

# logist\_regg

March 13, 2024

```
[1]: import pandas as pd
import numpy as np
```

```
[2]: cancer_data=pd.read_csv('/content/cancer.csv')
```

```
[3]: cancer_data.head()
```

```
[3]:
```

	index	id	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	1	842302	17.99	10.38	122.80	1001.0	
1	2	842517	20.57	17.77	132.90	1326.0	
2	3	84300903	19.69	21.25	130.00	1203.0	
3	4	84348301	11.42	20.38	77.58	386.1	
4	5	84358402	20.29	14.34	135.10	1297.0	

	smoothness_mean	compactness_mean	concavity_mean	concave_points_mean	\
0	0.11840	0.27760	0.3001	0.14710	
1	0.08474	0.07864	0.0869	0.07017	
2	0.10960	0.15990	0.1974	0.12790	
3	0.14250	0.28390	0.2414	0.10520	
4	0.10030	0.13280	0.1980	0.10430	

	...	smoothness_worst	compactness_worst	concavity_worst	\
0	...	0.1622	0.6656	0.7119	
1	...	0.1238	0.1866	0.2416	
2	...	0.1444	0.4245	0.4504	
3	...	0.2098	0.8663	0.6869	
4	...	0.1374	0.2050	0.4000	

	concave points_worst	symmetry_worst	fractal_dimension_worst	N Stage	\
0	0.2654	0.4601	0.11890	N1	
1	0.1860	0.2750	0.08902	N2	
2	0.2430	0.3613	0.08758	N3	
3	0.2575	0.6638	0.17300	N1	
4	0.1625	0.2364	0.07678	N1	

	6th Stage	differentiate	diagnosis
0	IIA	Poorly differentiated	M

1	IIIA	Moderately differentiated	M
2	IIIC	Moderately differentiated	M
3	IIA	Poorly differentiated	M
4	IIB	Poorly differentiated	M

[5 rows x 36 columns]

```
[4]: cancer_data.shape
```

```
[4]: (569, 36)
```

```
[5]: cancer_data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 36 columns):
#   Column                                Non-Null Count  Dtype
---  -
0   index                                569 non-null    int64
1   id                                    569 non-null    int64
2   radius_mean                          569 non-null    float64
3   texture_mean                         569 non-null    float64
4   perimeter_mean                      569 non-null    float64
5   area_mean                           569 non-null    float64
6   smoothness_mean                     569 non-null    float64
7   compactness_mean                    569 non-null    float64
8   concavity_mean                      552 non-null    float64
9   concave_points_mean                 550 non-null    float64
10  symmetry_mean                       568 non-null    float64
11  fractal_dimension                   569 non-null    float64
12  radius_se                           569 non-null    float64
13  texture_se                           569 non-null    float64
14  perimeter_se                        569 non-null    float64
15  area_se                             569 non-null    float64
16  smoothness_se                       569 non-null    float64
17  compactness_se                      569 non-null    float64
18  concavity_se                        554 non-null    float64
19  concave_points_se                   550 non-null    float64
20  symmetry_se                         569 non-null    float64
21  fractal_dimension_se                569 non-null    float64
22  radius_worst                       569 non-null    float64
23  texture_worst                       569 non-null    float64
24  texture_worst.1                     569 non-null    float64
25  area_worst                          569 non-null    float64
26  smoothness_worst                    569 non-null    float64
27  compactness_worst                   568 non-null    float64
28  concavity_worst                     562 non-null    float64
```

```

29 concave points_worst      563 non-null    float64
30 symmetry_worst            569 non-null    float64
31 fractal_dimension_worst   569 non-null    float64
32 N Stage                   569 non-null    object
33 6th Stage                  569 non-null    object
34 differentiate              569 non-null    object
35 diagnosis                  569 non-null    object
dtypes: float64(30), int64(2), object(4)
memory usage: 160.2+ KB

```

```
[6]: cancer_data.tail()
```

```

[6]:      index      id  radius_mean  texture_mean  perimeter_mean  area_mean  \
564    565  926424      21.56      22.39      142.00    1479.0
565    566  926682      20.13      28.25      131.20    1261.0
566    567  926954      16.60      28.08      108.30     858.1
567    568  927241      20.60      29.33      140.10    1265.0
568    569  92751      7.76      24.54      47.92     181.0

      smoothness_mean  compactness_mean  concavity_mean  concave_points_mean  \
564          0.11100          0.11590          0.24390          0.13890
565          0.09780          0.10340          0.14400          0.09791
566          0.08455          0.10230          0.09251          0.05302
567          0.11780          0.27700          0.35140          0.15200
568          0.05263          0.04362              NaN              NaN

      ...  smoothness_worst  compactness_worst  concavity_worst  \
564  ...          0.14100          0.21130          0.4107
565  ...          0.11660          0.19220          0.3215
566  ...          0.11390          0.30940          0.3403
567  ...          0.16500          0.86810          0.9387
568  ...          0.08996          0.06444              NaN

      concave points_worst  symmetry_worst  fractal_dimension_worst  N Stage  \
564          0.2216          0.2060          0.07115          N2
565          0.1628          0.2572          0.06637          N2
566          0.1418          0.2218          0.07820          N1
567          0.2650          0.4087          0.12400          N1
568              NaN          0.2871          0.07039          N3

      6th Stage      differentiate  diagnosis
564    IIIA  Moderately differentiated      M
565    IIIA    Poorly differentiated      M
566     IIA    Well differentiated      M
567     IIA    Well differentiated      M
568    IIIC    Well differentiated      B

```

[5 rows x 36 columns]

```
[7]: cancer_data.isnull().sum()
```

```
[7]: index          0
     id            0
     radius_mean   0
     texture_mean   0
     perimeter_mean 0
     area_mean      0
     smoothness_mean 0
     compactness_mean 0
     concavity_mean 17
     concave_points_mean 19
     symmetry_mean   1
     fractal_dimension 0
     radius_se       0
     texture_se       0
     perimeter_se     0
     area_se          0
     smoothness_se    0
     compactness_se    0
     concavity_se     15
     concave_points_se 19
     symmetry_se       0
     fractal_dimension_se 0
     radius_worst     0
     texture_worst     0
     texture_worst.1   0
     area_worst        0
     smoothness_worst  0
     compactness_worst 1
     concavity_worst   7
     concave points_worst 6
     symmetry_worst    0
     fractal_dimension_worst 0
     N Stage          0
     6th Stage         0
     differentiate     0
     diagnosis         0
     dtype: int64
```

```
[8]: cancer_data['concavity_mean'].fillna(cancer_data['concavity_mean'].
     ↪median(),inplace=True)
```

```
[9]: cancer_data['concave_points_se'].fillna(cancer_data['concave_points_se'].
     ↪median(),inplace=True)
```

```
cancer_data['concavity_mean'].fillna(cancer_data['concavity_mean'].
    ↪median(),inplace=True)
cancer_data['concave_points_mean'].fillna(cancer_data['concave_points_mean'].
    ↪median(),inplace=True)
```

```
[10]: cancer_data['concavity_worst'].fillna(cancer_data['concavity_worst'].mode().
    ↪values[0],inplace=True)
# if we have column with string datatype then replace null values with
    ↪mode,since mode represent object so do value[0]
```

```
[11]: cancer_data['concave points_worst'].fillna(cancer_data['concave points_worst'].
    ↪mode().values[0],inplace=True)
cancer_data['compactness_worst'].fillna(cancer_data['compactness_worst'].mode().
    ↪values[0],inplace=True)
```

```
[12]: cancer_data.isnull().sum()
```

```
[12]: index          0
id              0
radius_mean     0
texture_mean    0
perimeter_mean  0
area_mean       0
smoothness_mean 0
compactness_mean 0
concavity_mean  0
concave_points_mean 0
symmetry_mean   1
fractal_dimension 0
radius_se       0
texture_se      0
perimeter_se    0
area_se         0
smoothness_se   0
compactness_se  0
concavity_se    15
concave_points_se 0
symmetry_se     0
fractal_dimension_se 0
radius_worst    0
texture_worst   0
texture_worst.1 0
area_worst      0
smoothness_worst 0
compactness_worst 0
concavity_worst 0
concave points_worst 0
```

```

symmetry_worst          0
fractal_dimension_worst 0
N Stage                 0
6th Stage              0
differentiate           0
diagnosis               0
dtype: int64

```

```

[13]: cancer_data['symmetry_mean'].fillna(cancer_data['symmetry_mean'].
      ↪median(),inplace=True)
      cancer_data['concavity_se'].fillna(cancer_data['concavity_se'].
      ↪median(),inplace=True)

```

```

[14]: cancer_data.isnull().sum()

```

```

[14]: index          0
      id            0
      radius_mean   0
      texture_mean   0
      perimeter_mean 0
      area_mean      0
      smoothness_mean 0
      compactness_mean 0
      concavity_mean 0
      concave_points_mean 0
      symmetry_mean   0
      fractal_dimension 0
      radius_se       0
      texture_se       0
      perimeter_se     0
      area_se         0
      smoothness_se    0
      compactness_se   0
      concavity_se     0
      concave_points_se 0
      symmetry_se      0
      fractal_dimension_se 0
      radius_worst    0
      texture_worst    0
      texture_worst.1  0
      area_worst       0
      smoothness_worst 0
      compactness_worst 0
      concavity_worst  0
      concave points_worst 0
      symmetry_worst   0
      fractal_dimension_worst 0

```

```

N Stage          0
6th Stage        0
differentiate     0
diagnosis         0
dtype: int64

```

```

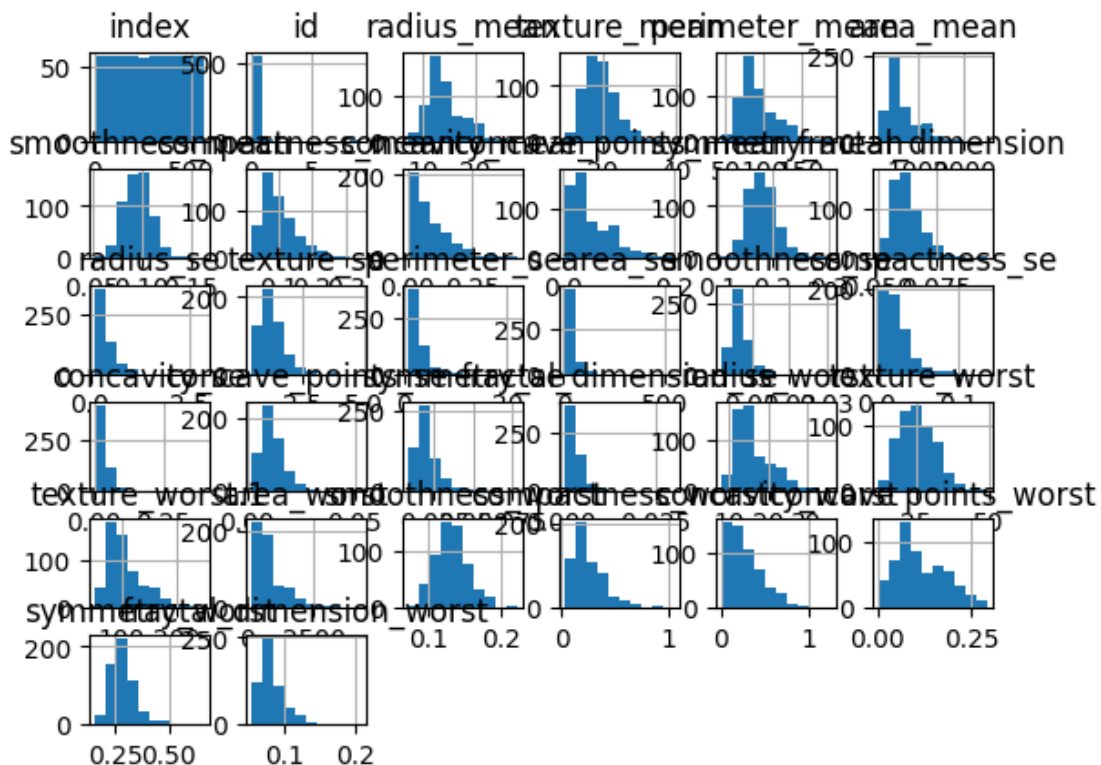
[15]: # now complete the non-normal distribution data into normal-distribution data
cancer_data.hist()

```

```

[15]: array([[<Axes: title={'center': 'index'}>,
<Axes: title={'center': 'id'}>,
<Axes: title={'center': 'radius_mean'}>,
<Axes: title={'center': 'texture_mean'}>,
<Axes: title={'center': 'perimeter_mean'}>,
<Axes: title={'center': 'area_mean'}>]],
[<Axes: title={'center': 'smoothness_mean'}>,
<Axes: title={'center': 'compactness_mean'}>,
<Axes: title={'center': 'concavity_mean'}>,
<Axes: title={'center': 'concave_points_mean'}>,
<Axes: title={'center': 'symmetry_mean'}>,
<Axes: title={'center': 'fractal_dimension'}>]],
[<Axes: title={'center': 'radius_se'}>,
<Axes: title={'center': 'texture_se'}>,
<Axes: title={'center': 'perimeter_se'}>,
<Axes: title={'center': 'area_se'}>,
<Axes: title={'center': 'smoothness_se'}>,
<Axes: title={'center': 'compactness_se'}>]],
[<Axes: title={'center': 'concavity_se'}>,
<Axes: title={'center': 'concave_points_se'}>,
<Axes: title={'center': 'symmetry_se'}>,
<Axes: title={'center': 'fractal_dimension_se'}>,
<Axes: title={'center': 'radius_worst'}>,
<Axes: title={'center': 'texture_worst'}>]],
[<Axes: title={'center': 'texture_worst.1'}>,
<Axes: title={'center': 'area_worst'}>,
<Axes: title={'center': 'smoothness_worst'}>,
<Axes: title={'center': 'compactness_worst'}>,
<Axes: title={'center': 'concavity_worst'}>,
<Axes: title={'center': 'concave points_worst'}>]],
[<Axes: title={'center': 'symmetry_worst'}>,
<Axes: title={'center': 'fractal_dimension_worst'}>, <Axes: >,
<Axes: >, <Axes: >, <Axes: >]], dtype=object)

```



```
[16]: cancer_data.skew()
```

<ipython-input-16-a3ad186019e1>:1: FutureWarning: The default value of numeric\_only in DataFrame.skew is deprecated. In a future version, it will default to False. In addition, specifying 'numeric\_only=None' is deprecated. Select only valid columns or specify the value of numeric\_only to silence this warning.

```
cancer_data.skew()
```

```
[16]: index          0.000000
      id           6.473752
      radius_mean   0.942380
      texture_mean   0.650450
      perimeter_mean 0.990650
      area_mean     1.645732
      smoothness_mean 0.456324
      compactness_mean 1.190123
      concavity_mean 1.449348
      concave_points_mean 1.233690
      symmetry_mean  0.725645
      fractal_dimension 1.304489
      radius_se      3.088612
```

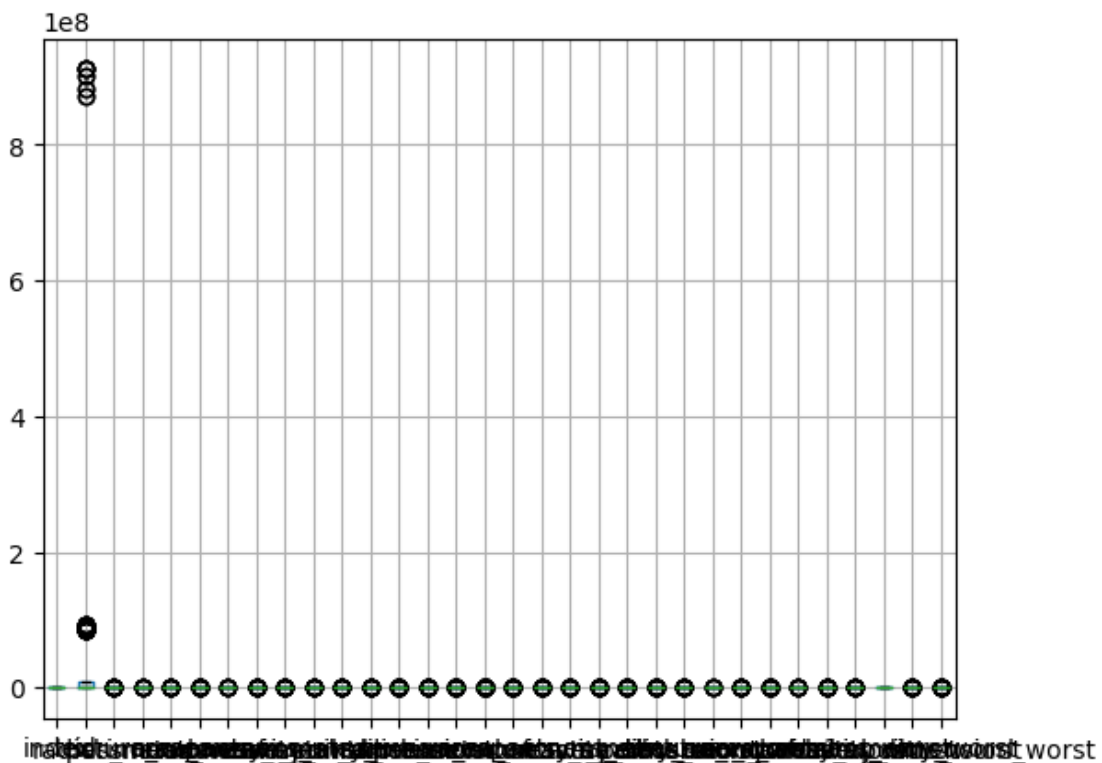


texture_se	1.646444
perimeter_se	3.443615
area_se	5.447186
smoothness_se	2.314450
compactness_se	1.902221
concavity_se	5.285191
concave_points_se	1.708892
symmetry_se	2.195133
fractal_dimension_se	3.923969
radius_worst	1.103115
texture_worst	0.498321
texture_worst.1	1.128164
area_worst	1.859373
smoothness_worst	0.415426
compactness_worst	1.479888
concavity_worst	1.149806
concave points_worst	0.492616
symmetry_worst	1.433928
fractal_dimension_worst	1.662579

dtype: float64

```
[17]: cancer_data.boxplot()
```

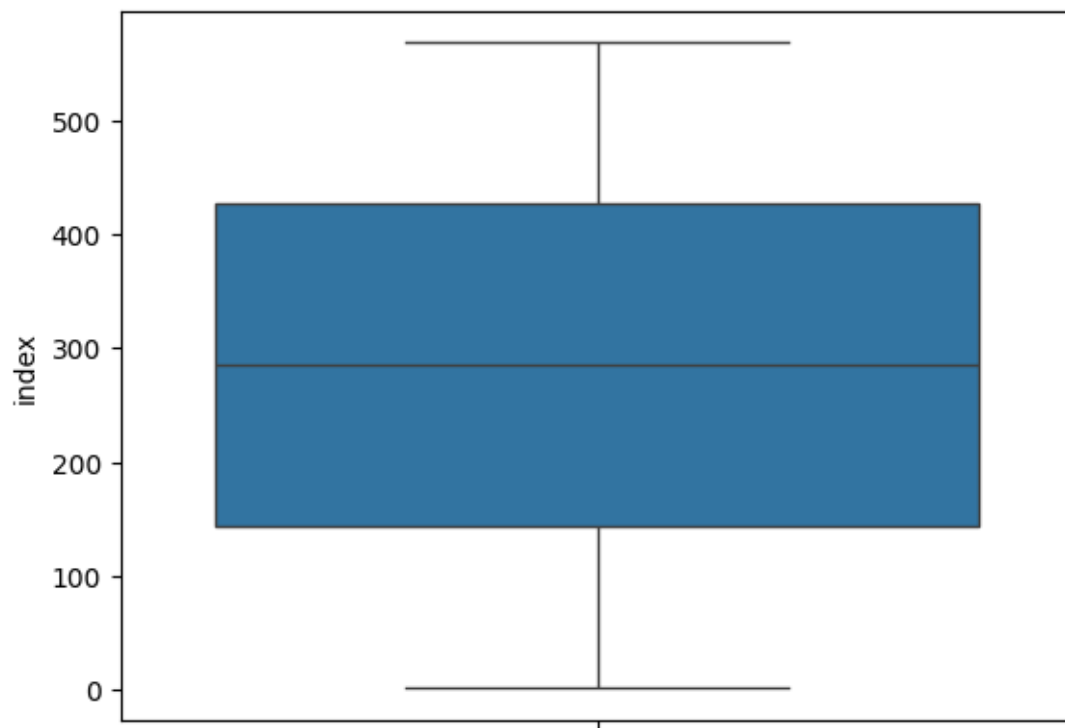
```
[17]: <Axes: >
```

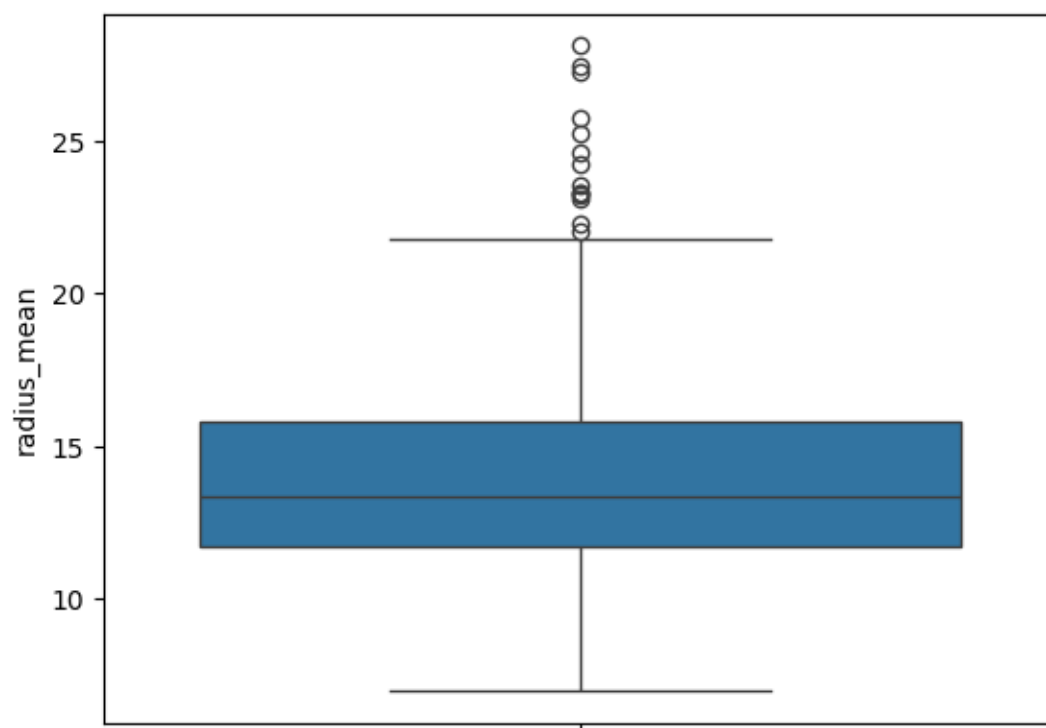
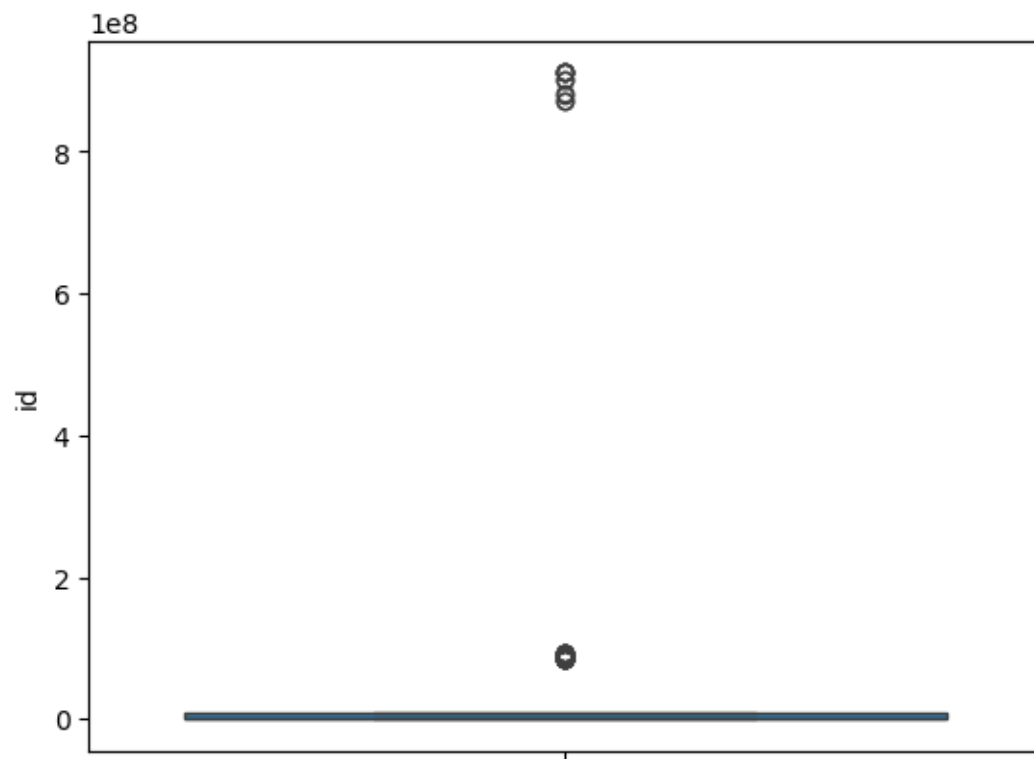


