0.1595
          460       251.2      4254.0      0.1357      0.4256      0.6833      0.2625

               Feature 29  Feature 30
          211      0.1648     0.05525
          460      0.2641     0.07427

          [2 rows x 32 columns]
```

```
In [148]: df[df['Feature 14'] > 500]
```

```
Out[148]:             ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  \
          211    8810703         M      28.11      18.47      188.5     2499.0
          460  911296202         M      27.42      26.27      186.9     2501.0

               Feature 5  Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  \
          211     0.1142     0.1516     0.3201     0.1595  ...       28.11       18.47
          460     0.1084     0.1988     0.3635     0.1689  ...       36.04       31.37

               Feature 23  Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  \
          211       188.5      2499.0      0.1142      0.1516      0.3201      0.1595
          460       251.2      4254.0      0.1357      0.4256      0.6833      0.2625
```

```
     Feature 29  Feature 30
211      0.1648     0.05525
460      0.2641     0.07427

[2 rows x 32 columns]
```

```
In [149]: df[df['Feature 15'] > 0.03]
```

```
Out[149]:            ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  \
212  881094802         M      17.42      25.56      114.5      948.0

     Feature 5  Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  \
212     0.1006     0.1146     0.1682    0.06597  ...       18.07       28.07

     Feature 23  Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  \
212       120.4      1021.0      0.1243      0.1793      0.2803      0.1099

     Feature 29  Feature 30
212      0.1603     0.06818

[1 rows x 32 columns]
```

```
In [150]: df[df['Feature 17'] > 0.28]
```

```
Out[150]:           ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  Feature 5  \
67    859471         B      9.029      17.33      58.79      250.5     0.1066
151  8710441         B      9.731      15.34      63.78      300.2     0.1072

     Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  Feature 23  \
67      0.1413     0.3130    0.04375  ...       10.31       22.65       65.50
151     0.1599     0.4108    0.07857  ...       11.02       19.49       71.04

     Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  Feature 29  \
67        324.7      0.1482      0.4365      1.2520      0.1750      0.4228
151       380.5      0.1292      0.2772      0.8216      0.1571      0.3108

     Feature 30
67       0.1175
151      0.1259

[2 rows x 32 columns]
```

```
In [151]: df[df['Feature 18'] > 0.05]
```

```
Out[151]:           ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  Feature 5  \
151  8710441         B      9.731      15.34      63.78      300.2     0.1072

     Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  Feature 23  \
```

```
151     0.1599     0.4108    0.07857  ...       11.02       19.49       71.04

     Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  Feature 29  \
151       380.5      0.1292      0.2772      0.8216      0.1571      0.3108

     Feature 30
151      0.1259

[1 rows x 32 columns]
```

```
In [152]: df[df['Feature 19'] > 0.07]
```

```
Out[152]:          ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  Feature 5  \
77  8610862         M      20.18      23.97      143.7     1245.0     0.1286

    Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  Feature 23  \
77     0.3454     0.3754     0.1604  ...       23.37       31.72       170.3

    Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  Feature 29  \
77      1623.0      0.1639      0.6164      0.7681      0.2508       0.544

    Feature 30
77     0.09964

[1 rows x 32 columns]
```

```
In [153]: df[df['Feature 20'] > 0.015]
```

```
Out[153]:            ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  \
70     859711         B      8.888      14.64      58.79      244.0
151   8710441         B      9.731      15.34      63.78      300.2
175    872608         B      9.904      18.06      64.60      302.4
289  89143602         B     14.410      19.73      96.03      651.0

     Feature 5  Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  \
70     0.09783     0.1531    0.08606    0.02872  ...       9.733       15.67
151    0.10720     0.1599    0.41080    0.07857  ...      11.020       19.49
175    0.09699     0.1294    0.13070    0.03716  ...      11.260       24.39
289    0.08757     0.1676    0.13620    0.06602  ...      15.770       22.13

     Feature 23  Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  \
70        62.56       284.4     0.12070      0.2436      0.1434     0.04786
151       71.04       380.5     0.12920      0.2772      0.8216     0.15710
175       73.07       390.2     0.13010      0.2950      0.3486     0.09910
289      101.70       767.3     0.09983      0.2472      0.2220     0.10210

     Feature 29  Feature 30
70       0.2254     0.10840
151      0.3108     0.12590
```

```
175      0.2614     0.11620
289      0.2272     0.08799

[4 rows x 32 columns]
```

```
In [154]: df[df['Feature 24'] > 4000]
```

```
Out[154]:            ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  \
460  911296202         M      27.42      26.27      186.9     2501.0

     Feature 5  Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  \
460     0.1084     0.1988     0.3635     0.1689  ...       36.04       31.37

     Feature 23  Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  \
460       251.2      4254.0      0.1357      0.4256      0.6833      0.2625

     Feature 29  Feature 30
460      0.2641     0.07427

[1 rows x 32 columns]
```

```
In [155]: df[df['Feature 29'] > 0.6]
```

```
Out[155]:          ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  Feature 5  \
2  84348301         M      11.42      20.38      77.58      386.1     0.1425

   Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  Feature 23  \
2     0.2839     0.2414     0.1052  ...       14.91        26.5       98.87

   Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  Feature 29  \
2       567.7      0.2098      0.8663      0.6869      0.2575      0.6638

   Feature 30
2       0.173

[1 rows x 32 columns]
```

```
In [156]: df[df['Feature 30'] > 0.16]
```

```
Out[156]:          ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  Feature 5  \
2  84348301         M      11.42      20.38      77.58      386.1     0.1425
8  84501001         M      12.46      24.04      83.97      475.9     0.1186

   Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  Feature 23  \
2     0.2839     0.2414    0.10520  ...       14.91       26.50       98.87
8     0.2396     0.2273    0.08543  ...       15.09       40.68       97.65

   Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  Feature 29  \
2       567.7      0.2098      0.8663      0.6869      0.2575      0.6638
```

```
8       711.4      0.1853       1.0580       1.1050       0.2210       0.4366

   Feature 30
2      0.1730
8      0.2075

[2 rows x 32 columns]
```

```
In [157]: df_spare = df.drop([238,249,211,460,191,212,67,151,77,70,175,289,2,8])
```

```
In [158]: df_spare
```

Out[158]:

	ID	Diagnosis	Feature 1	Feature 2	Feature 3	Feature 4	\
0	842517	M	20.570	17.77	132.90	1326.0	
1	84300903	M	19.690	21.25	130.00	1203.0	
3	84358402	M	20.290	14.34	135.10	1297.0	
4	843786	M	12.450	15.70	82.57	477.1	
5	844359	M	18.250	19.98	119.60	1040.0	
..	...	...	...	...	...	...	
545	922577	B	10.320	16.35	65.31	324.9	
546	922840	B	10.260	16.58	65.85	320.8	
547	923169	B	9.683	19.34	61.05	285.7	
548	923465	B	10.820	24.21	68.89	361.6	
549	842302	M	17.990	10.38	122.80	1001.0	

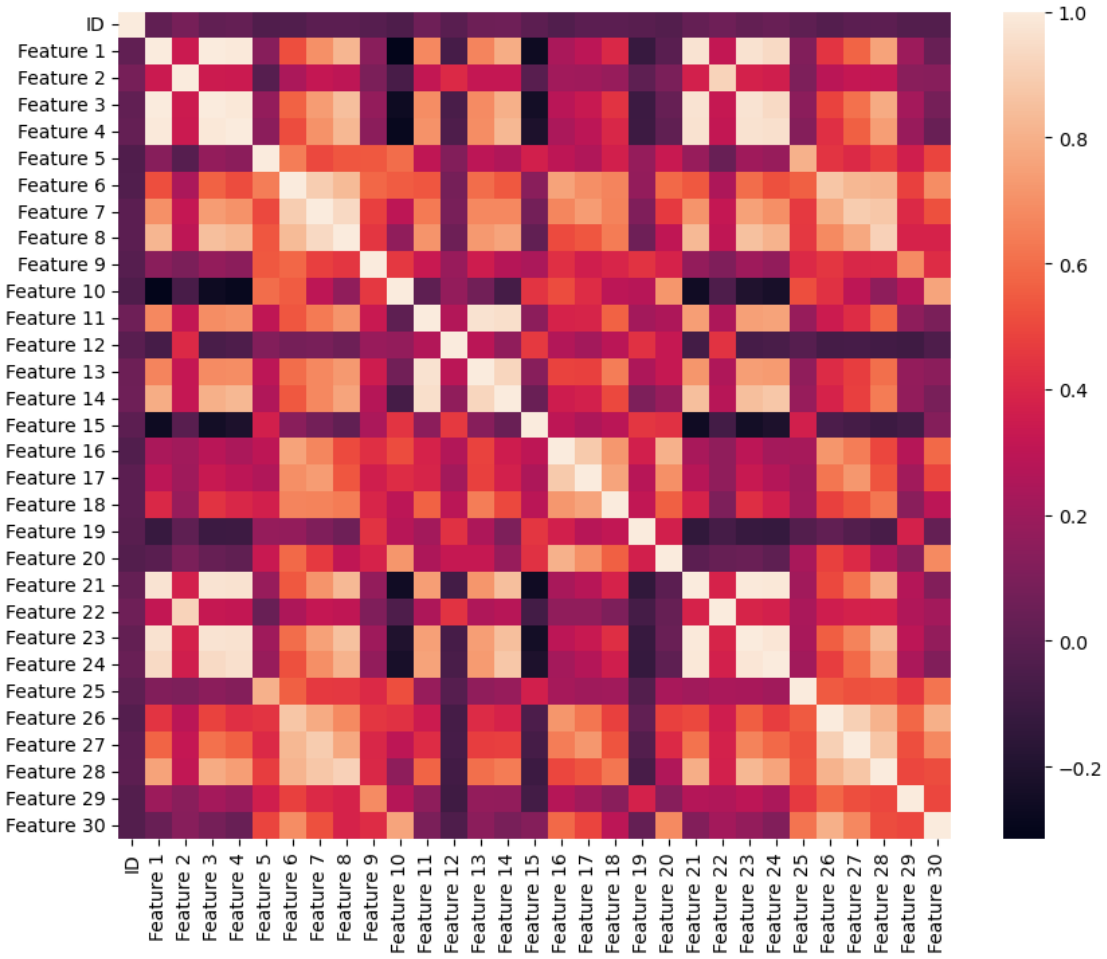
	Feature 5	Feature 6	Feature 7	Feature 8	...	Feature 21	Feature 22	\
0	0.08474	0.07864	0.08690	0.070170	...	24.99	23.41	
1	0.10960	0.15990	0.19740	0.127900	...	23.57	25.53	