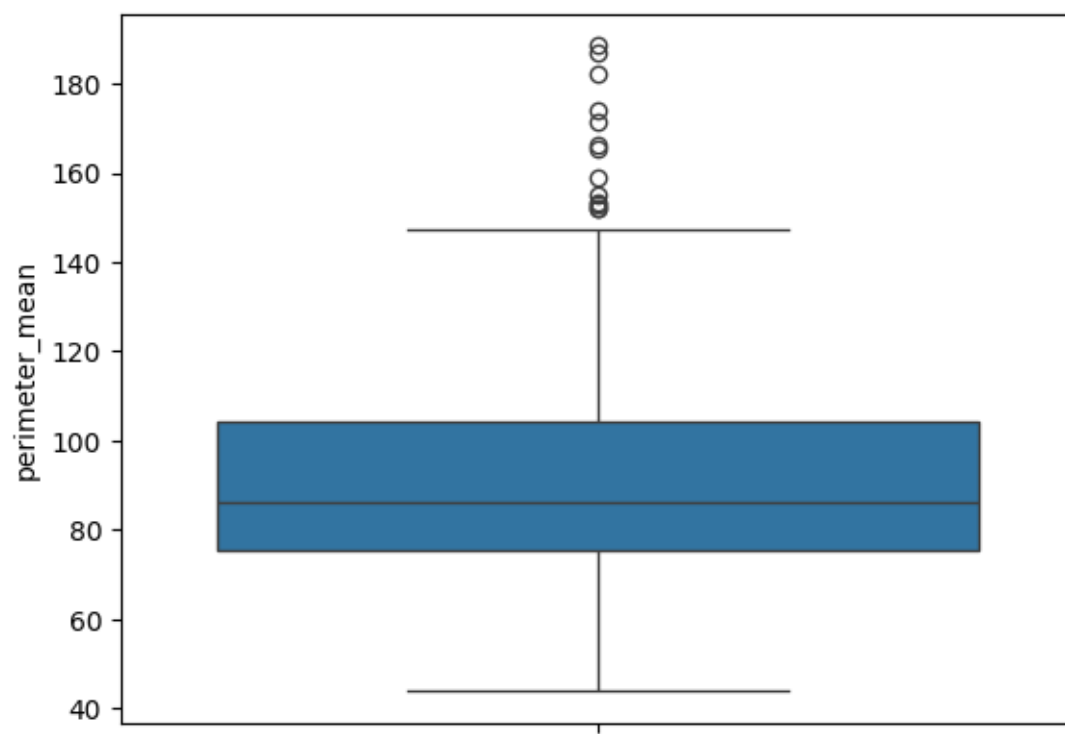
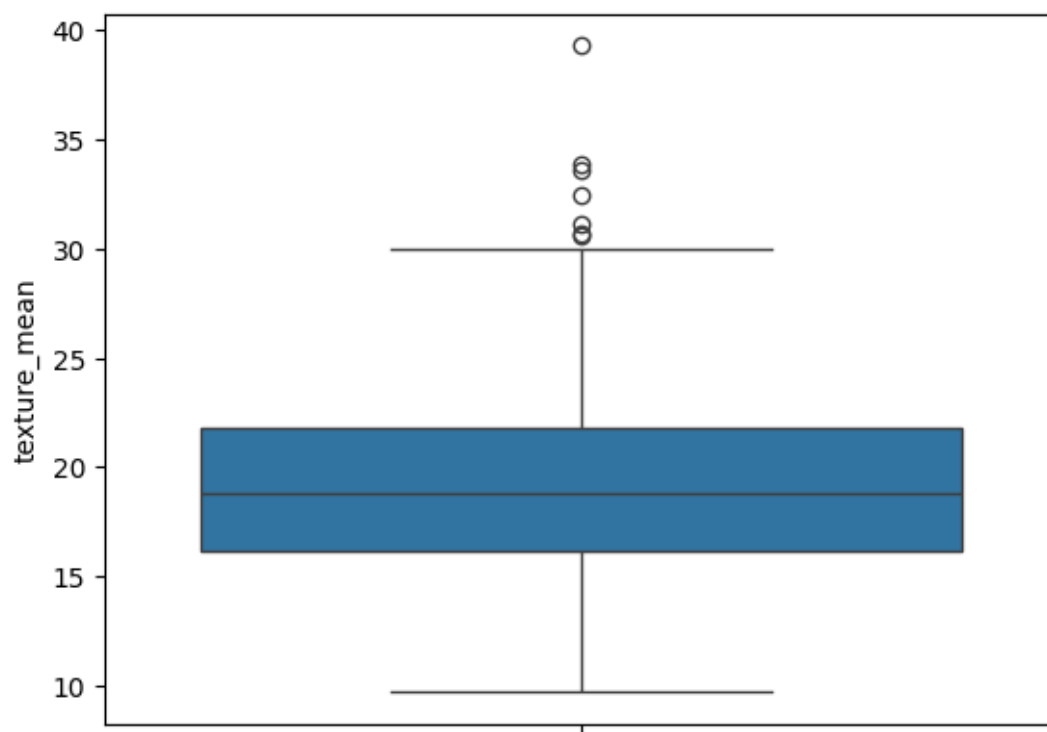
```
[18]: # removing outliers
import seaborn as sns
import matplotlib.pyplot as plt
```

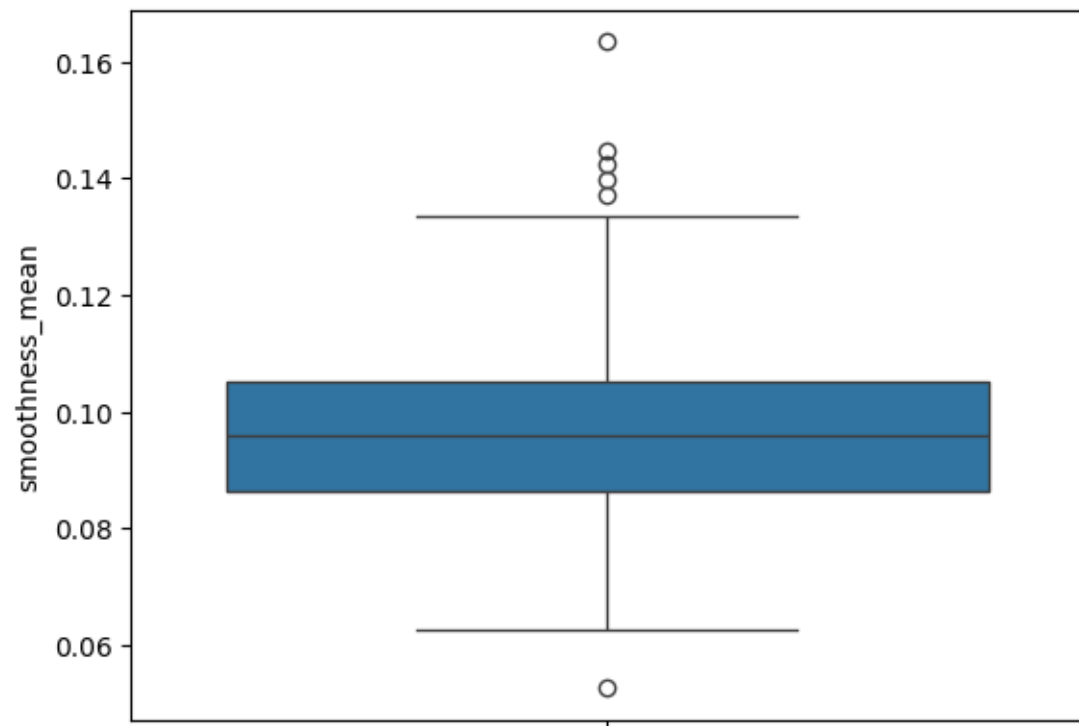
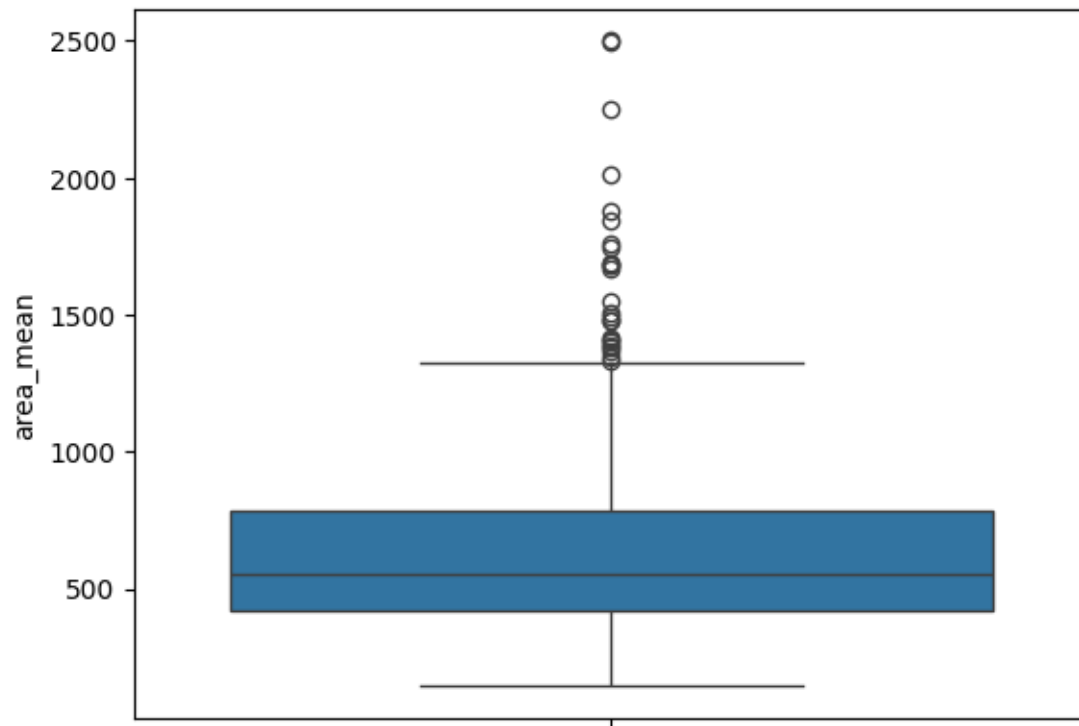
```
[19]: numerical_cols=cancer_data.select_dtypes(include='number').columns
for col in numerical_cols:
    sns.boxplot(cancer_data[col])

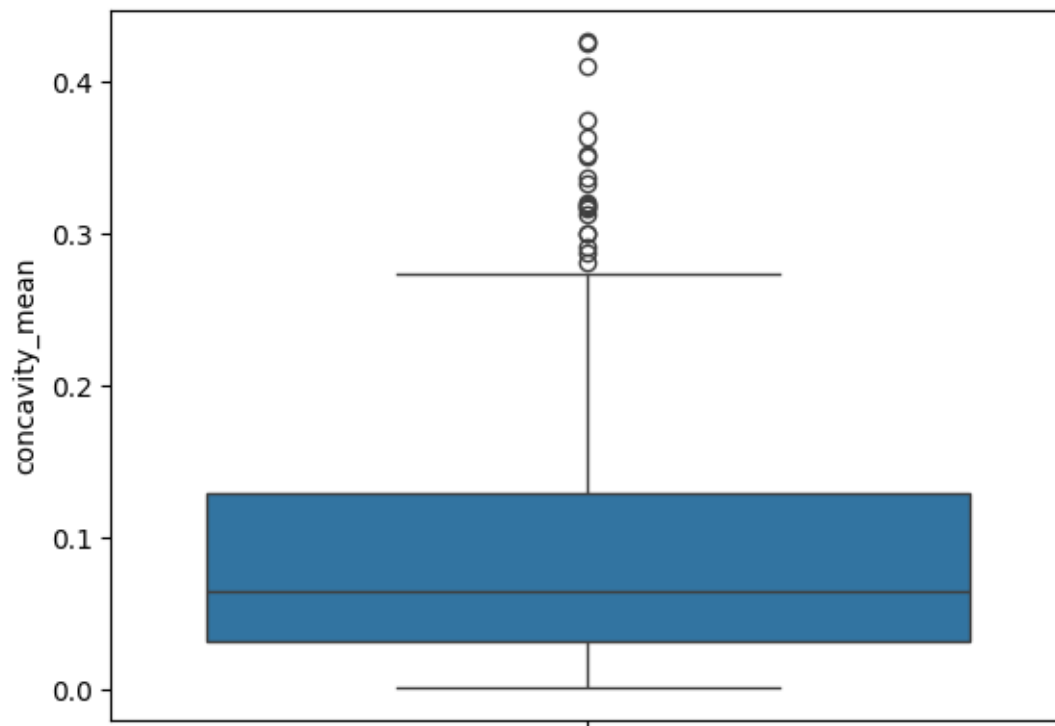
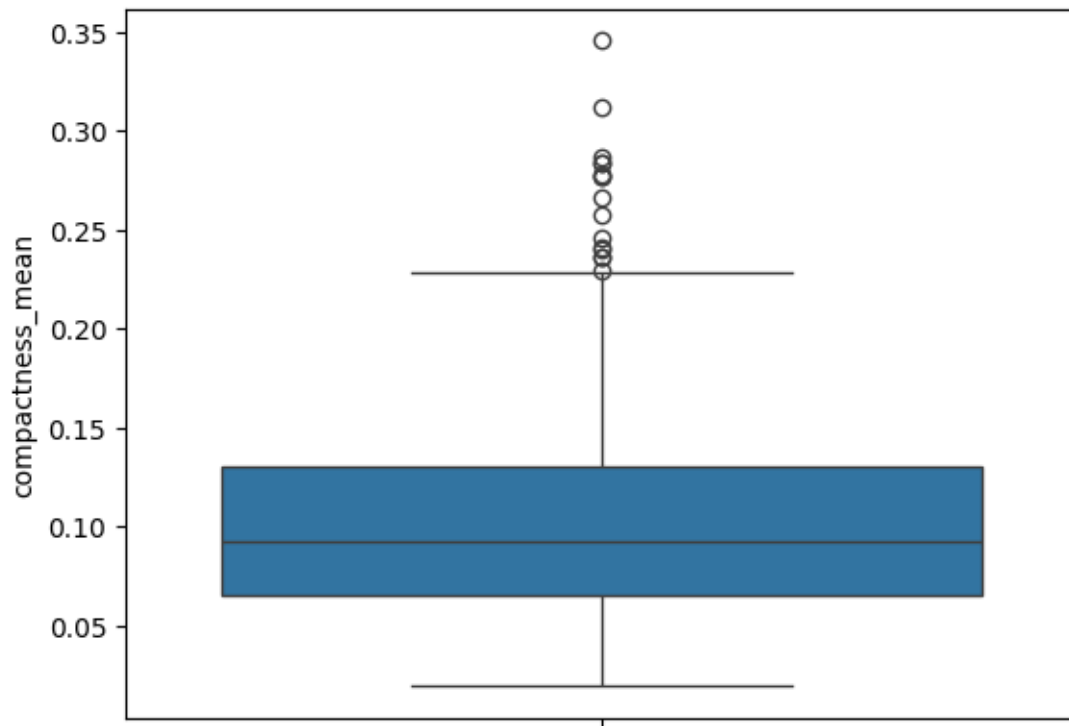
# show plot
plt.show()
```

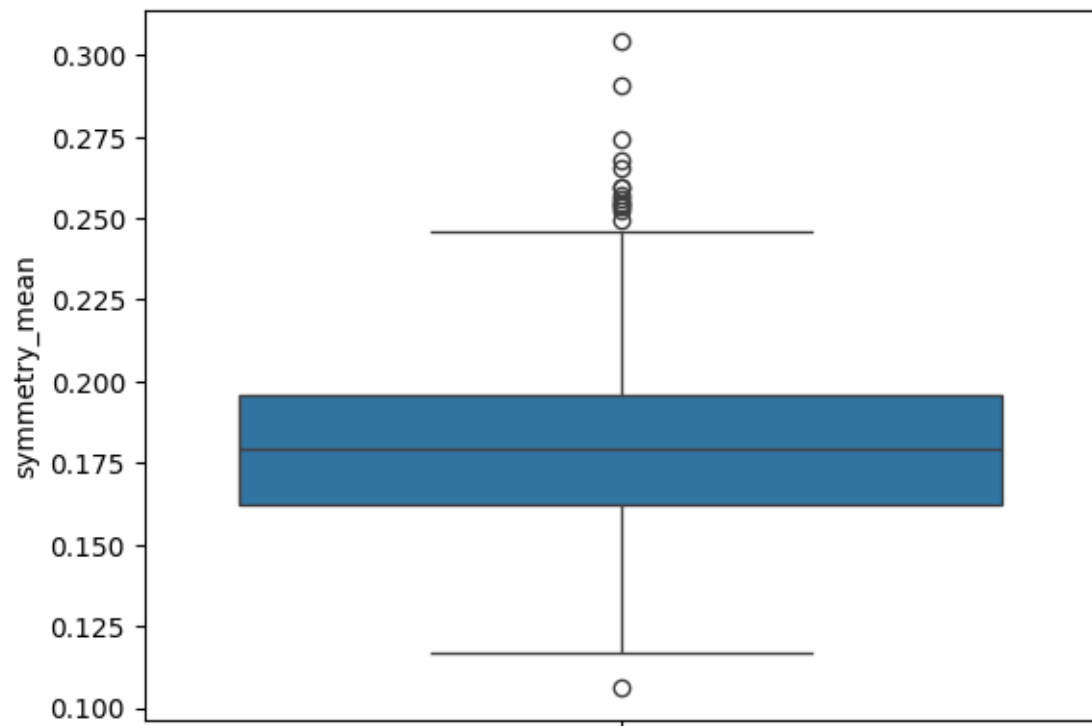
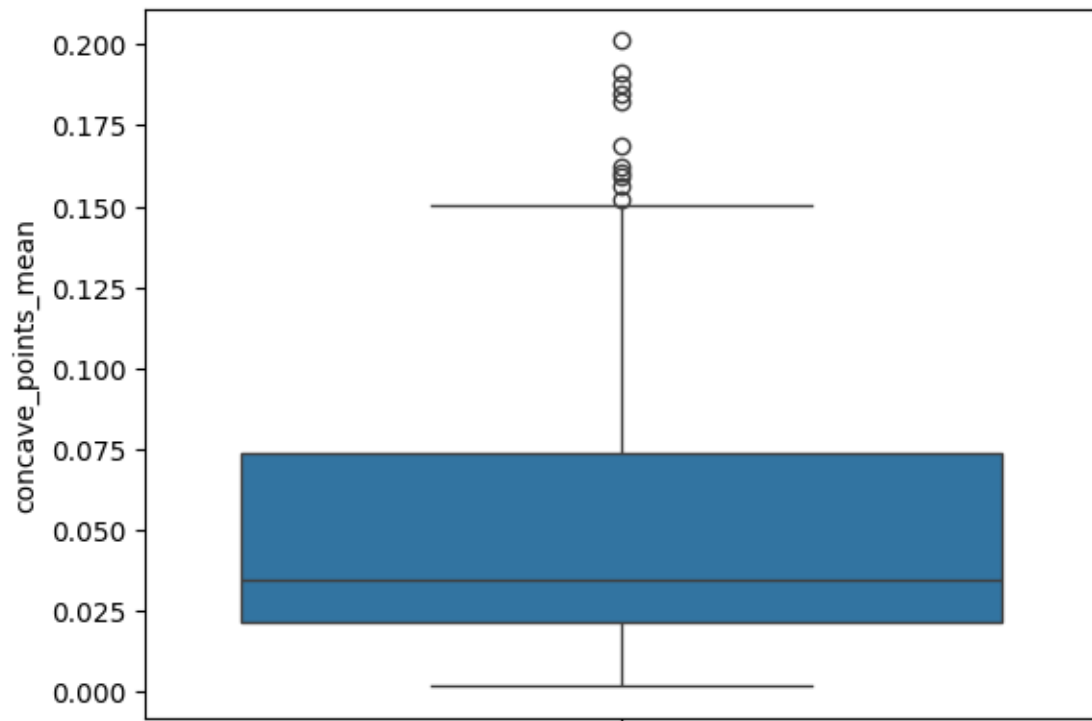