3	0.10030	0.13280	0.19800	0.104300	...	22.54	16.67	
4	0.12780	0.17000	0.15780	0.080890	...	15.47	23.75	
5	0.09463	0.10900	0.11270	0.074000	...	22.88	27.66	
..	...	...	...	...	...	...	...	
545	0.09434	0.04994	0.01012	0.005495	...	11.25	21.77	
546	0.08877	0.08066	0.04358	0.024380	...	10.83	22.04	
547	0.08491	0.05030	0.02337	0.009615	...	10.93	25.59	
548	0.08192	0.06602	0.01548	0.008160	...	13.03	31.45	
549	0.11840	0.27760	0.30010	0.147100	...	25.38	17.33	

	Feature 23	Feature 24	Feature 25	Feature 26	Feature 27	Feature 28	\
0	158.80	1956.0	0.1238	0.18660	0.24160	0.18600	
1	152.50	1709.0	0.1444	0.42450	0.45040	0.24300	
3	152.20	1575.0	0.1374	0.20500	0.40000	0.16250	
4	103.40	741.6	0.1791	0.52490	0.53550	0.17410	
5	153.20	1606.0	0.1442	0.25760	0.37840	0.19320	
..	...	...	...	...	...	...	
545	71.12	384.9	0.1285	0.08842	0.04384	0.02381	
546	71.08	357.4	0.1461	0.22460	0.17830	0.08333	
547	69.10	364.2	0.1199	0.09546	0.09350	0.03846	

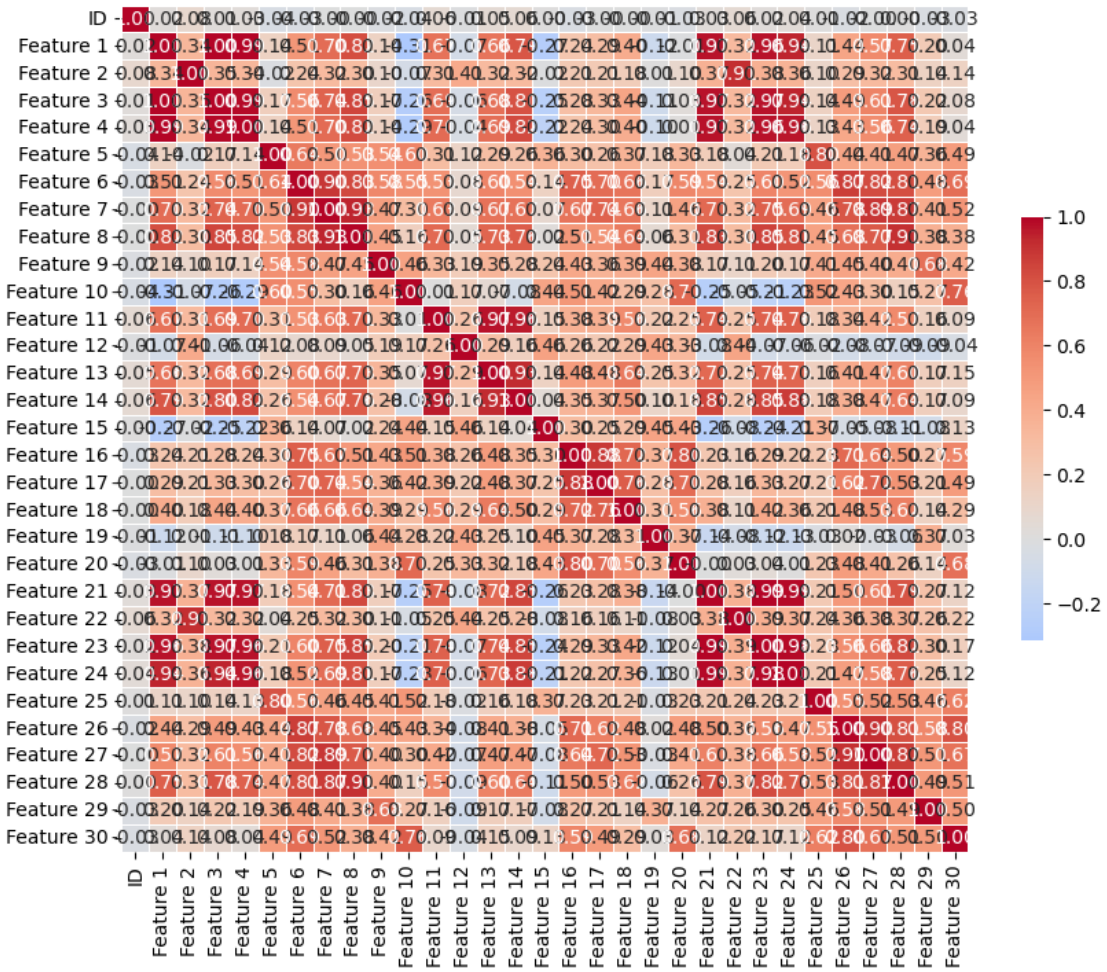
```
548       83.90       505.6      0.1204     0.16330     0.06194     0.03264
549      184.60      2019.0      0.1622     0.66560     0.71190     0.26540

     Feature 29  Feature 30
0        0.2750     0.08902
1        0.3613     0.08758
3        0.2364     0.07678
4        0.3985     0.12440
5        0.3063     0.08368
..          ...         ...
545      0.2681     0.07399
546      0.2691     0.09479
547      0.2552     0.07920
548      0.3059     0.07626
549      0.4601     0.11890

[536 rows x 32 columns]
```

C. Using the Seaborn library's heatmap() function, generate a plot showing the correlations between the numerical data in the data set. Show the commands used to generate the plot and include the plot in your output.

```
In [159]: corr = df_spare.corr()

/local_scratch/24614920/ipykernel_27037/484272153.py:1: FutureWarning: The default value of nu
  corr = df_spare.corr()


In [160]: plt.figure(figsize=(10,8))
          sns.heatmap(corr)

          plt.show()
```




```
In [161]: plt.figure(figsize=(10,8))
          sns.heatmap(corr, annot=True, fmt=".2f", cmap='coolwarm', center=0,
                      square=True, linewidths=.5, cbar_kws={"shrink": .5})

          plt.show() #more detailed plot
```



D. Label encode the column containing the diagnosis of the tumor cells with 0 or 1 (0 for benign and 1 for malignant).

```
In [162]: df['Diagnosis'] = df['Diagnosis'].map({'B': 0, 'M': 1})

In [165]: df
```

Out[165]:

	ID	Diagnosis	Feature 1	Feature 2	Feature 3	Feature 4	\
0	842517	1	20.570	17.77	132.90	1326.0	
1	84300903	1	19.690	21.25	130.00	1203.0	
2	84348301	1	11.420	20.38	77.58	386.1	
3	84358402	1	20.290	14.34	135.10	1297.0	
4	843786	1	12.450	15.70	82.57	477.1	
..	...	...	...	...	...	...	
545	922577	0	10.320	16.35	65.31	324.9	
546	922840	0	10.260	16.58	65.85	320.8	
547	923169	0	9.683	19.34	61.05	285.7	
548	923465	0	10.820	24.21	68.89	361.6	

```
549    842302          1     17.990      10.38     122.80     1001.0

     Feature 5  Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  \
0      0.08474    0.07864    0.08690   0.070170  ...       24.99       23.41
1      0.10960    0.15990    0.19740   0.127900  ...       23.57       25.53
2      0.14250    0.28390    0.24140   0.105200  ...       14.91       26.50
3      0.10030    0.13280    0.19800   0.104300  ...       22.54       16.67
4      0.12780    0.17000    0.15780   0.080890  ...       15.47       23.75
..         ...        ...        ...        ...  ...         ...         ...
545    0.09434    0.04994    0.01012   0.005495  ...       11.25       21.77
546    0.08877    0.08066    0.04358   0.024380  ...       10.83       22.04
547    0.08491    0.05030    0.02337   0.009615  ...       10.93       25.59
548    0.08192    0.06602    0.01548   0.008160  ...       13.03       31.45
549    0.11840    0.27760    0.30010   0.147100  ...       25.38       17.33

     Feature 23  Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  \
0        158.80      1956.0      0.1238      0.18660     0.24160     0.18600
1        152.50      1709.0      0.1444      0.42450     0.45040     0.24300
2         98.87       567.7      0.2098      0.86630     0.68690     0.25750
3        152.20      1575.0      0.1374      0.20500     0.40000     0.16250
4        103.40       741.6      0.1791      0.52490     0.53550     0.17410
..          ...         ...         ...          ...         ...         ...
545       71.12       384.9      0.1285      0.08842     0.04384     0.02381
546       71.08       357.4      0.1461      0.22460     0.17830     0.08333
547       69.10       364.2      0.1199      0.09546     0.09350     0.03846
548       83.90       505.6      0.1204      0.16330     0.06194     0.03264
549      184.60      2019.0      0.1622      0.66560     0.71190     0.26540

     Feature 29  Feature 30
0        0.2750     0.08902
1        0.3613     0.08758
2        0.6638     0.17300
3        0.2364     0.07678
4        0.3985     0.12440
..          ...         ...
545      0.2681     0.07399
546      0.2691     0.09479
547      0.2552     0.07920
548      0.3059     0.07626
549      0.4601     0.11890

[550 rows x 32 columns]
```

In [167]:
```
df_spare
```

Out[167]:
```
           ID Diagnosis  Feature 1  Feature 2  Feature 3  Feature 4  \
0      842517         M     20.570      17.77     132.90     1326.0
1    84300903         M     19.690      21.25     130.00     1203.0
```

```
3    84358402         M     20.290      14.34     135.10     1297.0
4      843786         M     12.450      15.70      82.57      477.1
5      844359         M     18.250      19.98     119.60     1040.0
..        ...       ...        ...        ...        ...        ...
545    922577         B     10.320      16.35      65.31      324.9
546    922840         B     10.260      16.58      65.85      320.8
547    923169         B      9.683      19.34      61.05      285.7
548    923465         B     10.820      24.21      68.89      361.6
549    842302         M     17.990      10.38     122.80     1001.0

     Feature 5  Feature 6  Feature 7  Feature 8  ...  Feature 21  Feature 22  \
0      0.08474    0.07864    0.08690   0.070170  ...       24.99       23.41
1      0.10960    0.15990    0.19740   0.127900  ...       23.57       25.53
3      0.10030    0.13280    0.19800   0.104300  ...       22.54       16.67
4      0.12780    0.17000    0.15780   0.080890  ...       15.47       23.75
5      0.09463    0.10900    0.11270   0.074000  ...       22.88       27.66
..         ...        ...        ...        ...  ...         ...         ...
545    0.09434    0.04994    0.01012   0.005495  ...       11.25       21.77
546    0.08877    0.08066    0.04358   0.024380  ...       10.83       22.04
547    0.08491    0.05030    0.02337   0.009615  ...       10.93       25.59
548    0.08192    0.06602    0.01548   0.008160  ...       13.03       31.45
549    0.11840    0.27760    0.30010   0.147100  ...       25.38       17.33

     Feature 23  Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  \
0        158.80      1956.0      0.1238      0.1866      0.2416      0.1860
1        152.50      1709.0      0.1444      0.4245      0.4504      0.2430
3        152.20      1575.0      0.1374      0.2050      0.4000      0.1625
4        103.40       741.6      0.1791      0.5249      0.5355      0.1741
5        153.20      1606.0      0.1442      0.2576      0.3784      0.1932
..          ...         ...         ...         ...         ...         ...
545       71.12       384.9      0.1285      0.0884      0.0438      0.0238
546       71.08       357.4      0.1461      0.2246      0.1783      0.0833
547       69.10       364.2      0.1199      0.0955      0.0935      0.0385
548       83.90       505.6      0.1204      0.1633      0.0619      0.0326
549      184.60      2019.0      0.1622      0.6656      0.7119      0.2654

     Feature 29  Feature 30
0        0.2750     0.08902
1        0.3613     0.08758
3        0.2364     0.07678
4        0.3985     0.12440
5        0.3063     0.08368
..          ...         ...
545      0.2681     0.07399
546      0.2691     0.09479
547      0.2552     0.07920
548      0.3059     0.07626
549      0.4601     0.11890
```

```
[536 rows x 32 columns]
```

E. Partition the data set so that a random sample of 80% of the data will be used for training and 20% will be used for testing a machine learning model.