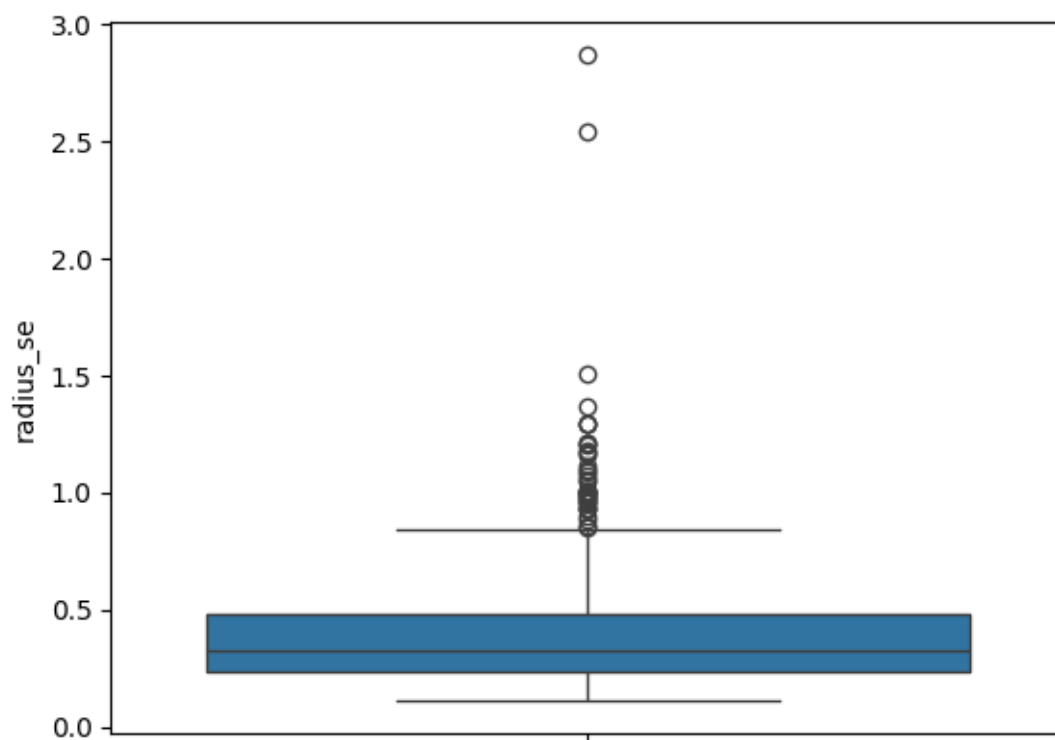
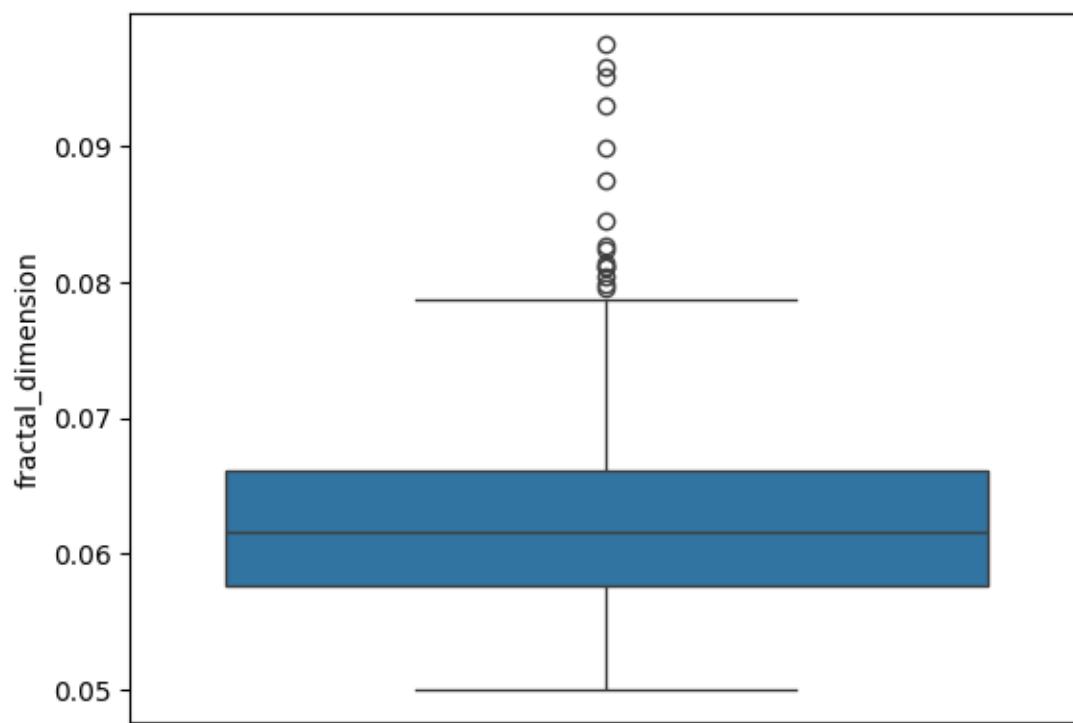




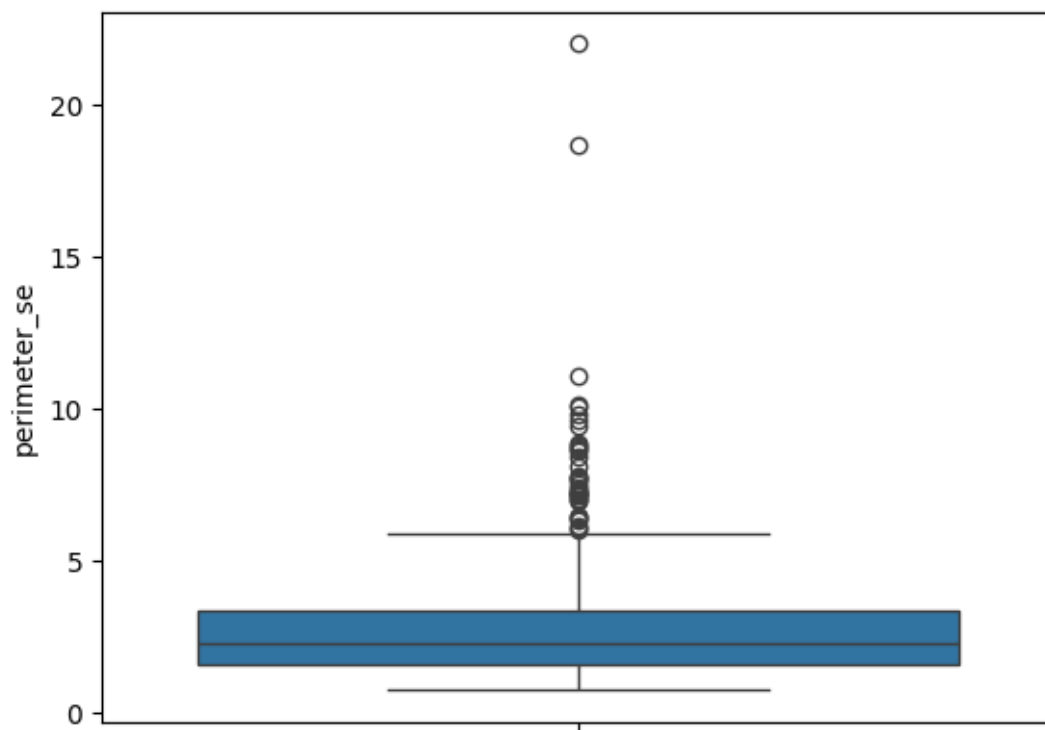
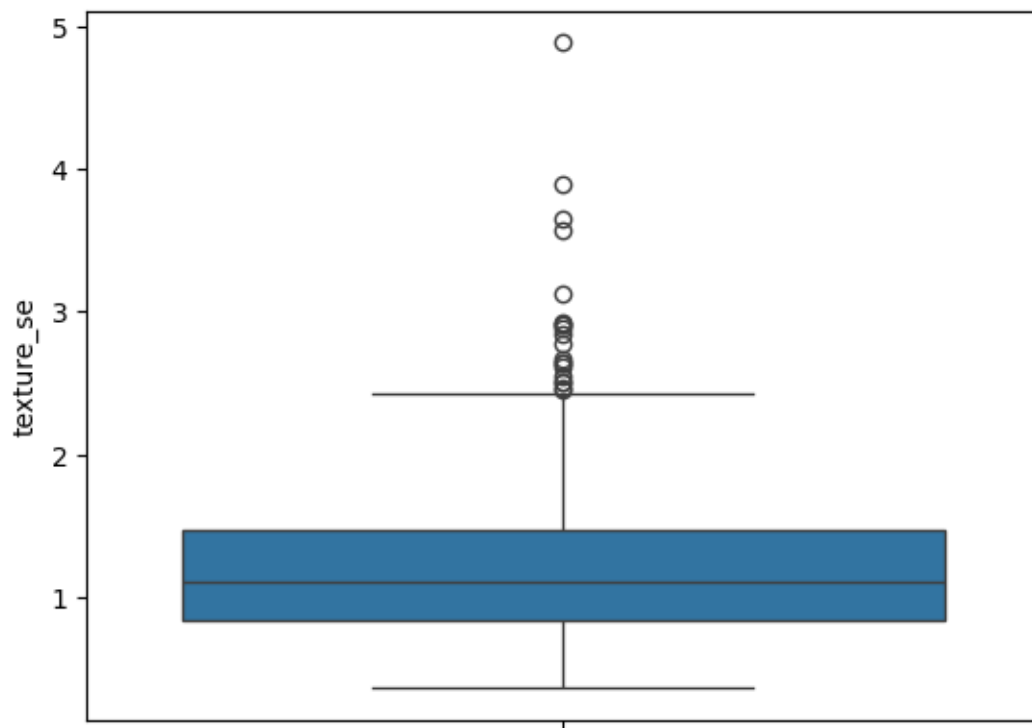


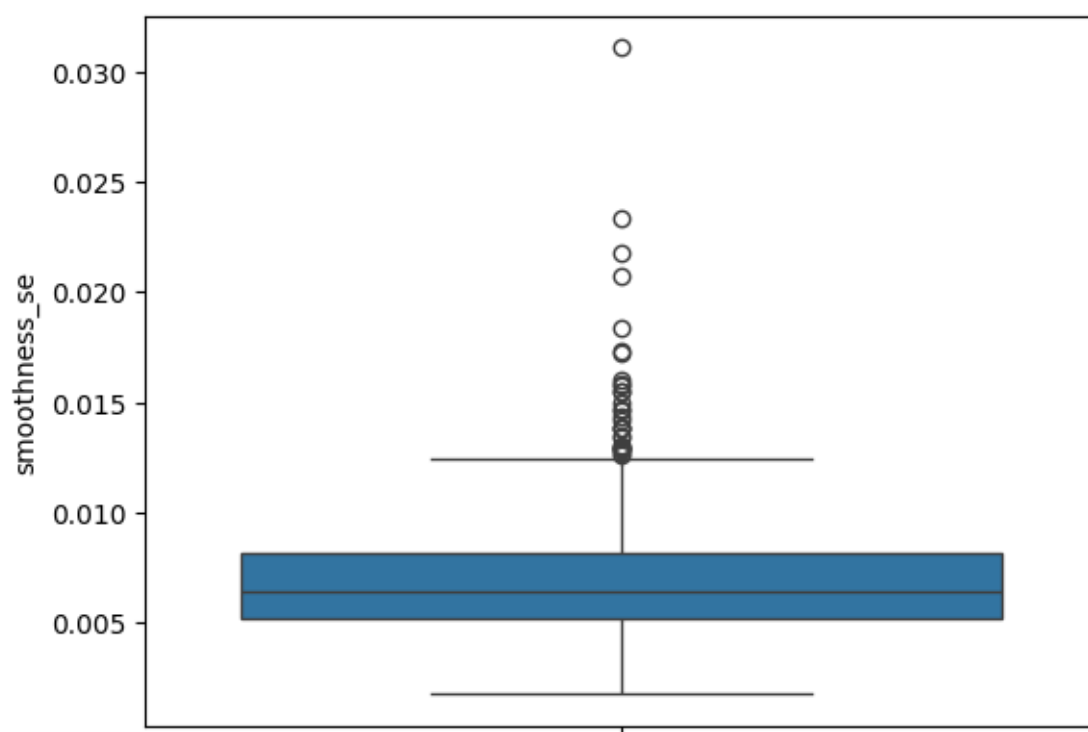
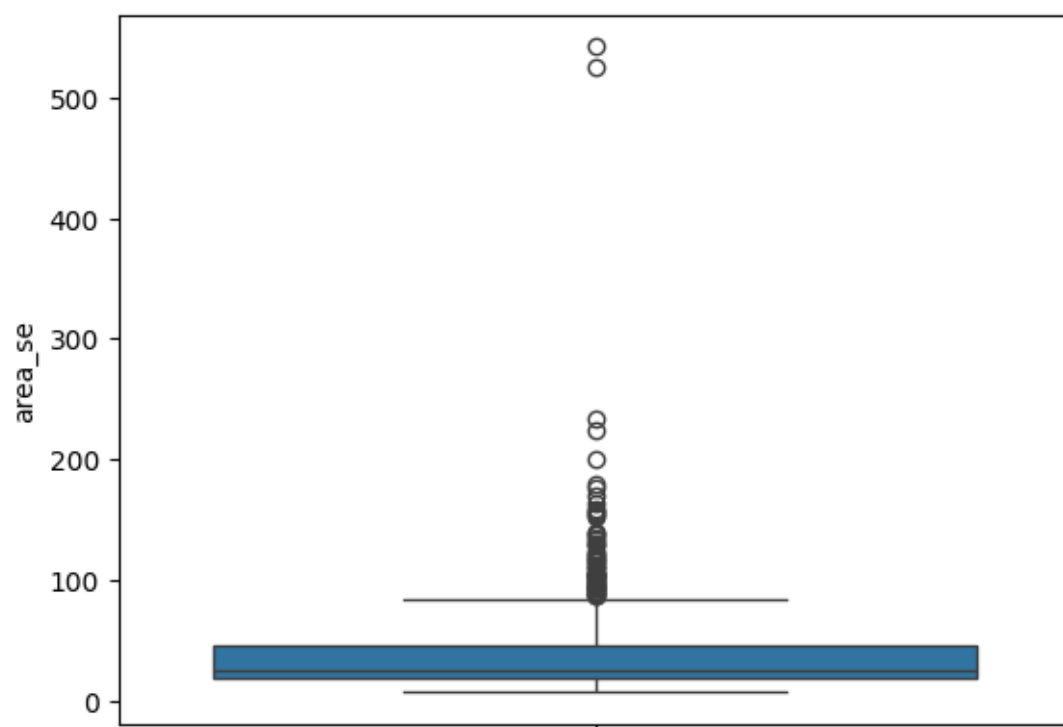


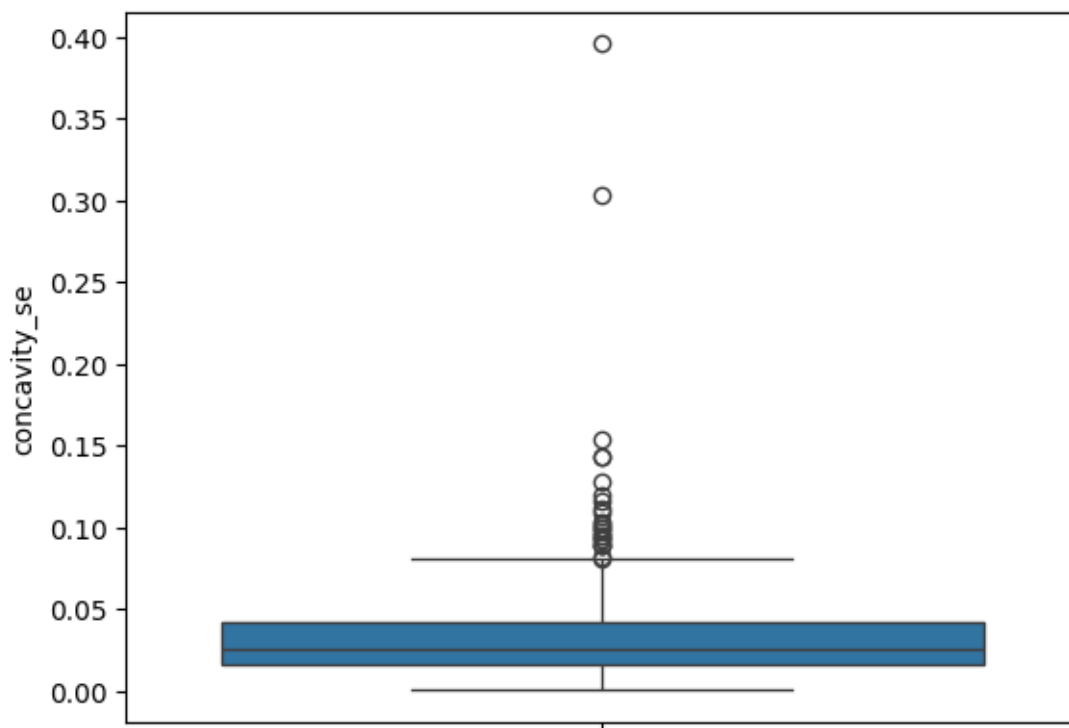
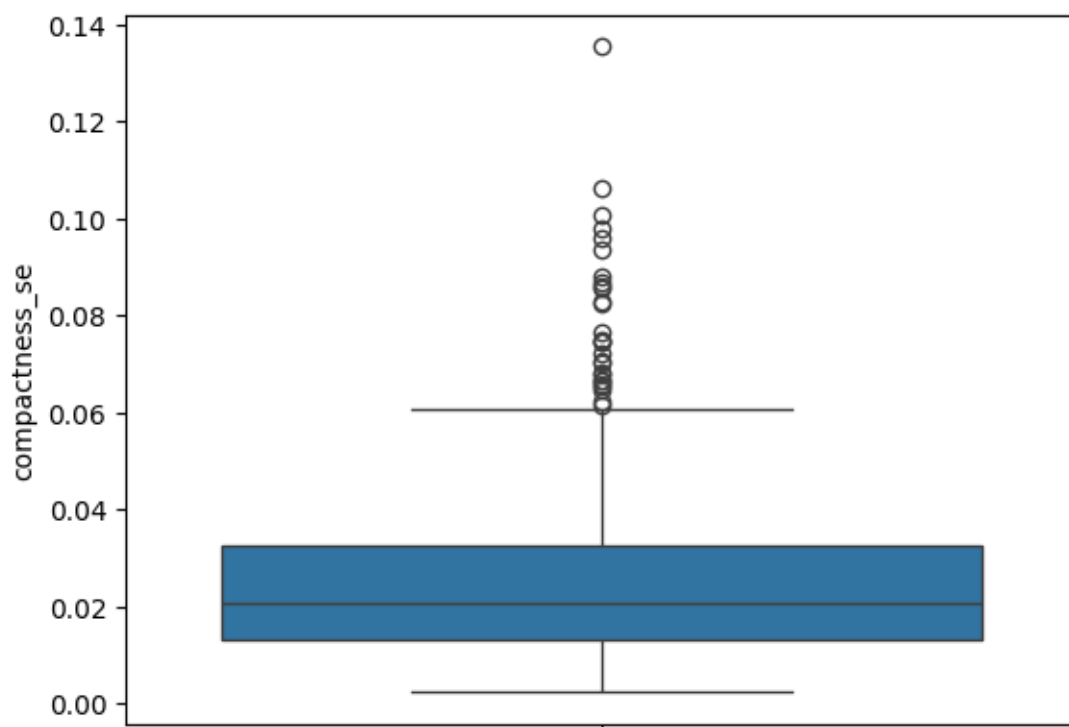


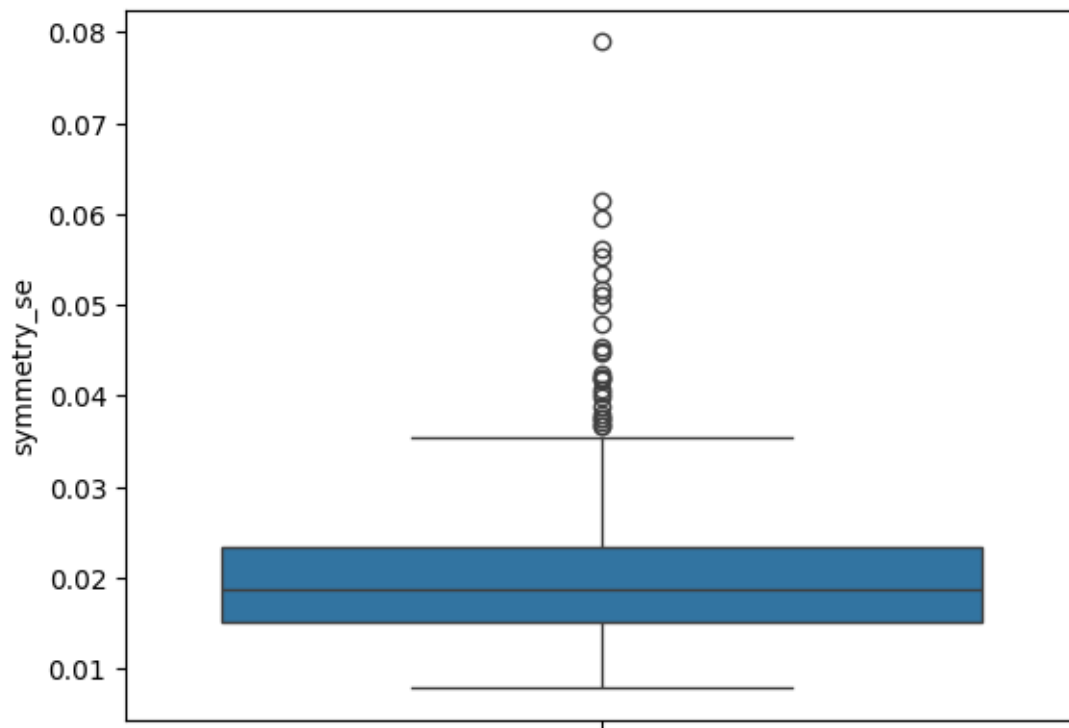
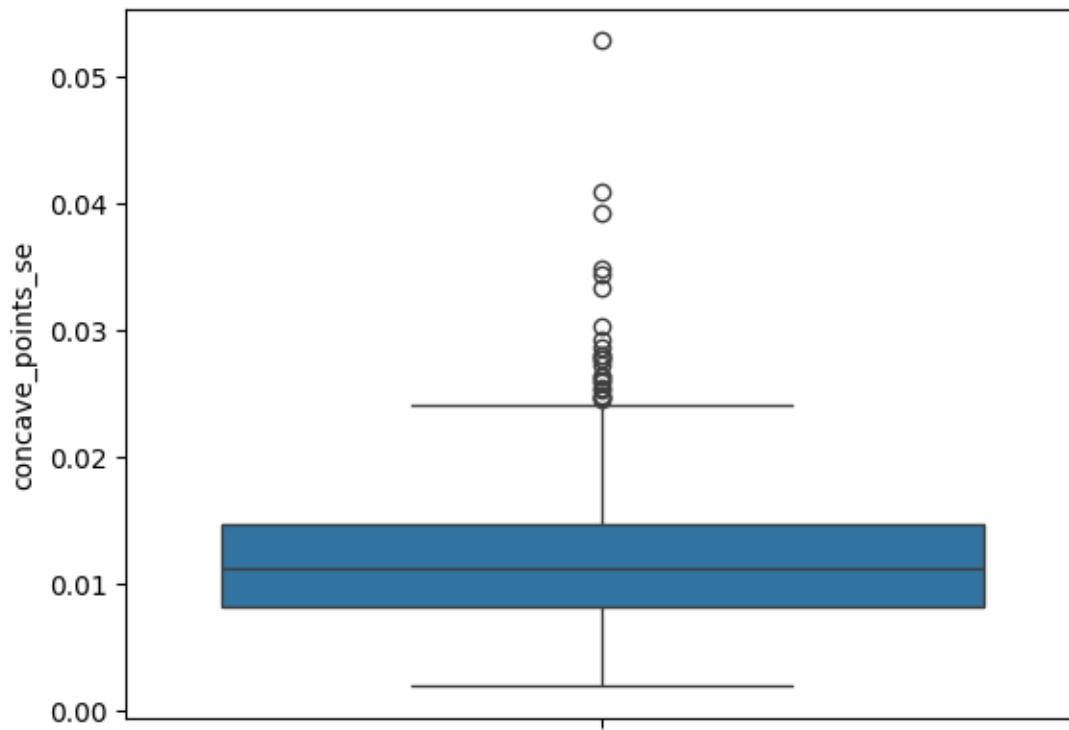