```
In [168]: from sklearn.model_selection import train_test_split

          X = df.drop(['Diagnosis','ID'], axis=1)  # Features
          y = df['Diagnosis']  # Target variable

          X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state

          # random_state is set to some number for reproducibility
```

F. Perform a standardization of the columns of data in the data set.

```
In [230]: from sklearn.preprocessing import StandardScaler

          scaler = StandardScaler()

          df_scaled = scaler.fit_transform(df.drop(['ID','Diagnosis'], axis=1))

          df_scaled = pd.DataFrame(df_scaled, columns=df.columns.drop(['ID','Diagnosis']))

          df_scaled
```

Out[230]:

	Feature 1	Feature 2	Feature 3	Feature 4	Feature 5	Feature 6	\
0	1.840343	-0.310881	1.697354	1.916615	-0.042679	-0.493187	
1	1.588445	0.528290	1.576849	1.565000	-0.042679	1.061470	
2	-0.778825	0.318497	-0.601393	-0.770239	-0.042678	3.433825	
3	1.760194	-1.137995	1.788772	1.833714	-0.042679	0.542996	
4	-0.483989	-0.810043	-0.394040	-0.510101	-0.042678	1.254702	
..	...	...	...	...	...	...	
545	-1.093697	-0.653301	-1.111256	-0.945189	-0.042679	-1.042272	
546	-1.110872	-0.597839	-1.088817	-0.956910	-0.042679	-0.454541	
547	-1.276037	0.067710	-1.288275	-1.057249	-0.042679	-1.035385	
548	-0.950574	1.242067	-0.962494	-0.840276	-0.042679	-0.734632	
549	1.101824	-2.092913	1.277662	0.987550	-0.042678	3.313294	

	Feature 7	Feature 8	Feature 9	Feature 10	...	Feature 21	Feature 22	\
0	-0.019331	0.554263	-0.012211	-0.867460	...	1.809080	-0.337037	
1	1.389774	2.061537	0.931463	-0.400582	...	1.513552	0.014996	
2	1.950865	1.468862	2.870218	4.865861	...	-0.288754	0.176068	
3	1.397425	1.445364	-0.023226	-0.563708	...	1.299190	-1.456238	
4	0.884791	0.834152	0.997557	1.869121	...	-0.172208	-0.280579	
..	...	...	...	...	...	...	...	
545	-0.998435	-1.134339	0.255837	-0.116518	...	-1.050468	-0.609365	
546	-0.571751	-0.641270	-0.537290	0.604894	...	-1.137878	-0.564530	

```
547  -0.829470  -1.026770  -0.864088   -0.068705  ...   -1.117066    0.024959
548  -0.930084  -1.064758   0.589978    0.062077  ...   -0.680017    0.998033
549   2.699412   2.562830   2.216622    2.231936  ...    1.890246   -1.346642

     Feature 23  Feature 24  Feature 25  Feature 26  Feature 27  Feature 28  \
0      1.542836    1.887845   -0.392689   -0.439945   -0.147477    1.095673
1      1.353713    1.453292    0.509358    1.100234    0.877996    1.976083
2     -0.256234   -0.554624    3.373139    3.960474    2.039510    2.200047
3      1.344707    1.217543    0.202837   -0.320823    0.630468    0.732697
4     -0.120246   -0.248677    2.028826    1.750229    1.295944    0.911868
..          ...         ...         ...         ...         ...         ...
545   -1.089276   -0.876228   -0.186882   -1.075569   -1.118729   -1.409480
546   -1.090477   -0.924610    0.583799   -0.193931   -0.458360   -0.490147
547   -1.149915   -0.912646   -0.563465   -1.029991   -0.874835   -1.183199
548   -0.705626   -0.663878   -0.541571   -0.590791   -1.029835   -1.273094
549    2.317340    1.998682    1.288797    2.661130    2.162292    2.322069

     Feature 29  Feature 30
0     -0.263805    0.276588
1      1.139731    0.196422
2      6.059426    4.951811
3     -0.891574   -0.404821
4      1.744732    2.246216
..          ...         ...
545   -0.376023   -0.560142
546   -0.359759    0.597808
547   -0.585821   -0.270098
548    0.238736   -0.433770
549    2.746560    1.940028