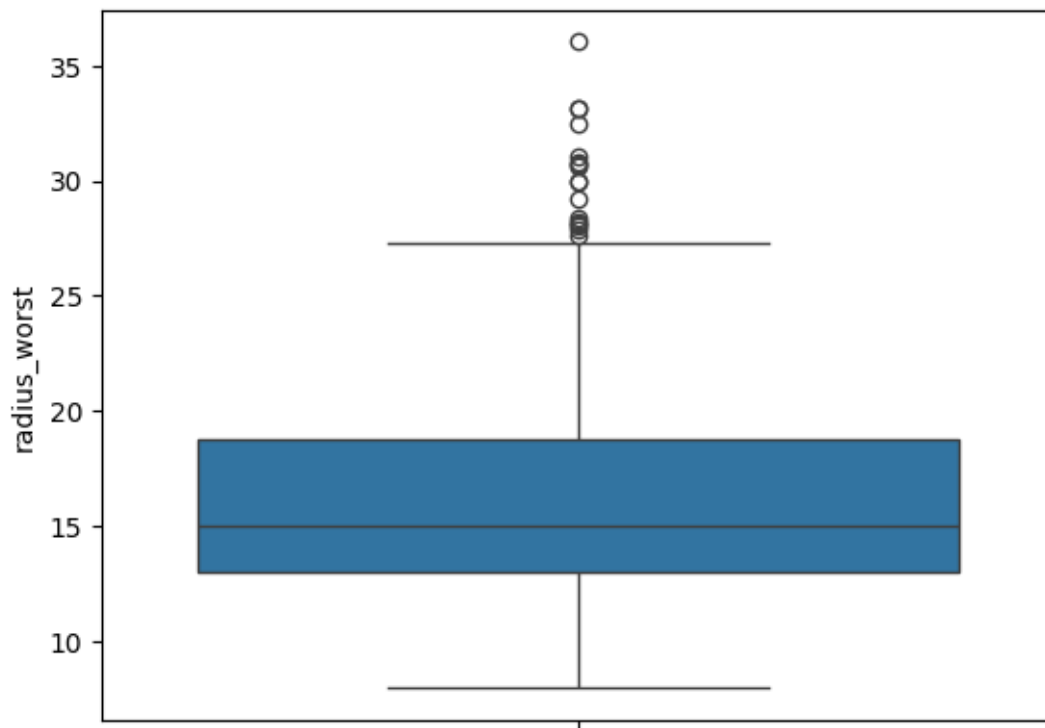
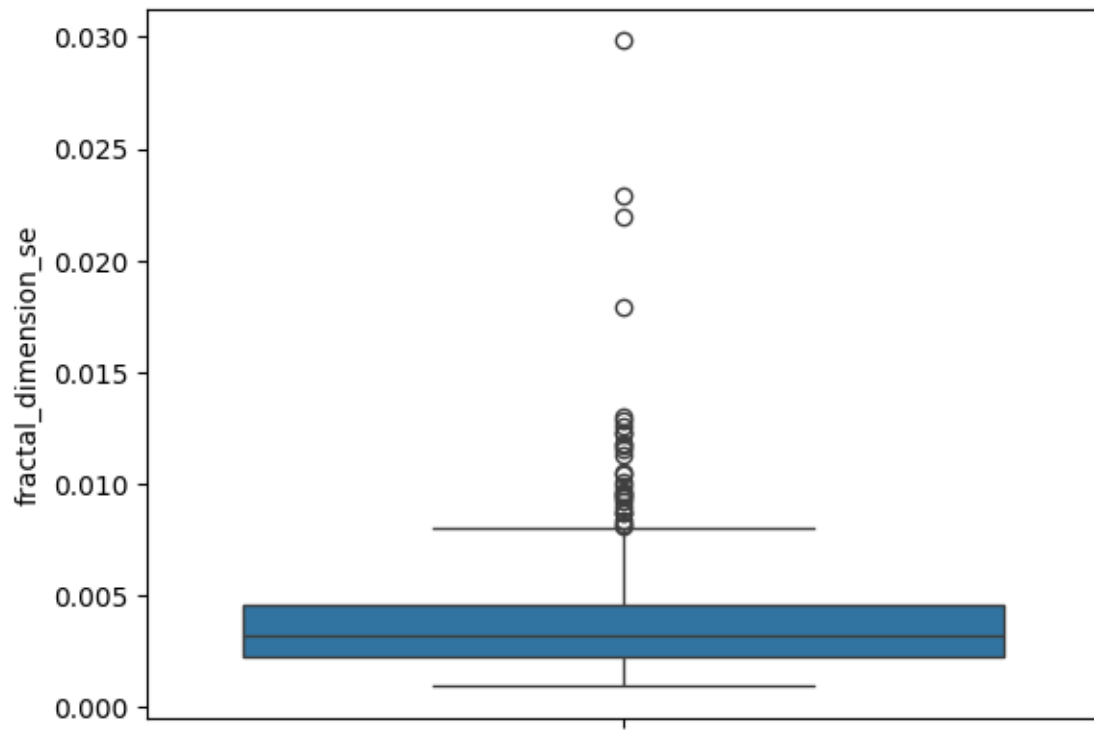


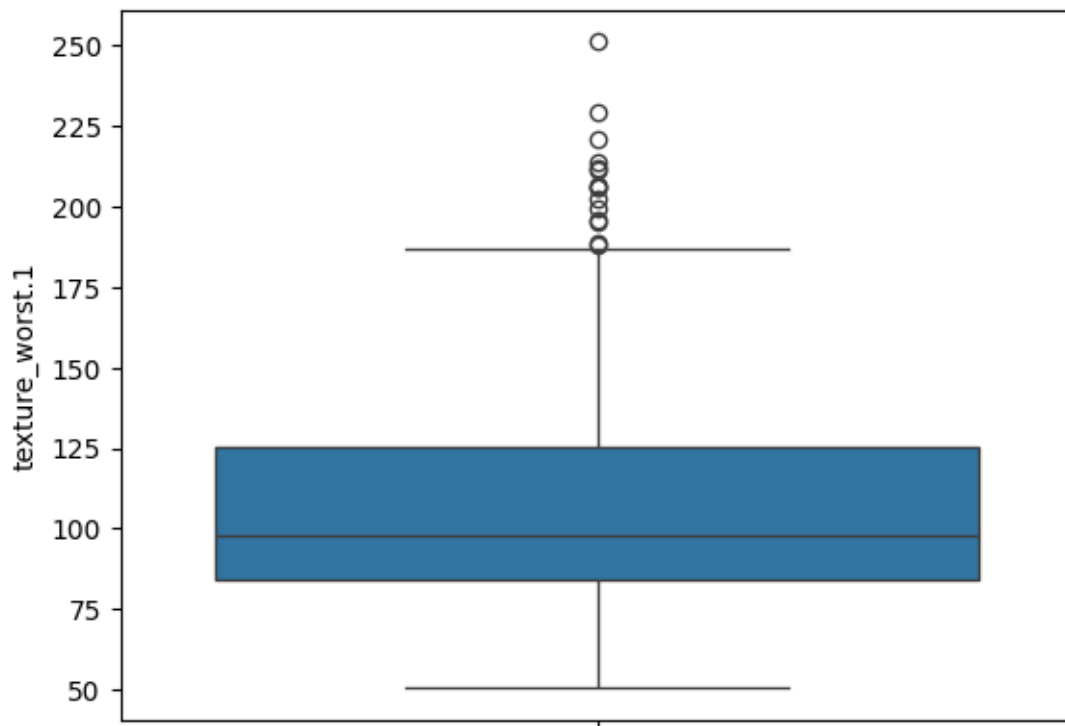
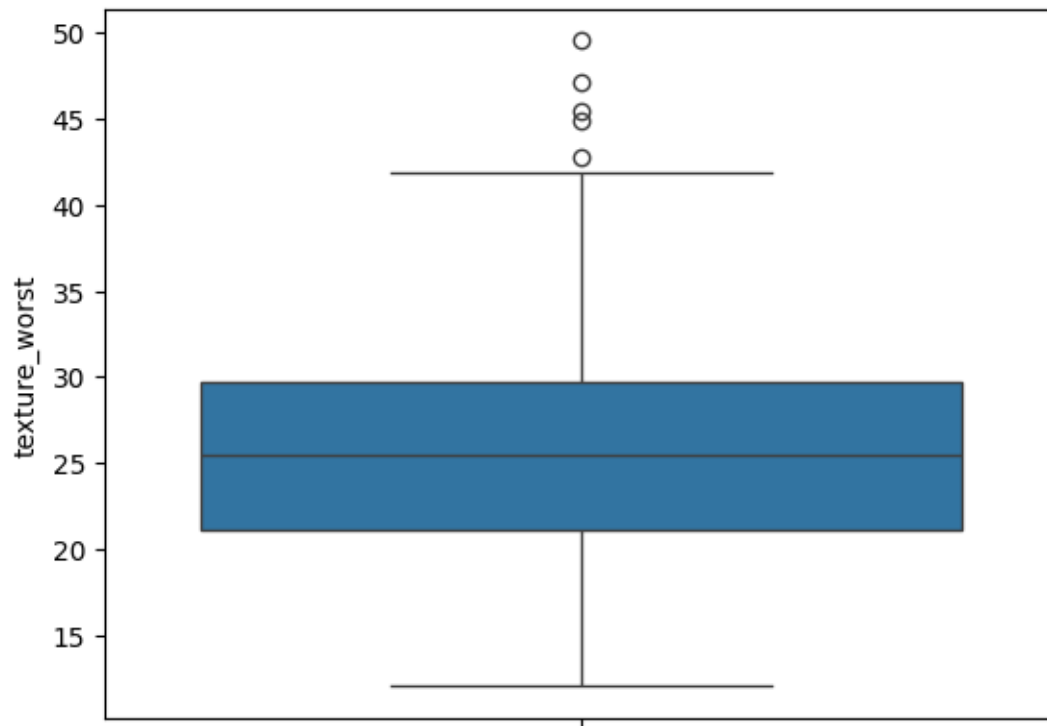


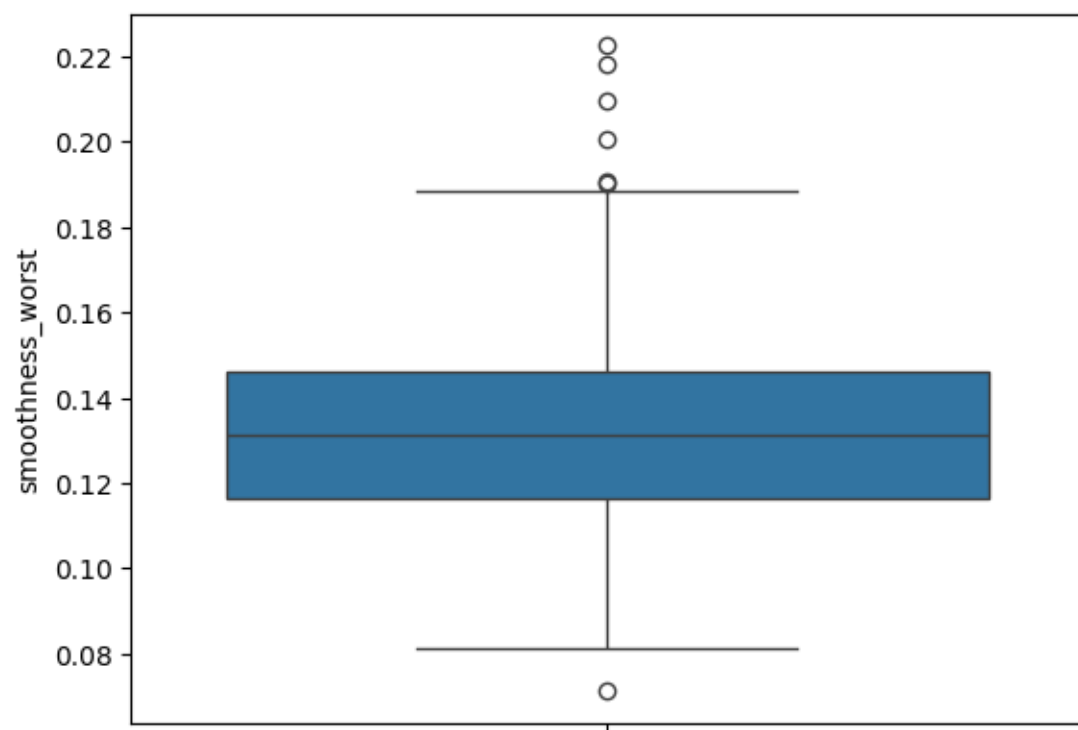
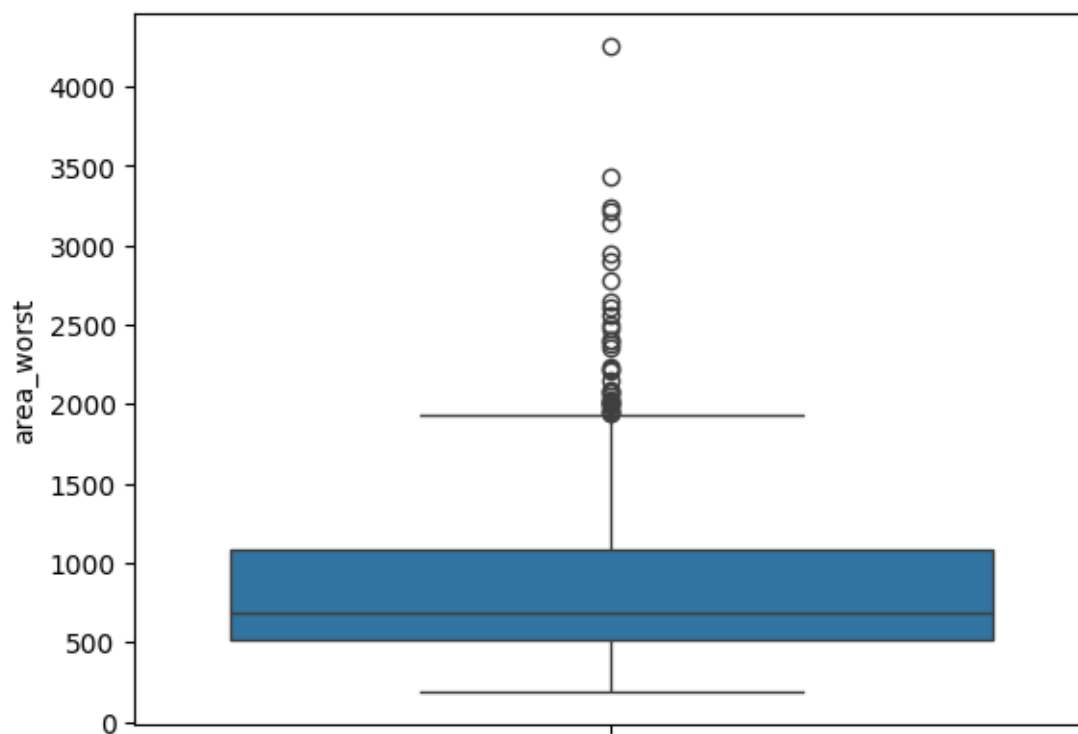


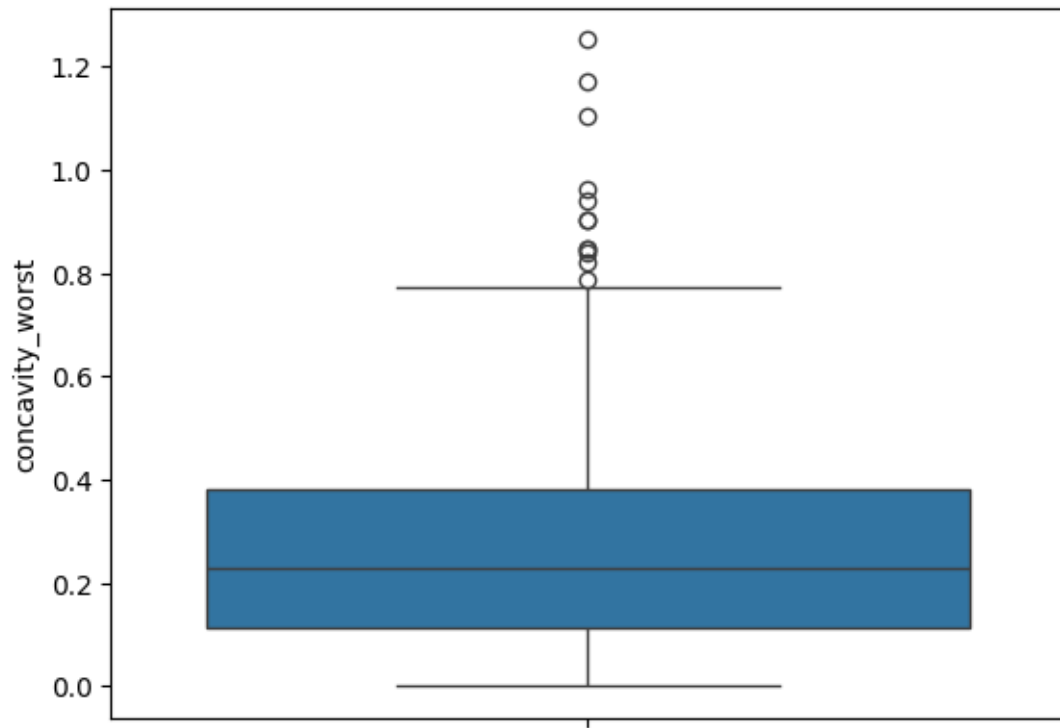
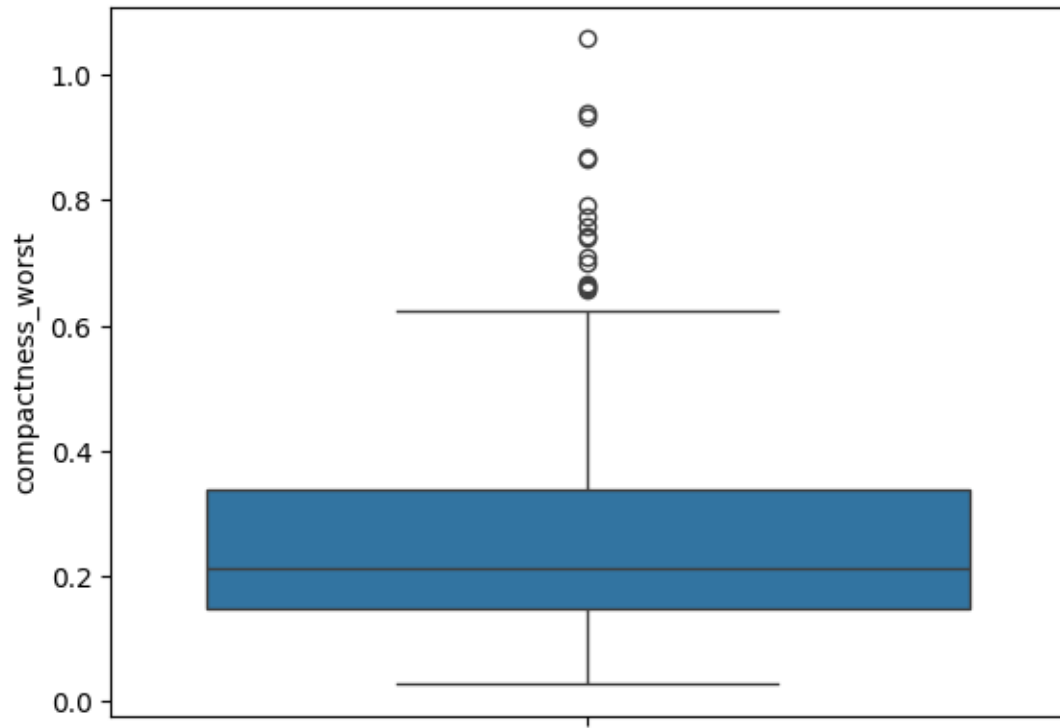




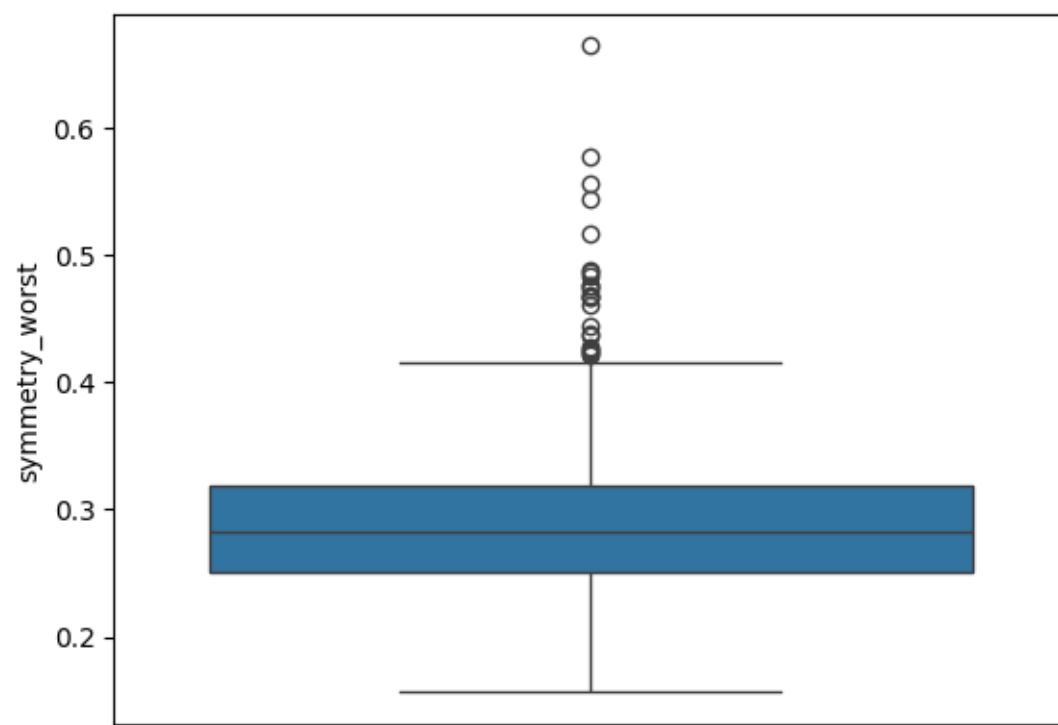
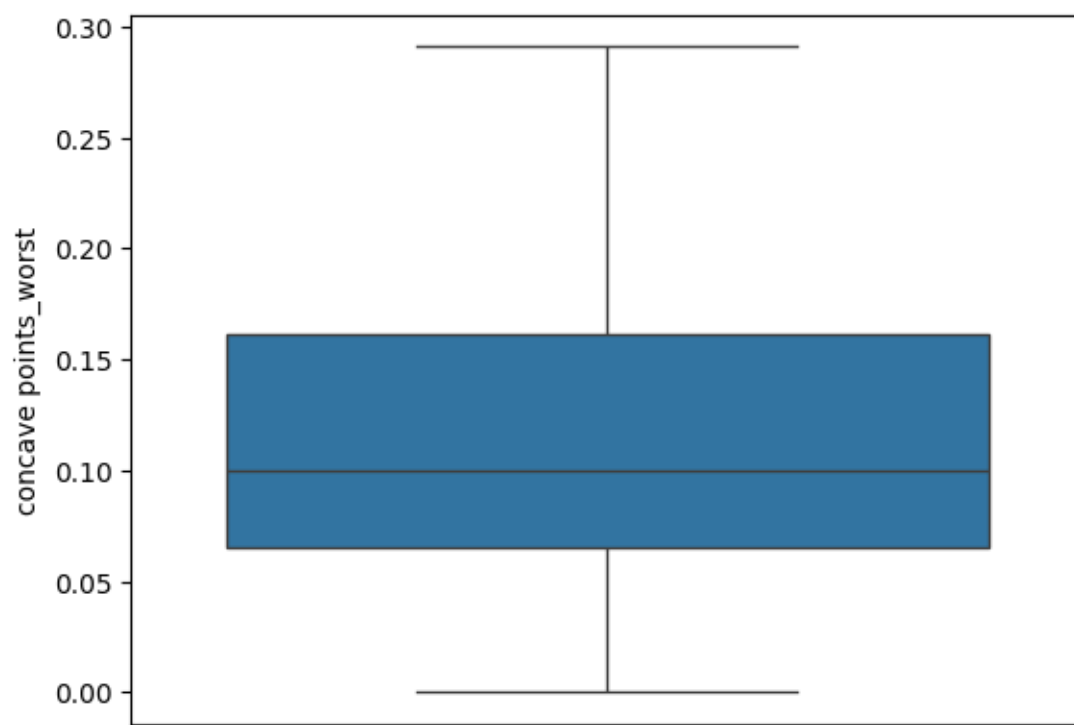