[550 rows x 30 columns]
```

I will apply principal component analysis (PCA) to reduce the number of all features in the data set from 30 to a smaller number. I will also justify the number of components selected. library.

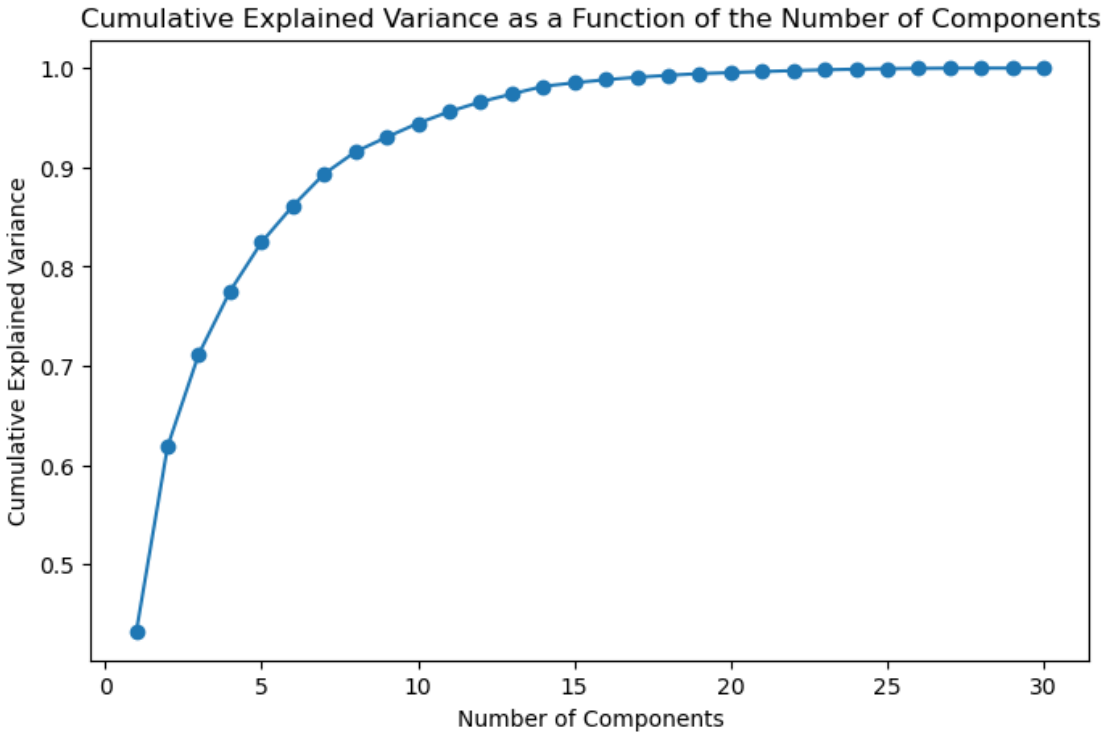
answer:

To find the number of components, I will graph a cumulative explained variance plot and take the number of components at which the cumulative explained variance is around 0.95 or 95%. This will help minimize the number of components while not taking away too much from the total variance.

According to the graph, this occurs at around 12 components, so that is what I will be using.

In [231]:
```
from sklearn.decomposition import PCA

pca = PCA()
pca.fit(df_scaled)

explained_var_ratio = pca.explained_variance_ratio_
cumulative_explained_variance = explained_var_ratio.cumsum()
```

```
# Plotting the cumulative variance to determine the number of components
import matplotlib.pyplot as plt

plt.figure(figsize=(8, 5))
plt.plot(range(1, len(cumulative_explained_variance)+1), cumulative_explained_varian
plt.title('Cumulative Explained Variance as a Function of the Number of Components')
plt.xlabel('Number of Components')
plt.ylabel('Cumulative Explained Variance')

plt.show()
```



In [232]:
```
pca = PCA(n_components=12)

df_pca = pca.fit_transform(df_scaled)

df_pca = pd.DataFrame(df_pca, columns=[f'PC{i+1}' for i in range(12)])

df_pca['Diagnosis'] = df['Diagnosis'].values

df_pca['ID'] = df['ID'].values

df_pca
```

Out[232]:
```
           PC1       PC2       PC3       PC4       PC5       PC6       PC7  \
0     2.587434 -3.601326 -0.376325 -1.241658  0.176109 -0.231313 -0.179083
1     5.706247 -1.039783 -0.467526 -0.851099 -0.487709  0.323322 -0.438519
2     6.556957  9.997883 -3.552778  0.194074 -4.203423  1.080593 -0.695179
3     3.963972 -1.849952  1.678046 -2.860082  0.326787 -1.220688  0.359283
4     1.985469  3.582114 -2.857792 -0.837771 -1.004940 -0.683544  0.382726
..         ...       ...       ...       ...       ...       ...       ...
545 -4.311050 -0.009418 -0.123576 -0.266163 -0.645609 -0.249375  0.327210
546 -2.704734  2.320246 -0.105277 -0.416950  0.347170 -0.772776  0.440303
547 -3.779907  0.518490  0.910258  0.692394  0.228941 -0.085353  0.163032
548 -2.409412  0.354669  1.280796  2.500620 -1.269512  0.186802  0.075004
549  9.016385  2.016723 -0.964481 -3.501965 -2.765369 -0.279642 -0.279578

           PC8       PC9      PC10      PC11      PC12  Diagnosis        ID
0    -0.129854  0.185328 -0.747952 -0.964888  0.790003          1    842517
1    -0.616032 -0.110898  0.035642 -0.548160 -0.551433          1  84300903
2     1.383369 -1.391978 -1.454793  0.976422 -0.912563          1  84348301
3    -1.241968 -0.137130 -0.238869 -0.363197  0.595826          1  84358402
4     0.416360  0.107473 -0.088778  0.536401  0.108046          1    843786
..         ...       ...       ...       ...       ...        ...       ...
545   0.239175  0.193812  0.502262 -0.586515  0.355696          0    922577
546  -0.226475 -0.631589 -0.506948 -0.058294 -0.023189          0    922840
547   0.449346 -0.268377  0.365838  0.194498  0.109323          0    923169
548   0.959030 -0.040272  0.368420 -0.342227 -0.012104          0    923465
549   1.950325  0.607976  0.024847  0.975559 -0.049020          1    842302

[550 rows x 14 columns]
```

H. Using the new features generated from PCA, construct a logistic regression model with Scikit-Learn to determine if the tumor cells are malignant or benign.

In [233]:
```python
from sklearn.model_selection import train_test_split

X_pca = df_pca.drop(['Diagnosis','ID'], axis=1)  # Features
y_pca = df_pca['Diagnosis']  # Target variable

X_train_PCA, X_test_PCA, y_train_PCA, y_test_PCA = train_test_split(X_pca, y_pca, tes