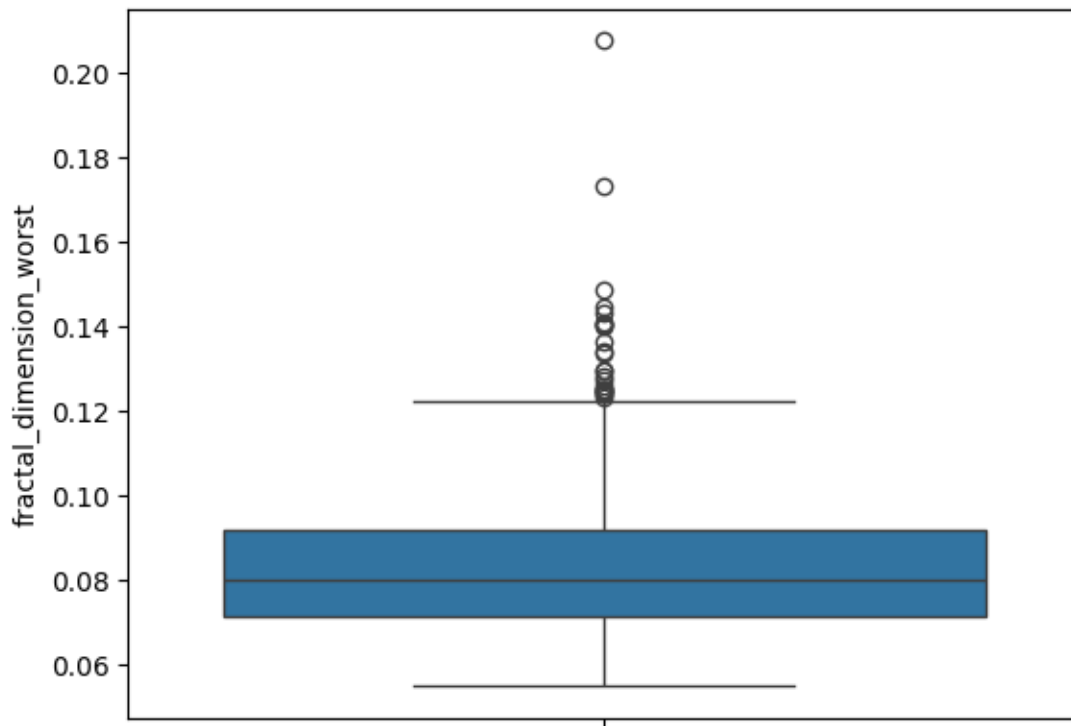






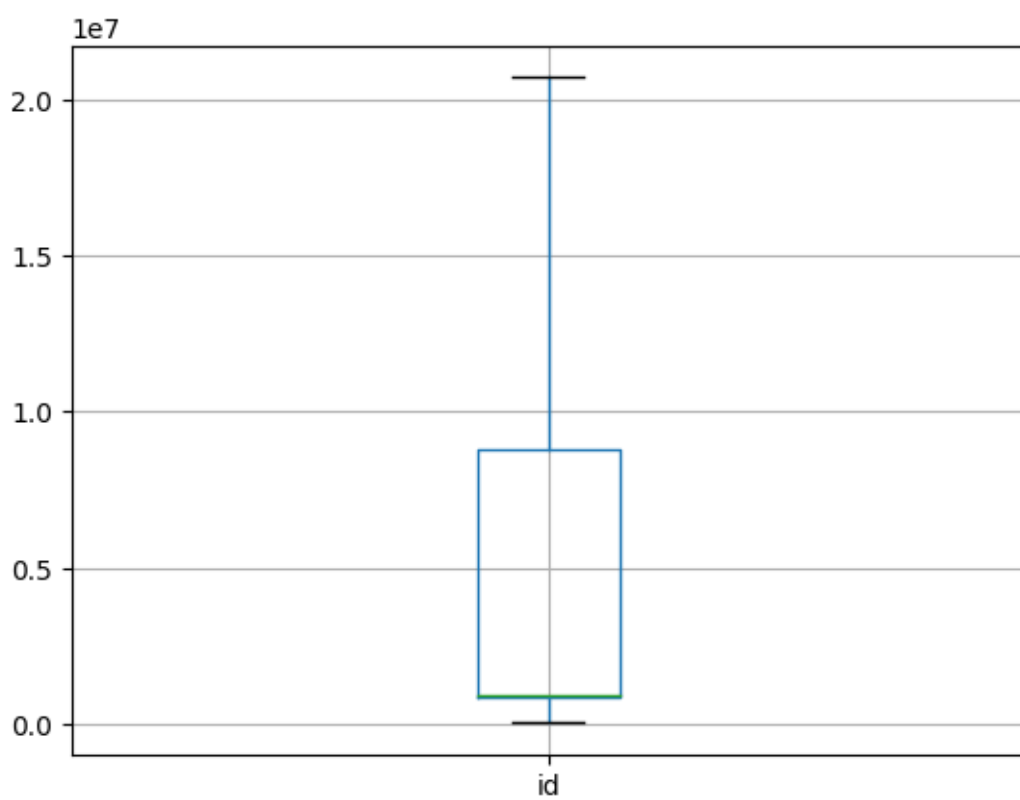
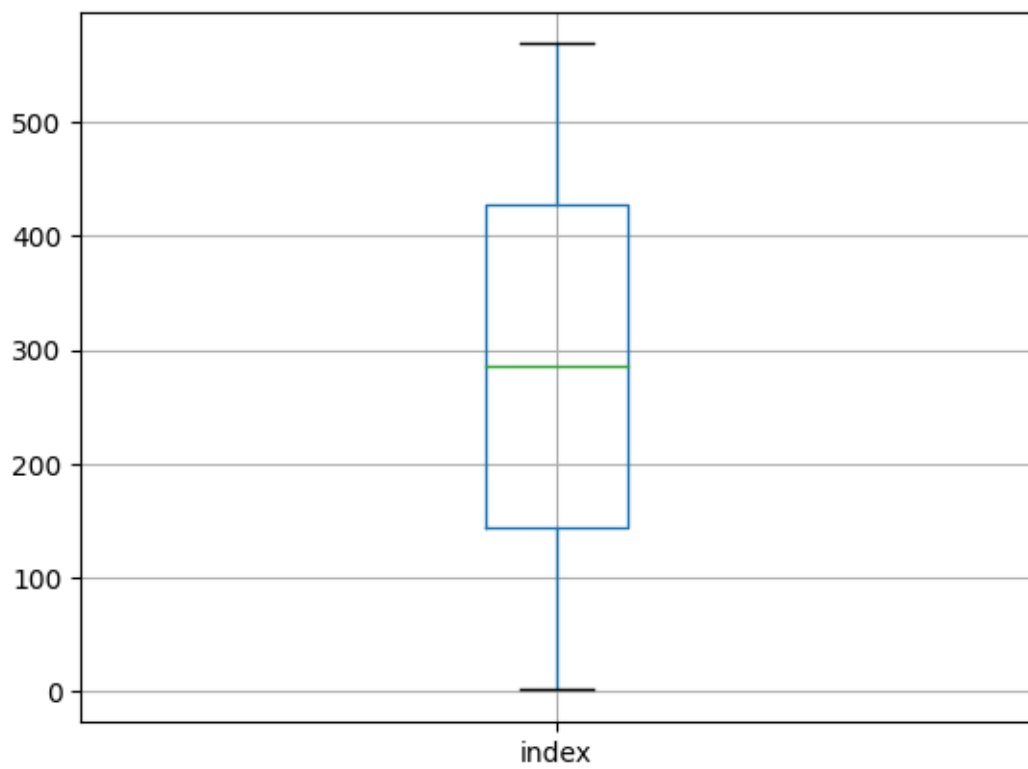


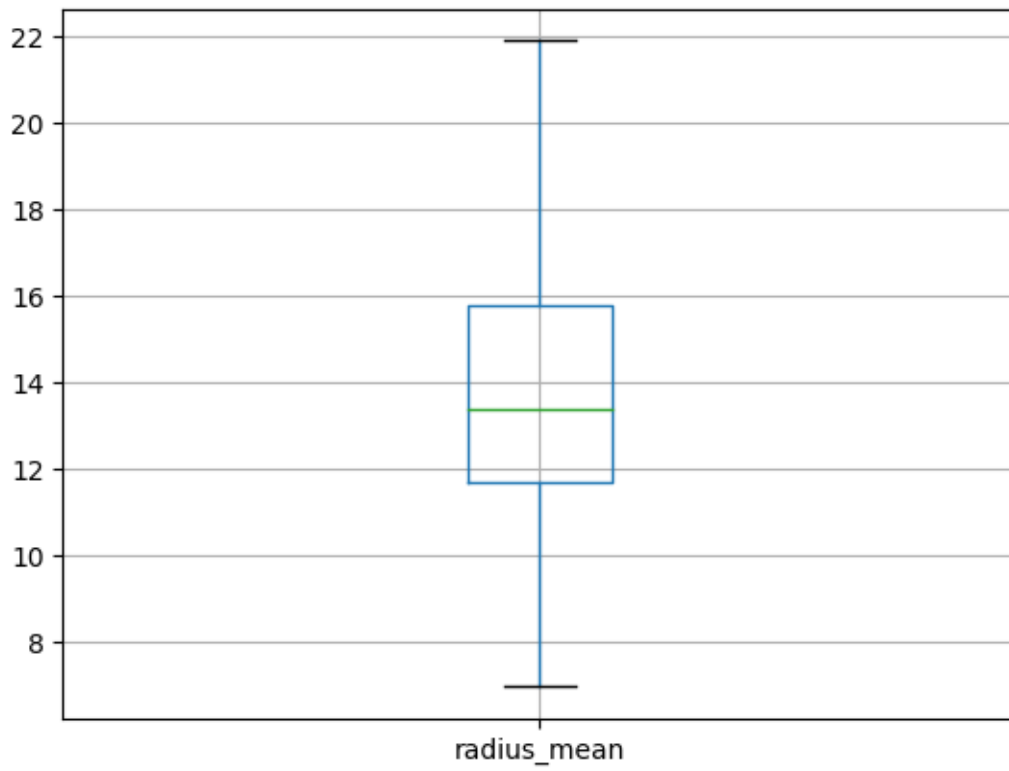


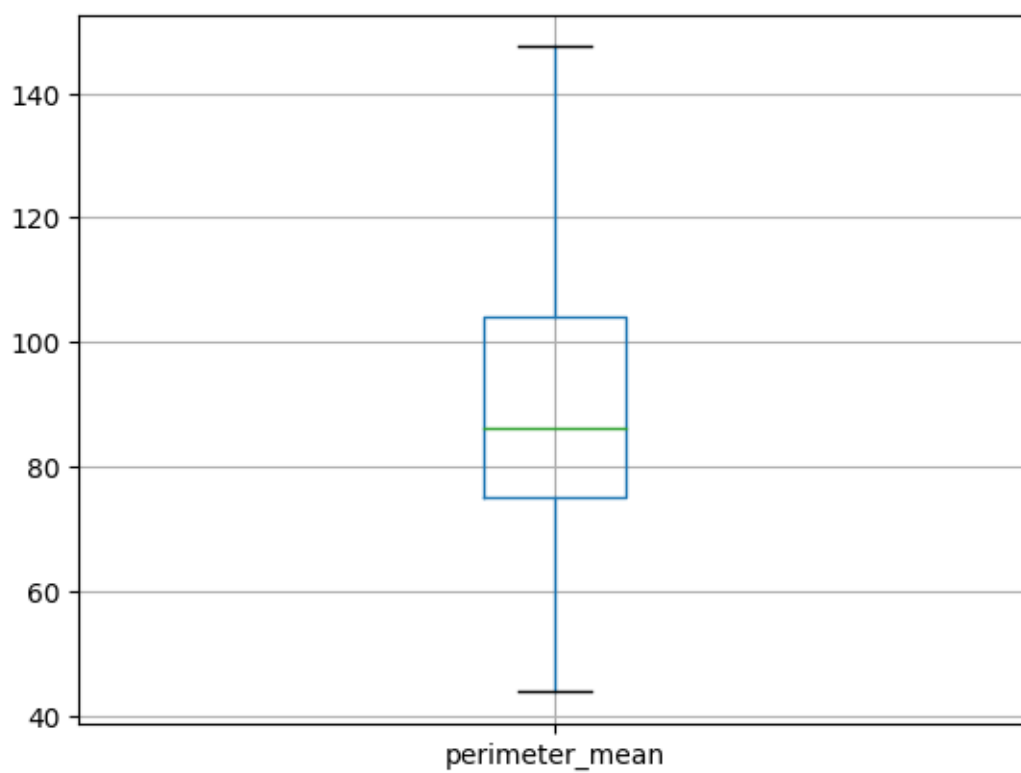
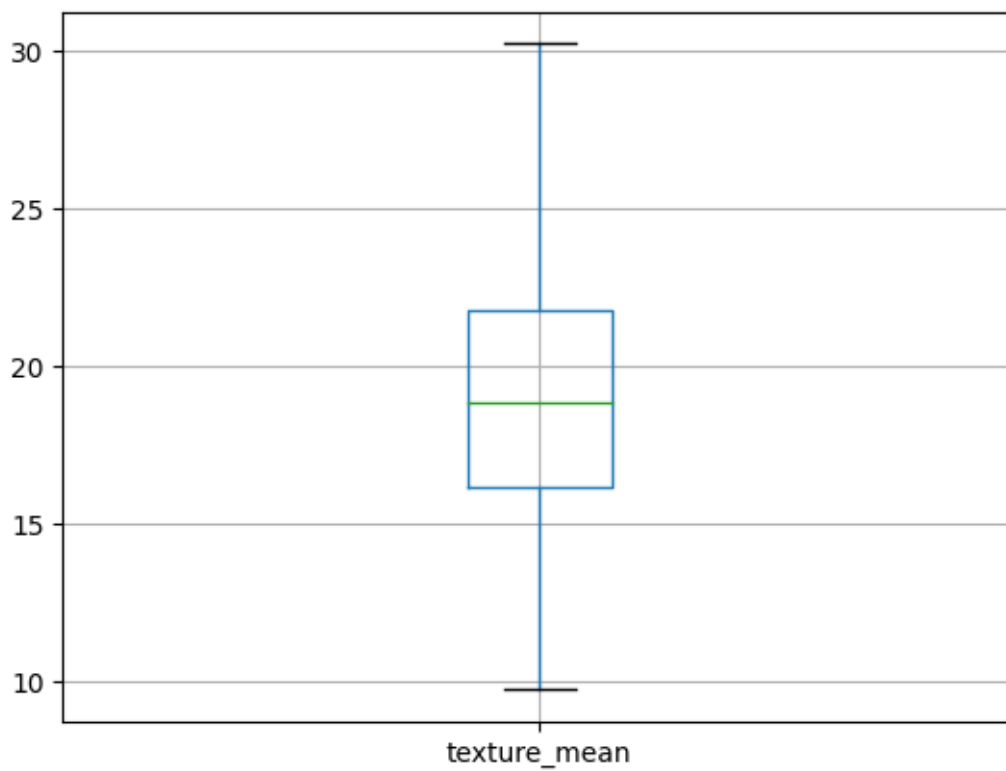


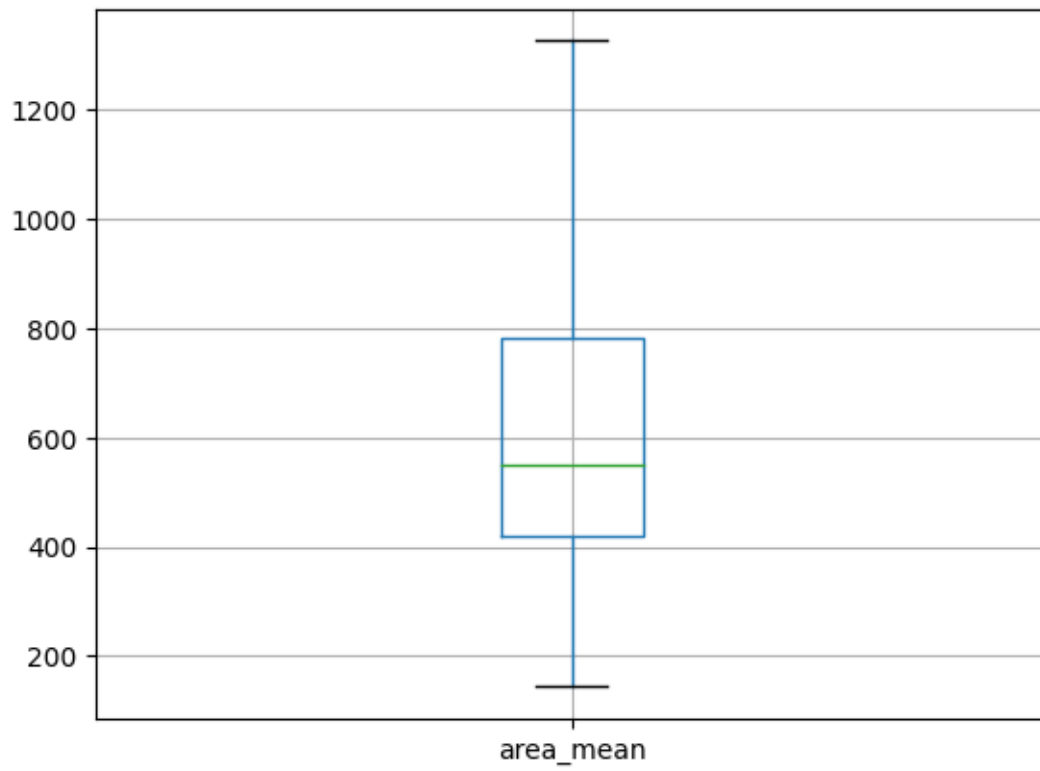
```
[20]: for column in numerical_cols:
    Q1 = cancer_data[column].quantile(.25)
    Q3 = cancer_data[column].quantile(.75)
    IQR = Q3 - Q1
    UB = Q3 + 1.5 * IQR
    LB = Q1 - 1.5 * IQR
    cancer_data.loc[cancer_data[column] >=UB, column]=UB
    cancer_data.loc[cancer_data[column] <=LB, column]=LB
    plt.figure()
    cancer_data[[column]].boxplot()
```

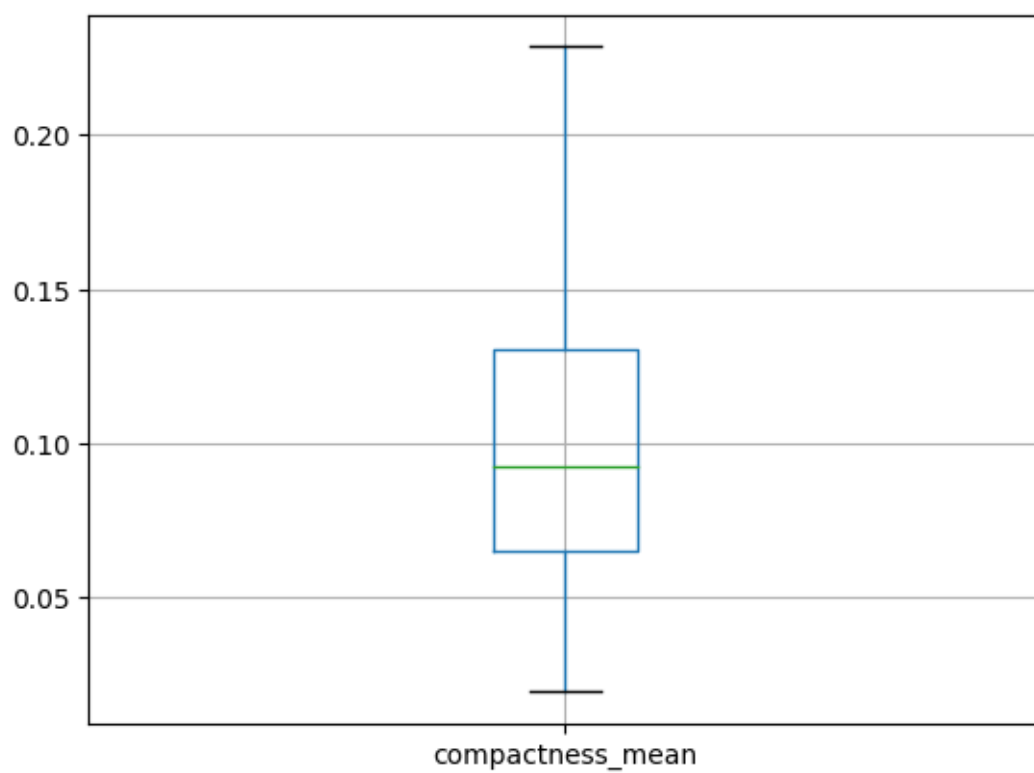
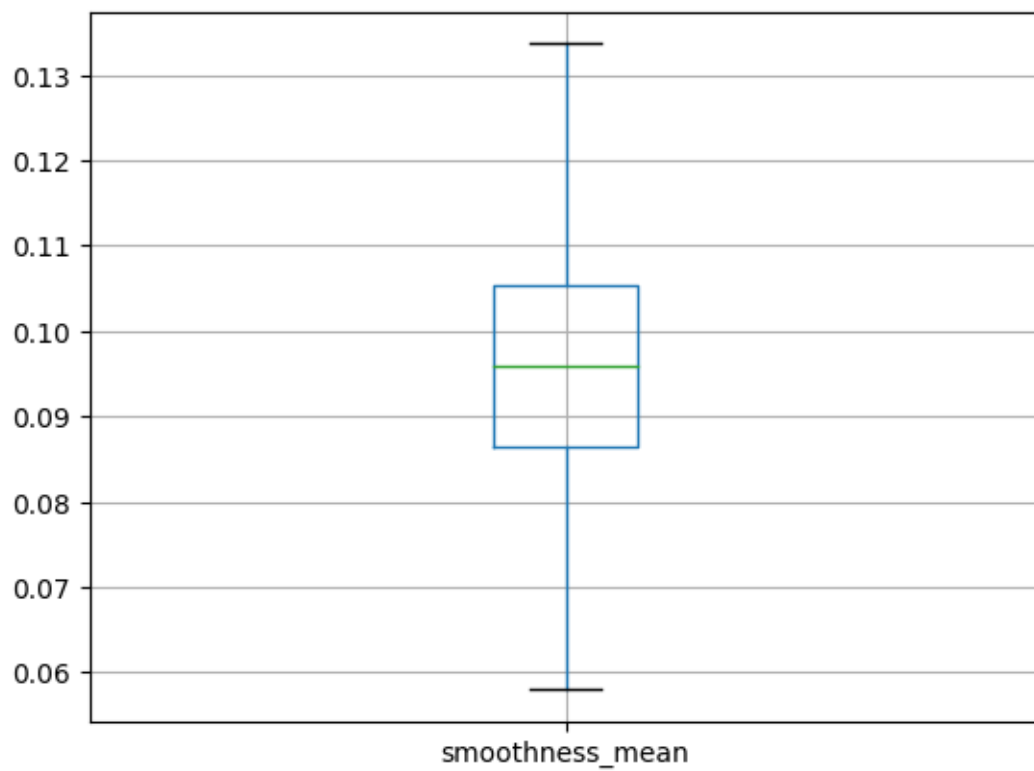
<ipython-input-20-0e36a88e36ee>:9: RuntimeWarning: More than 20 figures have been opened. Figures created through the pyplot interface (`matplotlib.pyplot.figure`) are retained until explicitly closed and may consume too much memory. (To control this warning, see the rcParam `figure.max_open_warning`). Consider using `matplotlib.pyplot.close()`.  
 plt.figure()

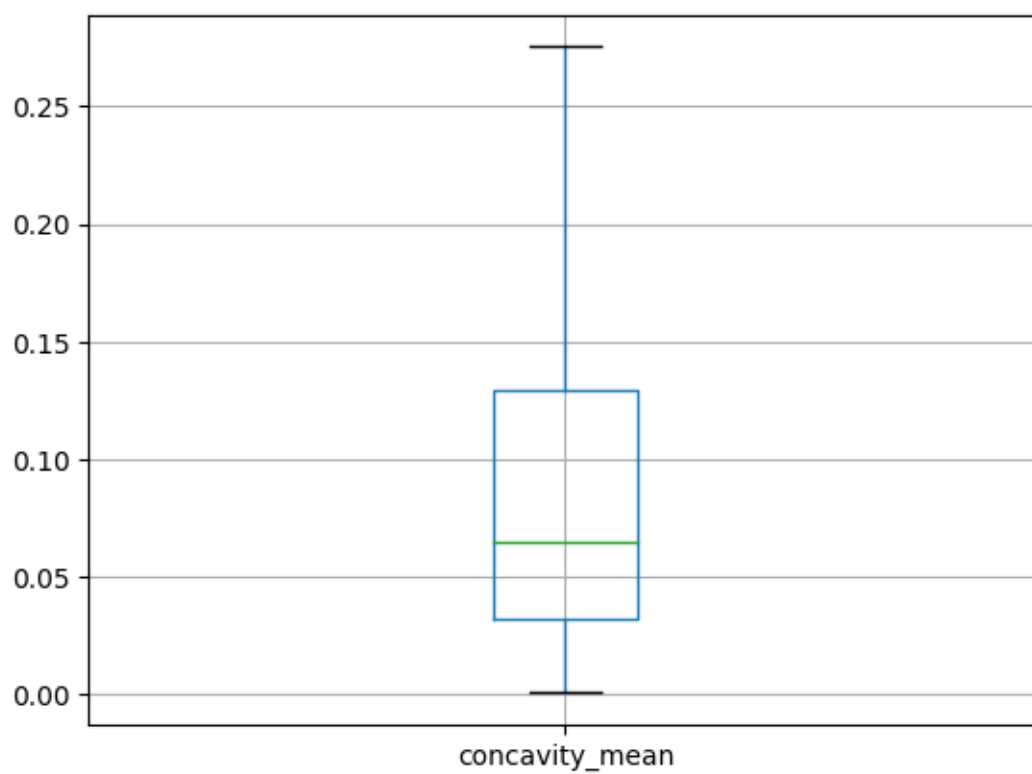




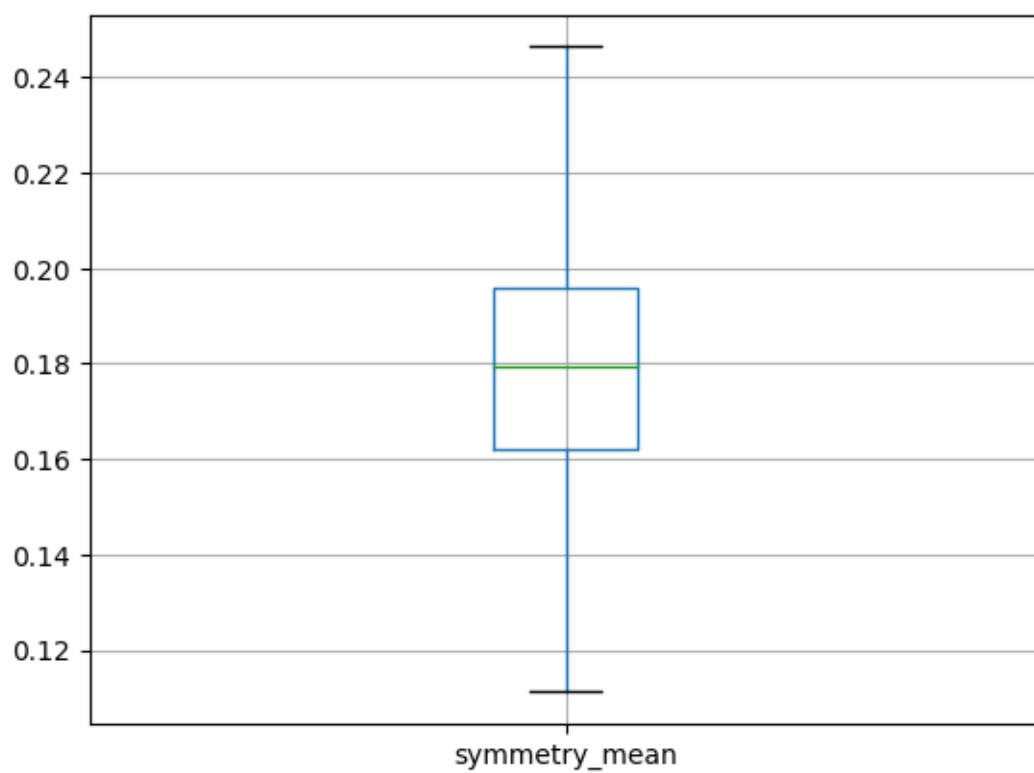
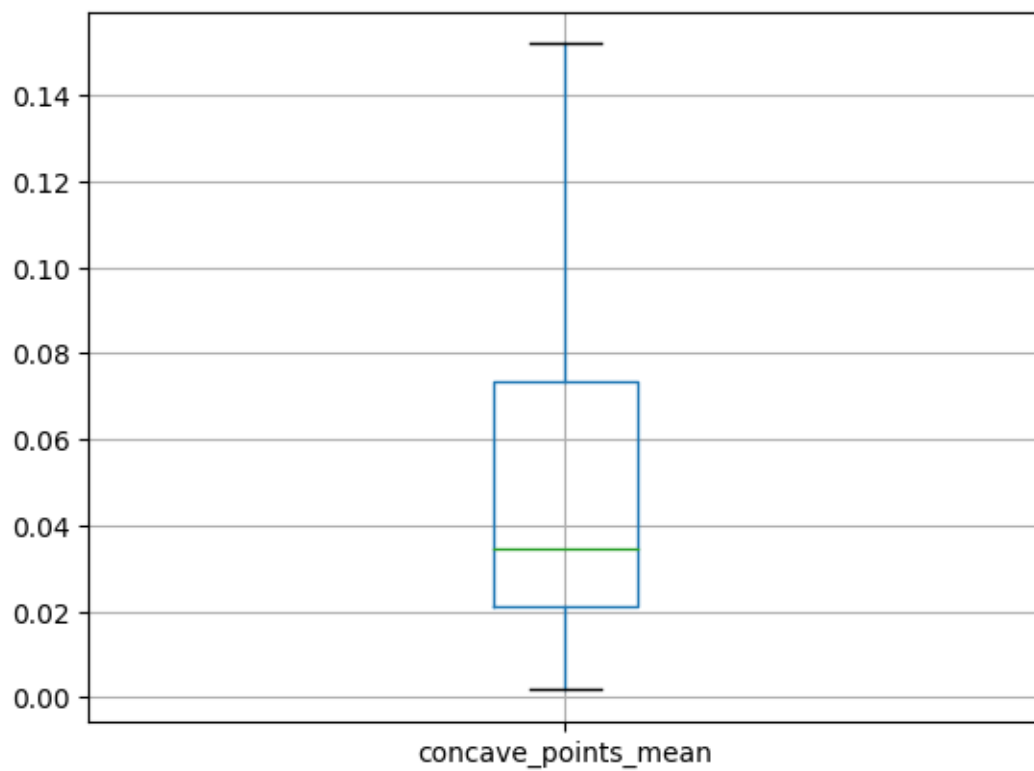


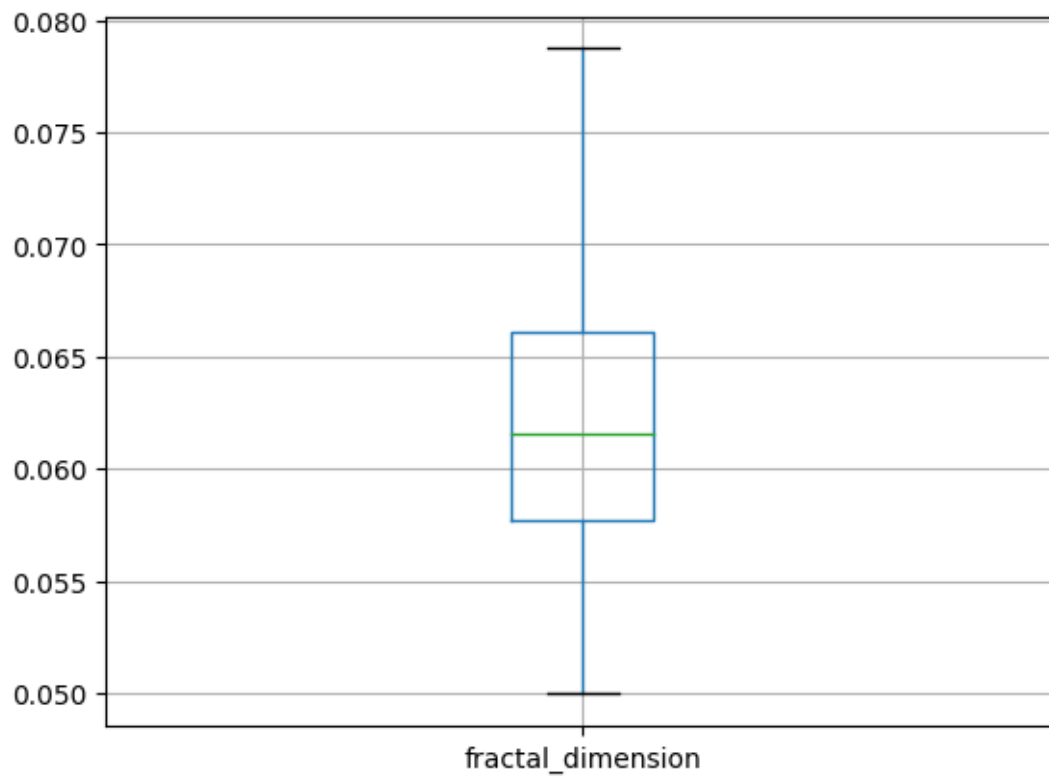


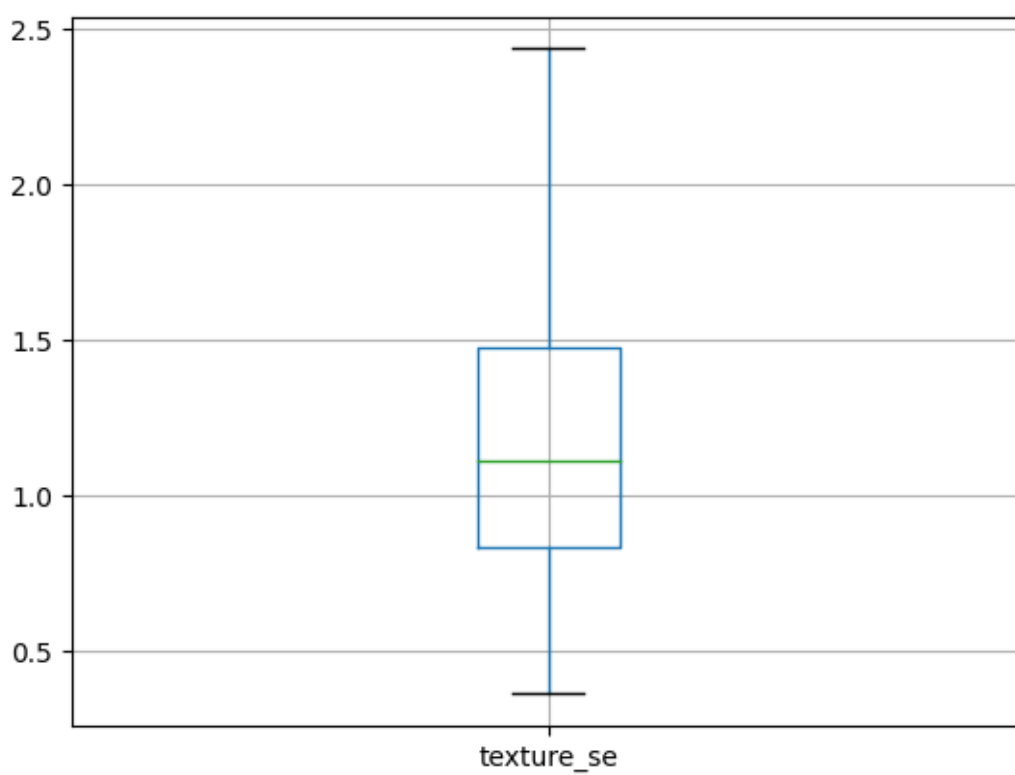
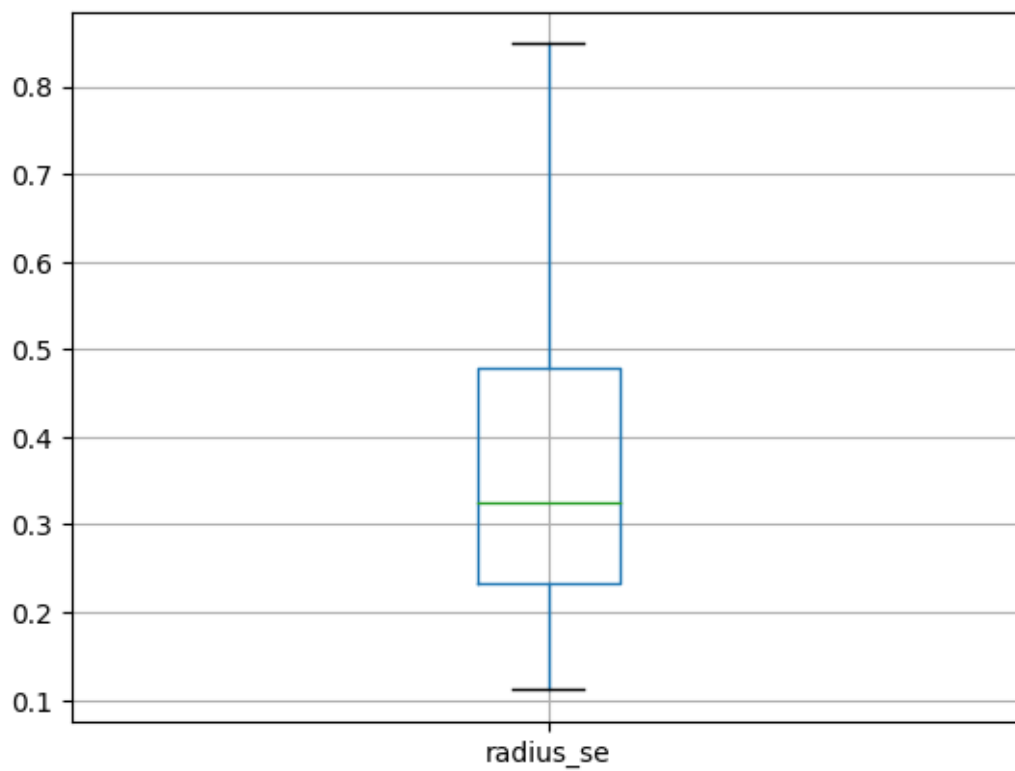


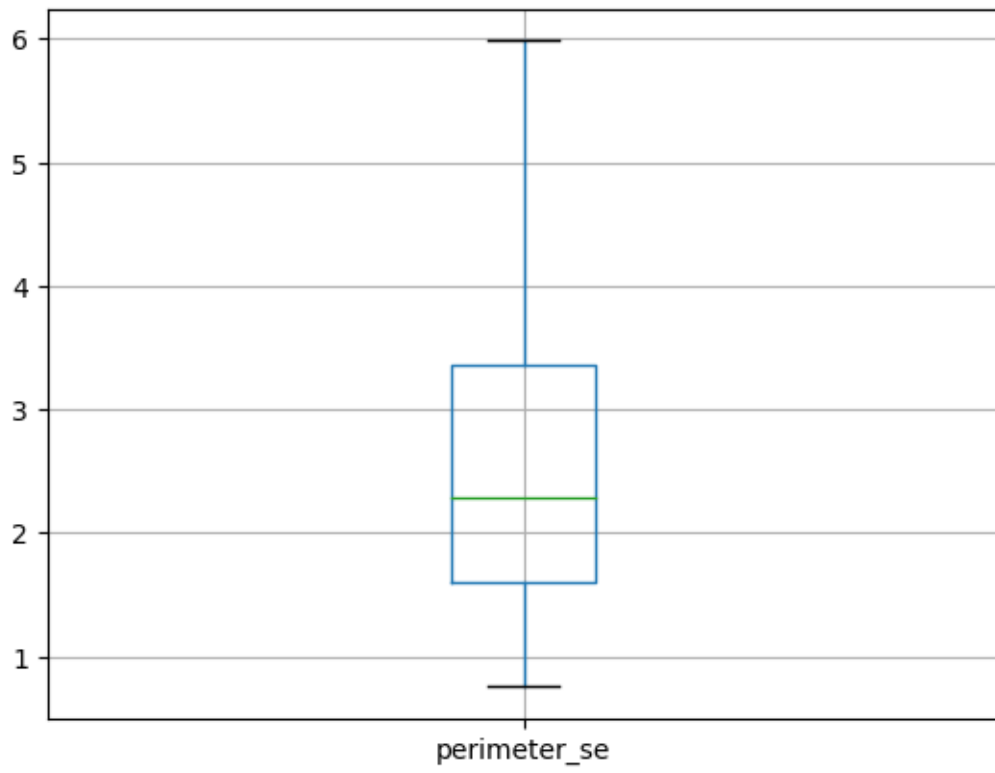


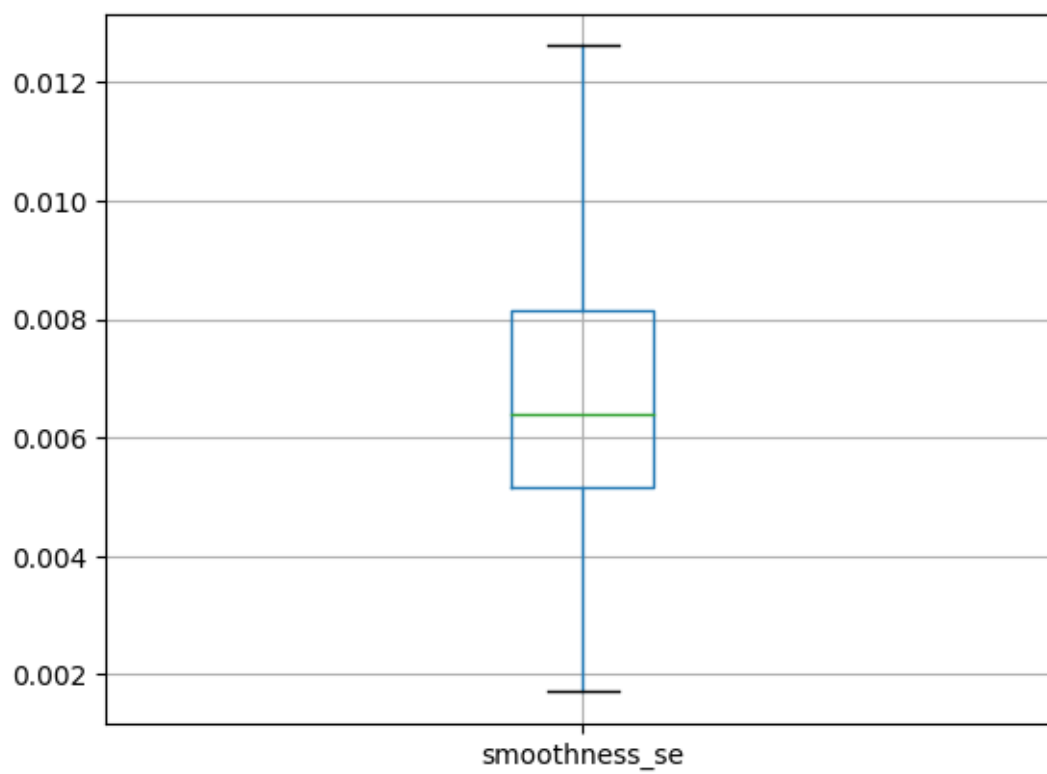
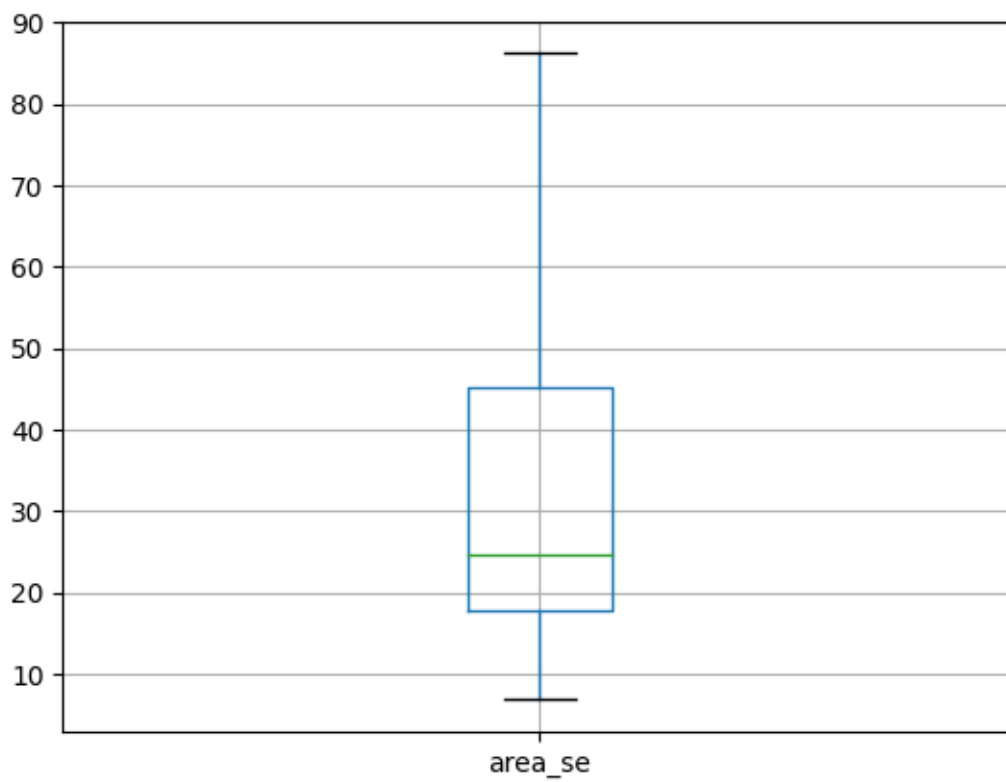