# random_state again is set to some different number for reproducibility
```

In [234]:
```python
X_train_PCA
```

Out[234]:
```
           PC1       PC2       PC3       PC4       PC5       PC6       PC7  \
457 -3.028087 -2.071467  0.053364  2.056696  0.522780 -0.139979  0.248794
488 -0.494312 -2.281269 -2.044199  0.195377 -1.127207  2.334826 -1.323309
35   1.291417  0.938873 -1.735180  0.794419  0.294593  0.604445 -0.276315
375  2.008091  6.814293  0.786530 -1.076432  3.835246  1.063594 -0.508196
24   6.900736  2.013076  0.153503 -1.996796 -3.002665 -0.140341 -0.054814
..         ...       ...       ...       ...       ...       ...       ...
```

```
16   4.234094  1.259233 -2.275159  0.421792 -1.034864 -1.102728  0.586782
58  -4.324247  2.137832 -1.006920 -1.716050 -1.400628 -1.510799  1.014744
277 -3.325414 -2.598148  0.041192  0.275126  0.512721  0.421758 -0.210814
255  6.607983 -1.480107  0.204645  1.526152  0.811515 -0.260269 -0.160489
320  2.107162 -4.092260  0.475338 -0.986990 -0.642993  1.168080 -0.816900

          PC8       PC9       PC10      PC11      PC12
457 -0.156660 -0.056691  0.424227 -0.717079 -0.266595
488  0.321888 -1.146209 -0.348800 -0.641757  0.574692
35  -0.094562 -0.619392  0.379166  0.293245  0.241627
375 -0.093593  0.900360  1.206910 -1.306294  0.457233
24   0.528268  1.889120  1.113624 -2.136325 -0.464392
..        ...       ...       ...       ...       ...
16   0.262718  0.686907  0.037458 -0.246790  0.026626
58  -0.048707 -0.880242  0.291605  0.416924  0.634970
277  0.234141  0.369960  0.165557  0.114981  0.342963
255  1.276332 -0.259639 -0.544192 -0.730308 -1.108929
320 -0.692044 -0.195339 -0.117856 -0.762373  0.286577

[440 rows x 12 columns]
```

```
In [235]: from sklearn.linear_model import LogisticRegression
          from sklearn.metrics import accuracy_score, classification_report

In [236]: logreg = LogisticRegression()
          logreg.fit(X_train_PCA, y_train_PCA)

Out[236]: LogisticRegression()
```

I. Perform k-fold cross validation (with 5 splits) with a logistic regression model using the training set. What is the average and standard deviation of the accuracy of the models? Comment on the accuracy and precision of the models.

Answer:

It appears that the model has an extremely high accuracy of 97%, which suggests that all the steps thus far including data manipulation, outlier handling, and other modifications to features have been done correctly and fruitfully. Additionally, the low standard deviation signifies that the model's performance is consistent across different folds. There isn't much variation in accuracy from one subset of data to another, which suggests the model should generalize well.

In terms of precision, here it should measure the proportion of positive identifications (in this case, malignant tumors) that were actually correct. A high precision model makes very few false positive predictions.

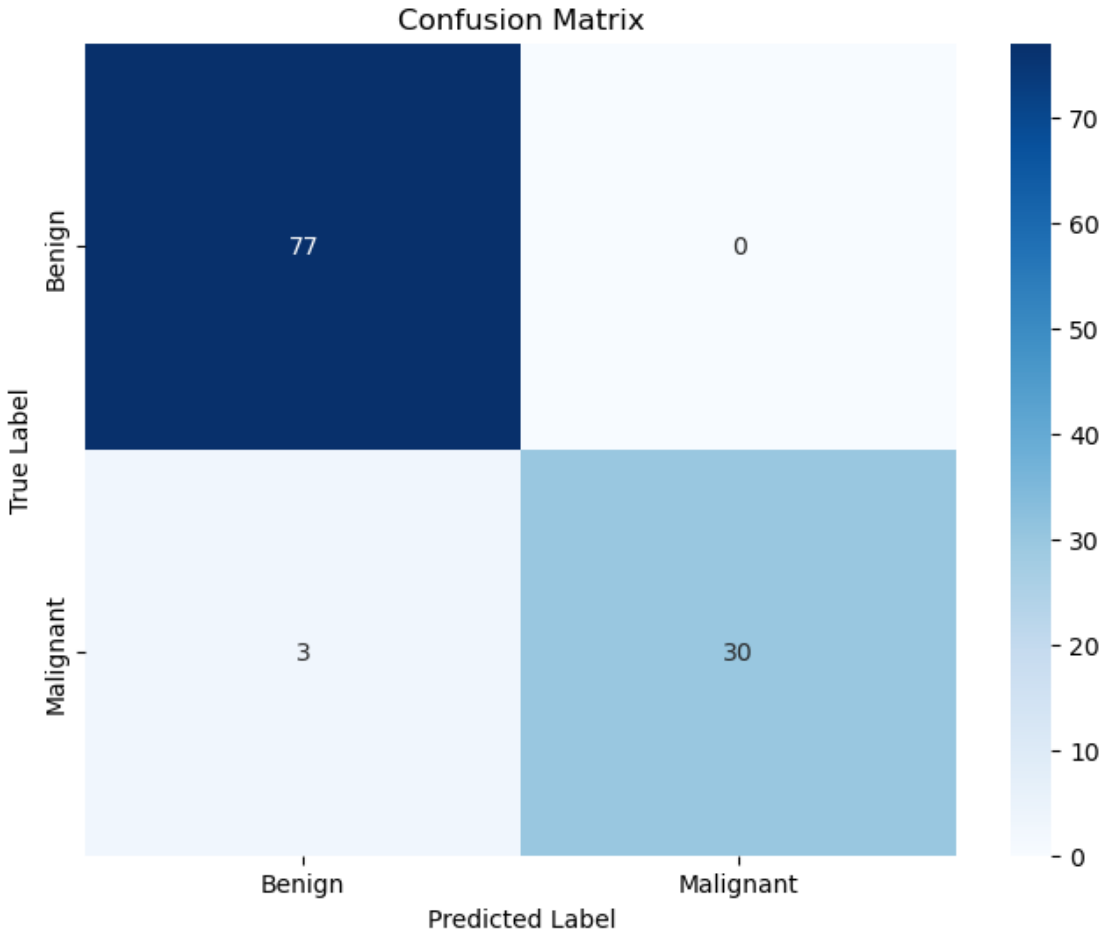
In this model, there are 3 malignant tumors that have been labeled benign, this is relatively accurate however for this model specifically this is extremely destructive due to the significance of false negatives. Because they lead a patient who needs treatment into not receiving it which results in the malignant tumor spreading.

It is not realistic for the precision to always be 100% however this model still is not 100% reliable and should not be used with full trust especially when it results in a benign tumor. Since all predictions of malignance were correct.