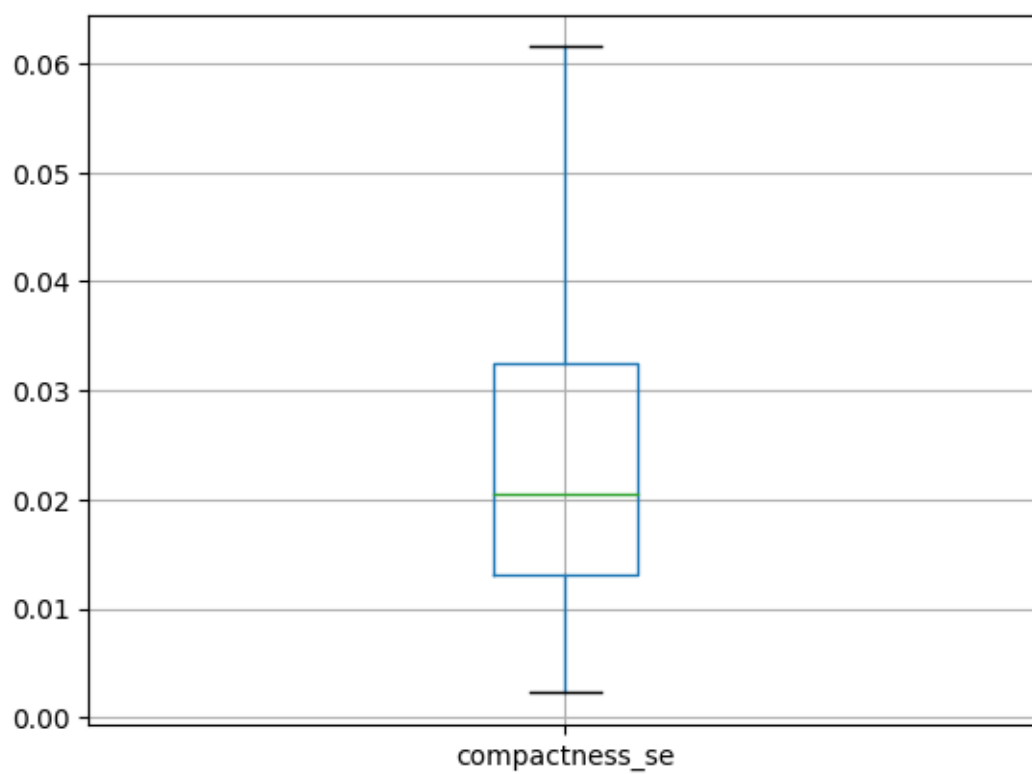


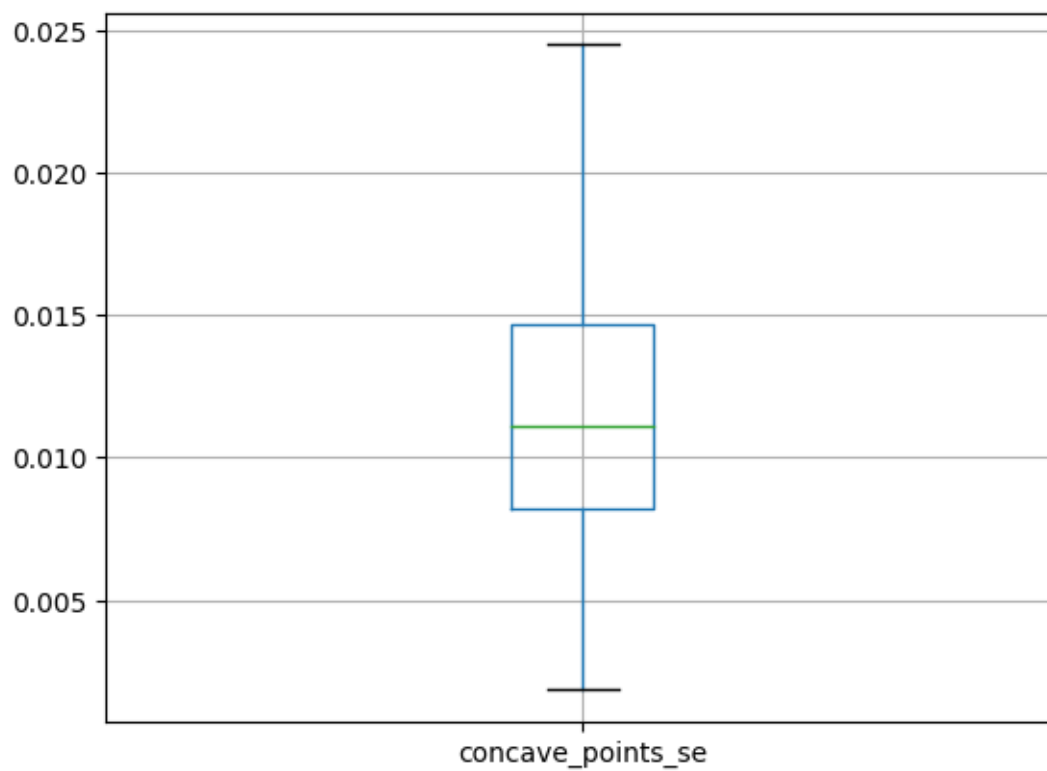
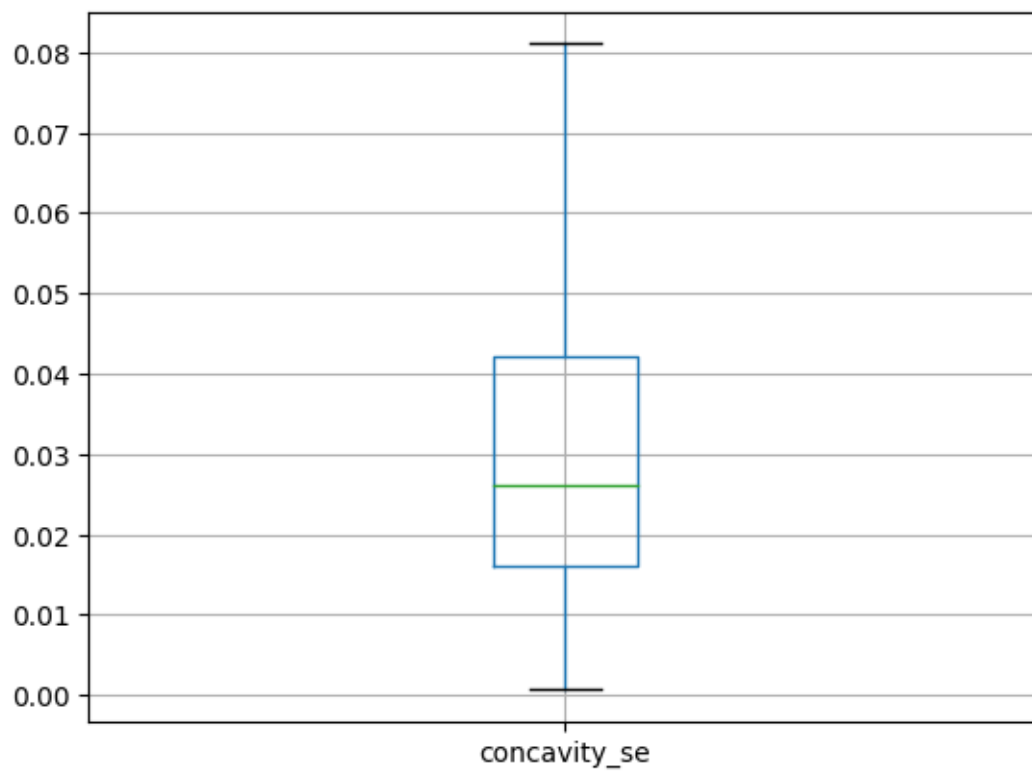


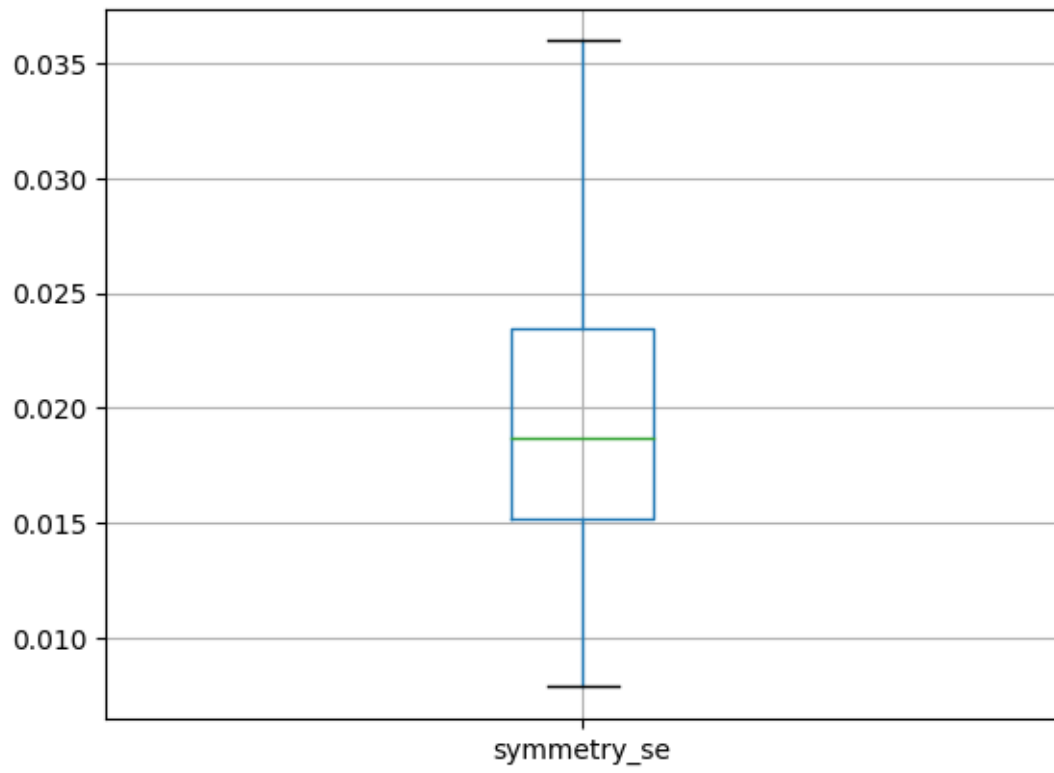




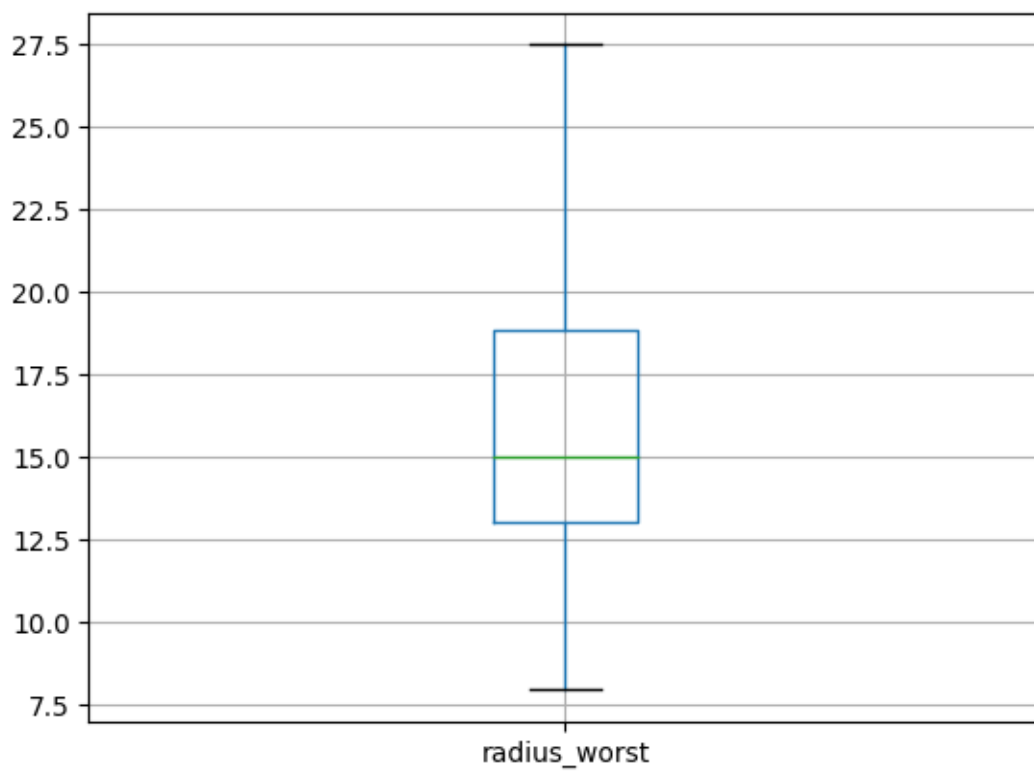
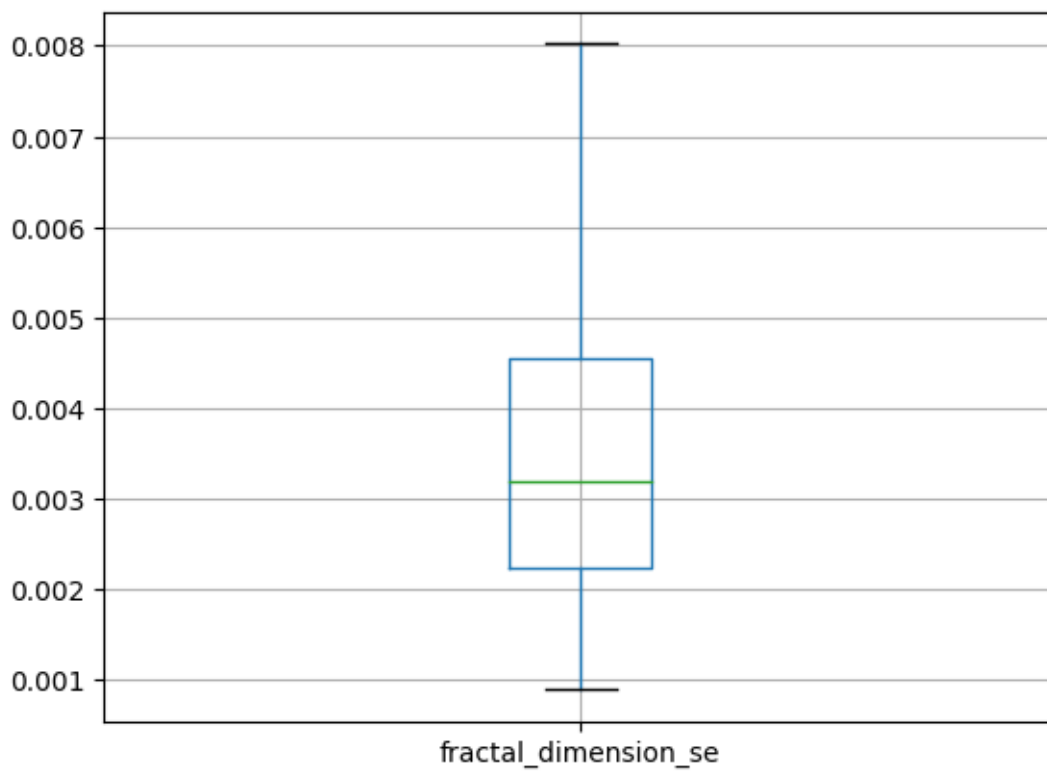


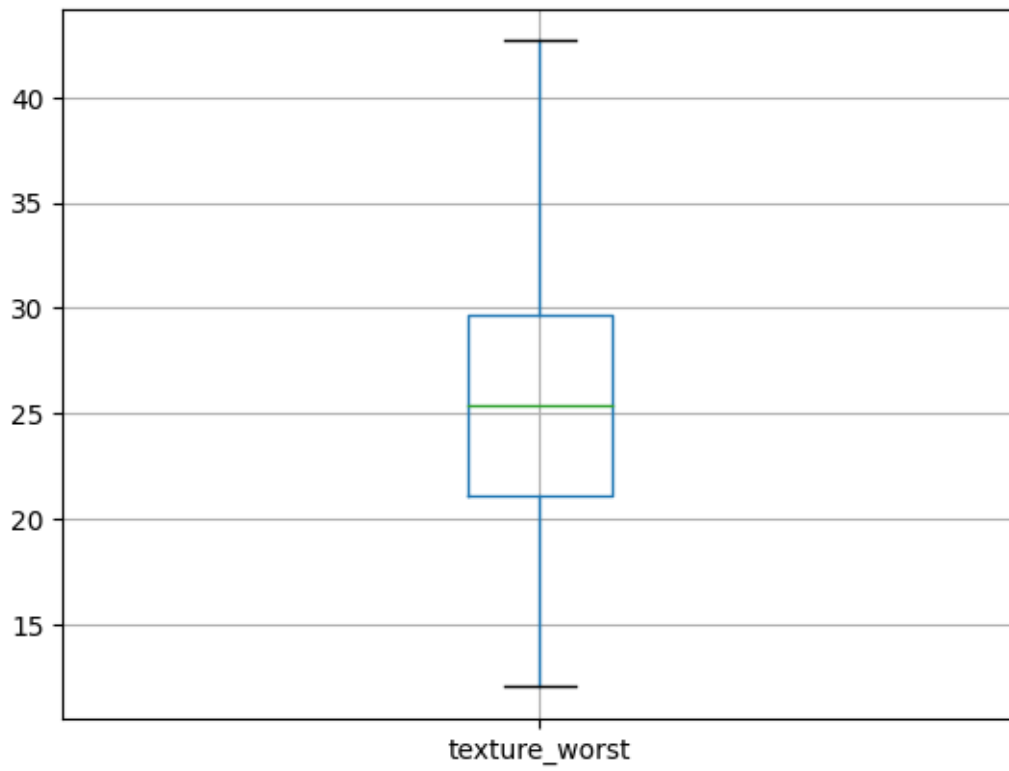


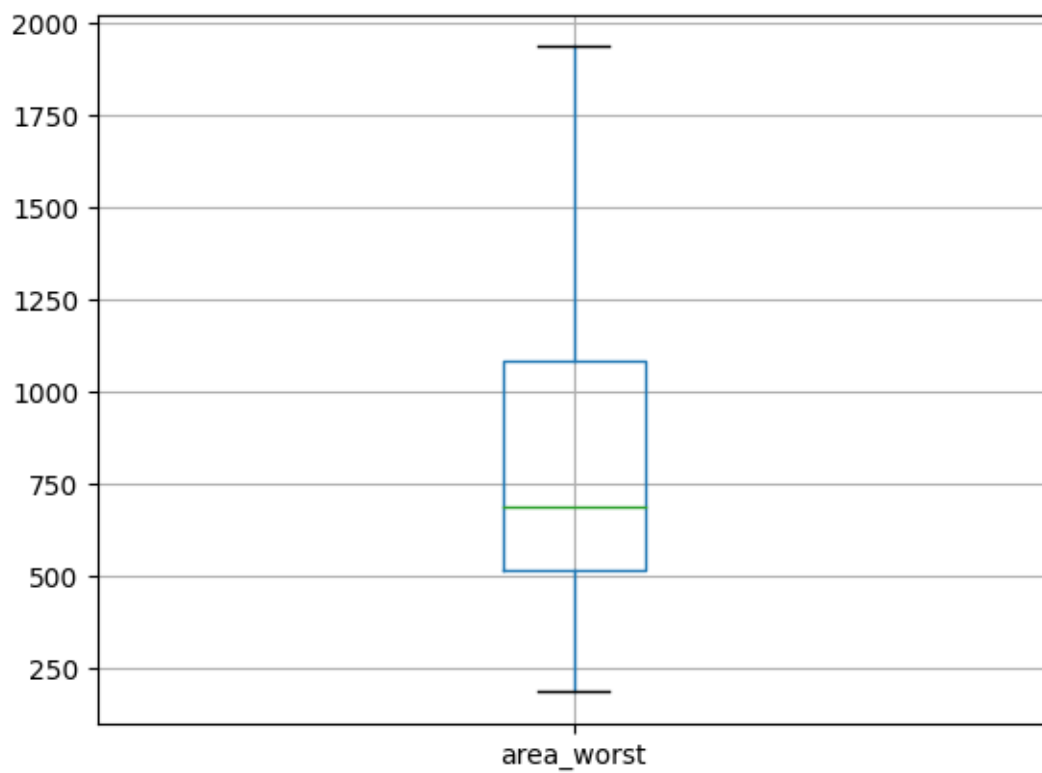
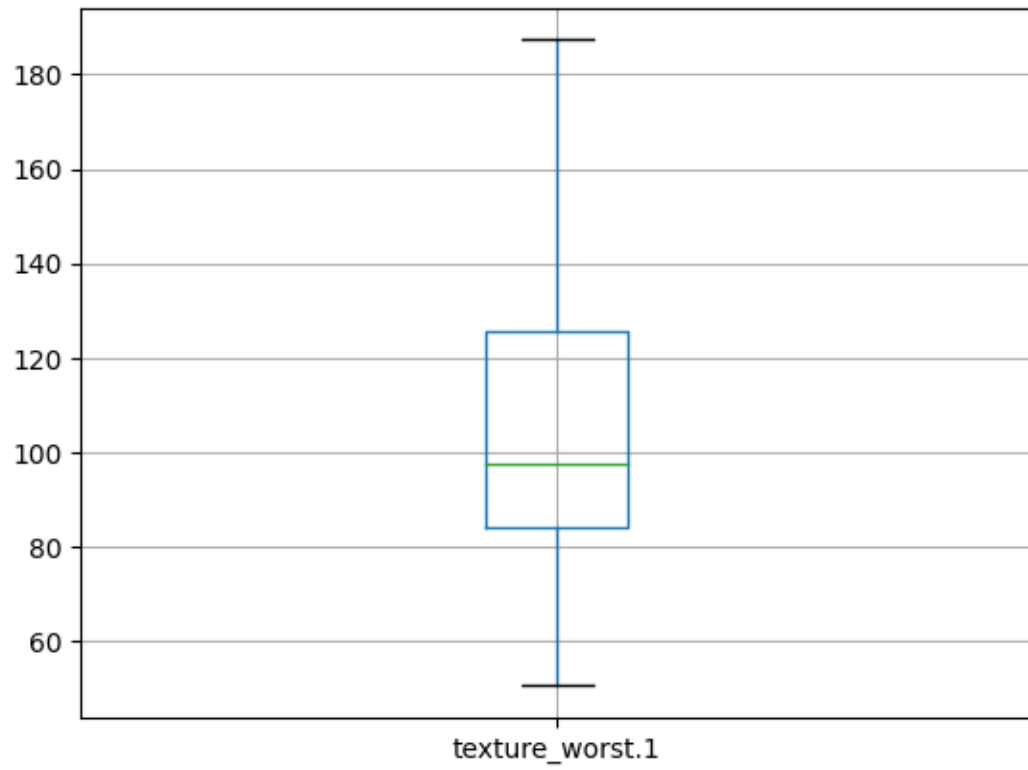