```
In [237]: from sklearn.model_selection import cross_val_score

In [238]: scores = cross_val_score(logreg, X_train_PCA, y_train_PCA, cv=5)

In [239]: mean_accuracy = scores.mean()
          std_dev_accuracy = scores.std()

          print(f"Mean Accuracy: {mean_accuracy:.2f}")
          print(f"Standard Deviation of Accuracy: {std_dev_accuracy:.2f}")

Mean Accuracy: 0.97
Standard Deviation of Accuracy: 0.02


In [240]: scores

Out[240]: array([1.        , 0.97727273, 0.95454545, 0.95454545, 0.98863636])
```

J. Perform a final validation test on the test set. What is the accuracy? Generate a confusion matrix for the results.

```
In [241]: y_pred = logreg.predict(X_test_PCA)

In [242]: accuracy = accuracy_score(y_test_PCA,y_pred)
          print(f"Accuracy: {accuracy:.2f}")

Accuracy: 0.97


In [243]: from sklearn.metrics import confusion_matrix

          conf_mat = confusion_matrix(y_test_PCA, y_pred)
          plt.figure(figsize=(8, 6))
          sns.heatmap(conf_mat, annot=True, fmt='d', cmap='Blues', xticklabels=['Benign', 'Mali
          plt.xlabel('Predicted Label')
          plt.ylabel('True Label')
          plt.title('Confusion Matrix')
          plt.show()
```




```
In [244]: # top left : True Negative
          # top right: False Positive
          # bottom left: False Negative
          # bottom right: True Positive
```

K. A new patient has been admitted to the hospital, and images of tumors have been taken and analyzed. This new data is presented in /public/bmort/python/new_patient.pkl, which is a pickle file containing a list that has 31 elements. The first element represents the ID of the patient (removed), and the other 30 elements represent the numerical measurements of the tumor cell features in the same order of features as the original data set. Based on the developed logistic regression model, are the cells of this patient benign or malignant?

Answer:

```
The model has predicted that the tumor is benign.
```

```
In [245]: import pickle

          with open('/public/bmort/python/new_patient.pkl', 'rb') as file:
```

```
    patient = pickle.load(file)

patient_features = pd.DataFrame([patient[1:]])
patient_features.columns = ['Feature 1', 'Feature 2','Feature 3','Feature 4','Feature
patient_features
```

Out[245]:

	Feature 1	Feature 2	Feature 3	Feature 4	Feature 5	Feature 6	Feature 7	Feature 8	Feature 9	Feature 10	...	Feature 21	Feature 22	Feature 23	Feature 24	Feature 25	Feature 26	Feature 27	Feature 28	Feature 29	Feature 30
0	7.76	24.54	47.92	181.0	0.05263	0.04362	0.0	0.0	0.1587	0.05884	...	9.456	30.37	59.16	268.6	0.08996	0.06444	0.0	0.0	0.2871	0.07039

[1 rows x 30 columns]

```
In [246]: patient_features_scaled = scaler.transform(patient_features)
          patient_features_scaled
```

```
Out[246]: array([[-1.826492  ,  1.32164358, -1.83387378, -1.35655034, -0.04267998,
                  -1.16318585, -1.12748635, -1.27780791, -0.8383844 , -0.56230195,
                  -0.06677329,  0.43466502, -0.15201599, -0.46348818,  0.06014199,
                  -1.15410177, -1.04894892, -1.93191293,  0.75343063, -0.37640848,
                  -1.4238324 ,  0.81869496, -1.44830958, -1.08083746, -1.87449885,
                  -1.2308165 , -1.33403862, -1.77724452, -0.06701726, -0.76055646]])
```

```
In [248]: patient_features_reduced = pca.transform(patient_features_scaled)
          patient_features_reduced
```

```
/software/anaconda3/2023.07-2/lib/python3.11/site-packages/sklearn/base.py:464: UserWarning: X
  warnings.warn(
```

```
Out[248]: array([[-5.05834785, -0.27651245,  1.18852839,  2.37275371, -0.69348176,
                   0.70438563, -0.1072332 ,  1.50752842, -0.89783311,  0.23668163,
                   0.01649923, -0.22730707]])
```

```
In [254]: newpatient_df = pd.DataFrame(patient_features_reduced)
```

```
In [255]: newpatient_df.columns = ['PC1','PC2','PC3','PC4','PC5','PC6','PC7','PC8','PC9','PC10
```

```
In [256]: newpatient_df
```

Out[256]:

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
0	-5.058348	-0.276512	1.188528	2.372754	-0.693482	0.704386	-0.107233	1.507528	-0.897833	0.236682	0.016499	-0.227307

```
In [266]: prediction = logreg.predict(newpatient_df)
```

```
In [271]: if prediction[0] == 0:
              print("The model predicts the patient's tumor cells are benign.")
          else:
              print("The model predicts the patient's tumor cells are malignant.")
```

```
The model predicts the patient's tumor cells are benign.
```