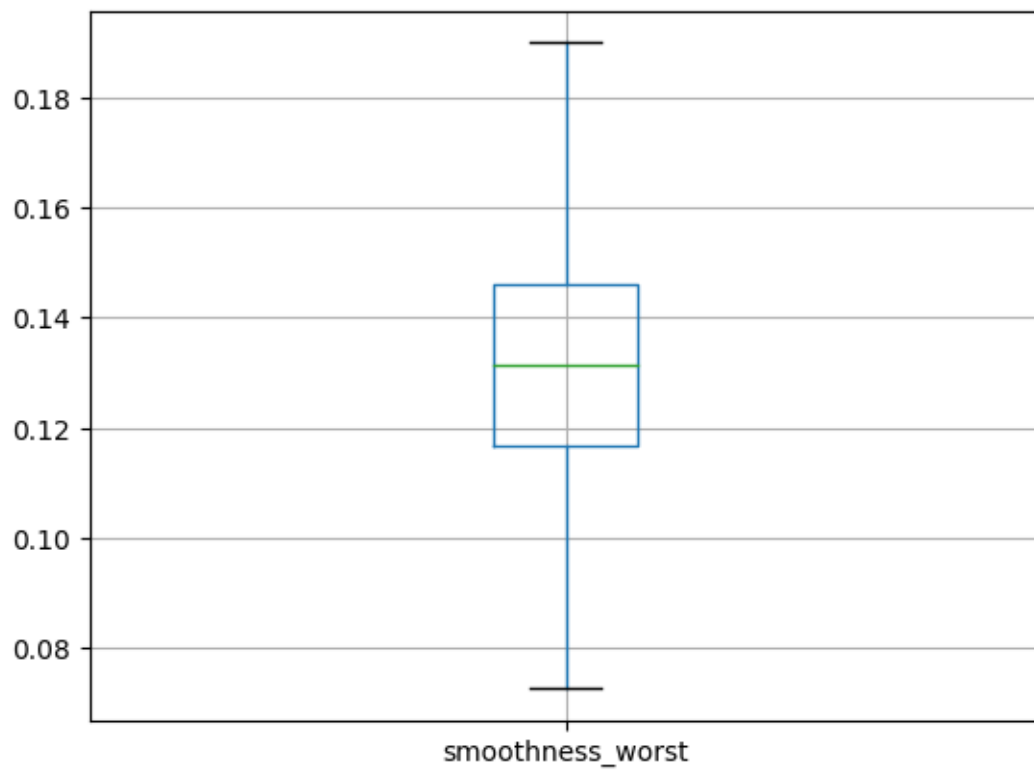


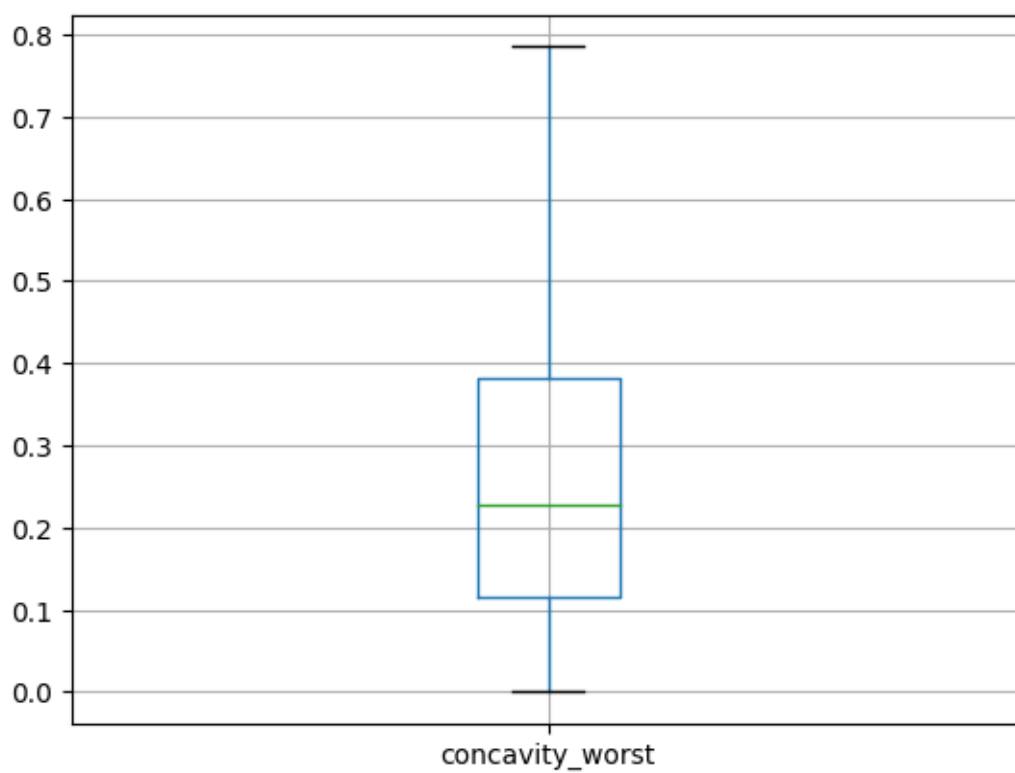
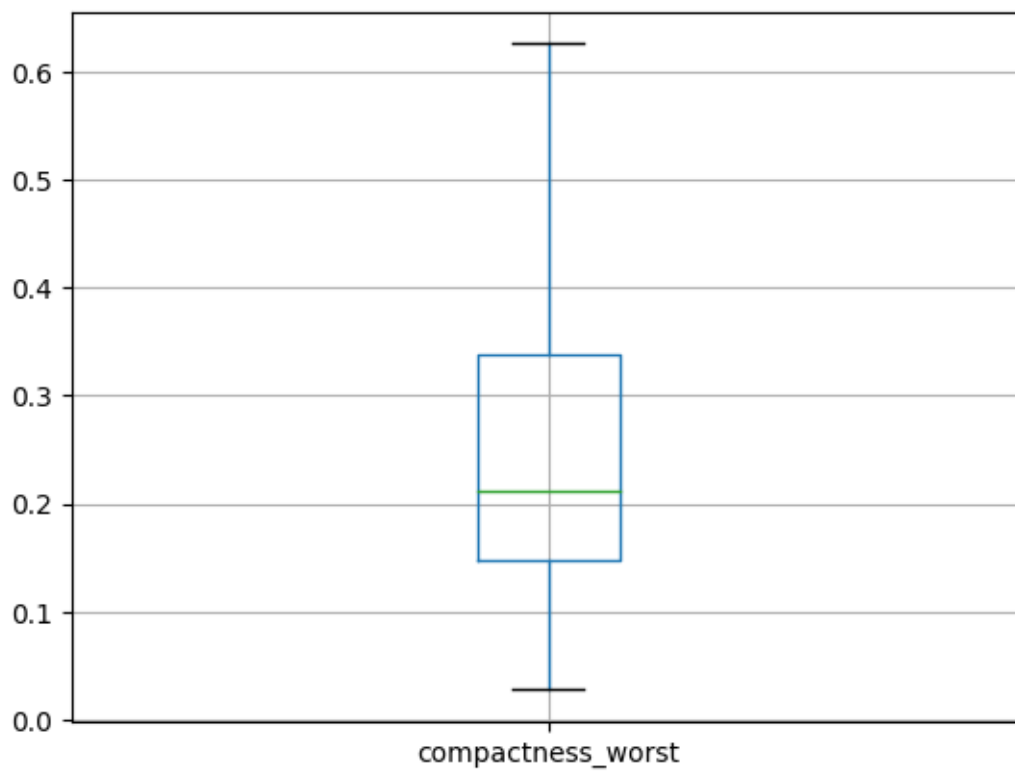


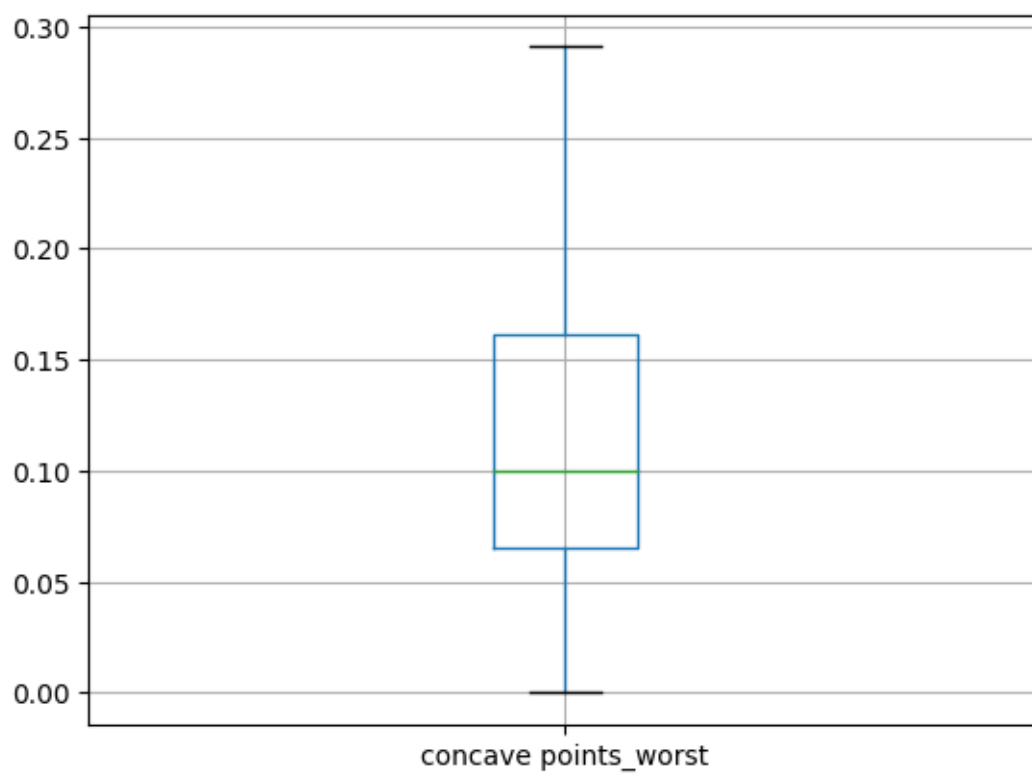


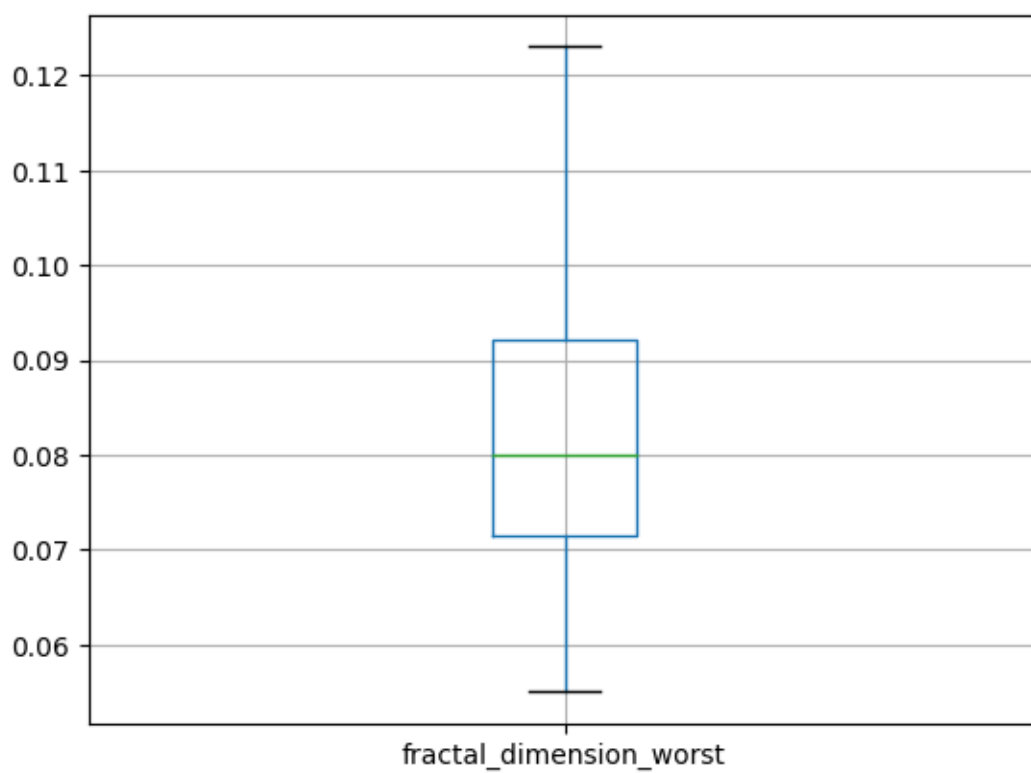
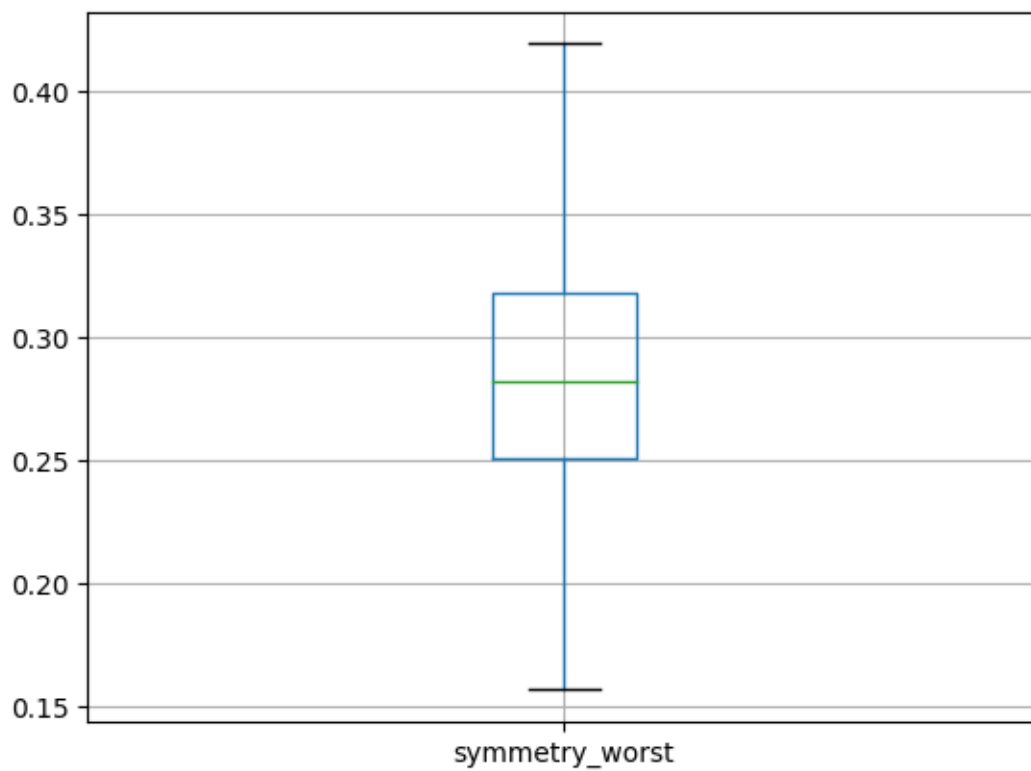








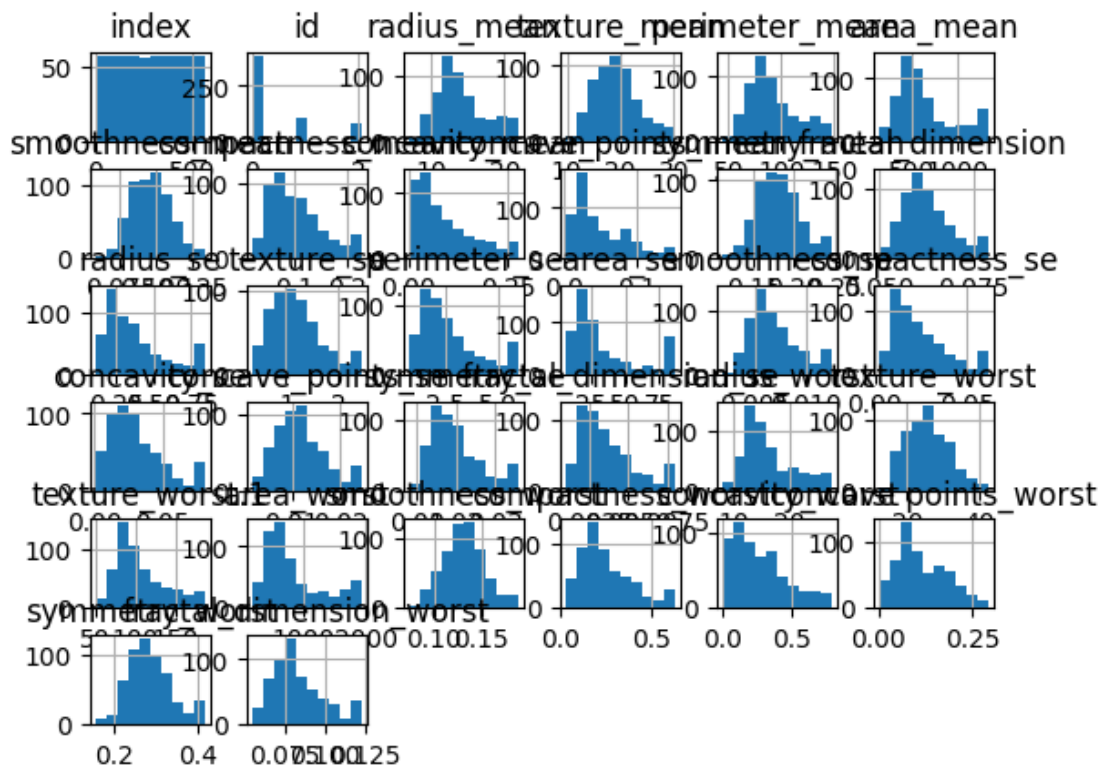




```
[21]: cancer_data.hist()
```

```
[21]: array([[<Axes: title={'center': 'index'}>,
  <Axes: title={'center': 'id'}>,
  <Axes: title={'center': 'radius_mean'}>,
  <Axes: title={'center': 'texture_mean'}>,
  <Axes: title={'center': 'perimeter_mean'}>,
  <Axes: title={'center': 'area_mean'}>],
[<Axes: title={'center': 'smoothness_mean'}>,
  <Axes: title={'center': 'compactness_mean'}>,
  <Axes: title={'center': 'concavity_mean'}>,
  <Axes: title={'center': 'concave_points_mean'}>,
  <Axes: title={'center': 'symmetry_mean'}>,
  <Axes: title={'center': 'fractal_dimension'}>]],
[<Axes: title={'center': 'radius_se'}>,
  <Axes: title={'center': 'texture_se'}>,
  <Axes: title={'center': 'perimeter_se'}>,
  <Axes: title={'center': 'area_se'}>,
  <Axes: title={'center': 'smoothness_se'}>,
  <Axes: title={'center': 'compactness_se'}>],
[<Axes: title={'center': 'concavity_se'}>,
  <Axes: title={'center': 'concave_points_se'}>,
  <Axes: title={'center': 'symmetry_se'}>,
  <Axes: title={'center': 'fractal_dimension_se'}>,
  <Axes: title={'center': 'radius_worst'}>,
  <Axes: title={'center': 'texture_worst'}>],
[<Axes: title={'center': 'texture_worst.1'}>,
  <Axes: title={'center': 'area_worst'}>,
  <Axes: title={'center': 'smoothness_worst'}>,
  <Axes: title={'center': 'compactness_worst'}>,
  <Axes: title={'center': 'concavity_worst'}>,
  <Axes: title={'center': 'concave points_worst'}>]],
[<Axes: title={'center': 'symmetry_worst'}>,
  <Axes: title={'center': 'fractal_dimension_worst'}>, <Axes: >,
  <Axes: >, <Axes: >]], dtype=object)
```





```
[22]: cancer_data.skew()
```

<ipython-input-22-a3ad186019e1>:1: FutureWarning: The default value of numeric\_only in DataFrame.skew is deprecated. In a future version, it will default to False. In addition, specifying 'numeric\_only=None' is deprecated. Select only valid columns or specify the value of numeric\_only to silence this warning.

```
cancer_data.skew()
```

```
[22]: index          0.000000
      id           1.418571
      radius_mean   0.655953
      texture_mean   0.449700
      perimeter_mean 0.701081
      area_mean     0.922884
      smoothness_mean 0.257712
      compactness_mean 0.826755
      concavity_mean 1.030074
      concave_points_mean 1.047545
      symmetry_mean  0.403661
      fractal_dimension 0.682430
      radius_se      1.025031
```

```

texture_se          0.740987
perimeter_se        1.034389
area_se             1.130940
smoothness_se       0.780923
compactness_se      0.990285
concavity_se        0.950588
concave_points_se   0.682343
symmetry_se         0.869297
fractal_dimension_se 0.979344
radius_worst        0.849779
texture_worst       0.386858
texture_worst.1     0.874870
area_worst          1.048970
smoothness_worst    0.247199
compactness_worst   0.919246
concavity_worst     0.808771
concave points_worst 0.492616
symmetry_worst      0.521772
fractal_dimension_worst 0.831581
dtype: float64

```

```
[23]: cancer_data['diagnosis'].value_counts()
```

```

[23]: B    357
      M    212
      Name: diagnosis, dtype: int64

```

```

[24]: from sklearn.preprocessing import LabelEncoder
      # loading the label Encoder function
      label_encode=LabelEncoder()
      labels=label_encode.fit_transform(cancer_data.diagnosis)
      # appending labels to the dataframe
      cancer_data['target']=labels

```

```
[25]: cancer_data['target'].value_counts()
```

```

[25]: 0    357
      1    212
      Name: target, dtype: int64

```

```
[26]: cancer_data
```

```

[26]:   index      id  radius_mean  texture_mean  perimeter_mean  area_mean  \
0      1  842302.0      17.99      10.38      122.80      1001.0
1      2  842517.0      20.57      17.77      132.90      1326.0
2      3  20728995.5      19.69      21.25      130.00      1203.0
3      4  20728995.5      11.42      20.38      77.58      386.1

```

4	5	20728995.5	20.29	14.34	135.10	1297.0
..	...	...	...	...	...	...
564	565	926424.0	21.56	22.39	142.00	1326.3
565	566	926682.0	20.13	28.25	131.20	1261.0
566	567	926954.0	16.60	28.08	108.30	858.1
567	568	927241.0	20.60	29.33	140.10	1265.0
568	569	92751.0	7.76	24.54	47.92	181.0

	smoothness_mean	compactness_mean	concavity_mean	concave_points_mean	\
0	0.118400	0.22862	0.275355	0.147100	
1	0.084740	0.07864	0.086900	0.070170	
2	0.109600	0.15990	0.197400	0.127900	
3	0.133695	0.22862	0.241400	0.105200	
4	0.100300	0.13280	0.198000	0.104300	
..	...	...	...	...	
564	0.111000	0.11590	0.243900	0.138900	
565	0.097800	0.10340	0.144000	0.097910	
566	0.084550	0.10230	0.092510	0.053020	
567	0.117800	0.22862	0.275355	0.151970	
568	0.057975	0.04362	0.064905	0.034605	

	compactness_worst	concavity_worst	concave points_worst	\
0	0.62620	0.7119	0.2654	
1	0.18660	0.2416	0.1860	
2	0.42450	0.4504	0.2430	
3	0.62620	0.6869	0.2575	
4	0.20500	0.4000	0.1625	
..	...	...	...	
564	0.21130	0.4107	0.2216	
565	0.19220	0.3215	0.1628	
566	0.30940	0.3403	0.1418	
567	0.62620	0.7855	0.2650	
568	0.06444	0.0000	0.0000	

	symmetry_worst	fractal_dimension_worst	N Stage	6th Stage	\
0	0.41915	0.11890	N1	IIA	
1	0.27500	0.08902	N2	IIIA	
2	0.36130	0.08758	N3	IIIC	
3	0.41915	0.12301	N1	IIA	
4	0.23640	0.07678	N1	IIB	
..	...	...	...	...	
564	0.20600	0.07115	N2	IIIA	
565	0.25720	0.06637	N2	IIIA	
566	0.22180	0.07820	N1	IIA	
567	0.40870	0.12301	N1	IIA	
568	0.28710	0.07039	N3	IIIC	

	differentiate	diagnosis	target
0	Poorly differentiated	M	1
1	Moderately differentiated	M	1
2	Moderately differentiated	M	1
3	Poorly differentiated	M	1
4	Poorly differentiated	M	1
..	...	...	...
564	Moderately differentiated	M	1
565	Poorly differentiated	M	1
566	Well differentiated	M	1
567	Well differentiated	M	1
568	Well differentiated	B	0

[569 rows x 37 columns]

```
[28]: # data standardization
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score

scaler=StandardScaler()
```

[ ]:

[ ]:	index	id	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	1	842302.0	17.99	10.38	122.80	1001.0	
1	2	842517.0	20.57	17.77	132.90	1326.0	
2	3	20728995.5	19.69	21.25	130.00	1203.0	
3	4	20728995.5	11.42	20.38	77.58	386.1	
4	5	20728995.5	20.29	14.34	135.10	1297.0	
..	...	...	...	...	...	...	
564	565	926424.0	21.56	22.39	142.00	1326.3	
565	566	926682.0	20.13	28.25	131.20	1261.0	
566	567	926954.0	16.60	28.08	108.30	858.1	
567	568	927241.0	20.60	29.33	140.10	1265.0	
568	569	92751.0	7.76	24.54	47.92	181.0	

	smoothness_mean	compactness_mean	concavity_mean	concave_points_mean	\
0	0.118400	0.22862	0.275355	0.147100	
1	0.084740	0.07864	0.086900	0.070170	
2	0.109600	0.15990	0.197400	0.127900	
3	0.133695	0.22862	0.241400	0.105200	
4	0.100300	0.13280	0.198000	0.104300	
..	...	...	...	...	
564	0.111000	0.11590	0.243900	0.138900	
565	0.097800	0.10340	0.144000	0.097910	
566	0.084550	0.10230	0.092510	0.053020	

567	0.117800	0.22862	0.275355	0.151970
568	0.057975	0.04362	0.064905	0.034605

	smoothness_worst	compactness_worst	concavity_worst	\
0	0.16220	0.62620	0.7119	
1	0.12380	0.18660	0.2416	
2	0.14440	0.42450	0.4504	
3	0.19010	0.62620	0.6869	
4	0.13740	0.20500	0.4000	
..	...	...	...	
564	0.14100	0.21130	0.4107	
565	0.11660	0.19220	0.3215	
566	0.11390	0.30940	0.3403	
567	0.16500	0.62620	0.7855	
568	0.08996	0.06444	0.0000	

	concave points_worst	symmetry_worst	fractal_dimension_worst	N Stage	\
0	0.2654	0.41915	0.11890	N1	
1	0.1860	0.27500	0.08902	N2	
2	0.2430	0.36130	0.08758	N3	
3	0.2575	0.41915	0.12301	N1	
4	0.1625	0.23640	0.07678	N1	
..	...	...	...	...	
564	0.2216	0.20600	0.07115	N2	
565	0.1628	0.25720	0.06637	N2	
566	0.1418	0.22180	0.07820	N1	
567	0.2650	0.40870	0.12301	N1	
568	0.0000	0.28710	0.07039	N3	

	6th Stage	differentiate	diagnosis
0	IIA Poorly	differentiated	M
1	IIIA Moderately	differentiated	M
2	IIIC Moderately	differentiated	M
3	IIA Poorly	differentiated	M
4	IIB Poorly	differentiated	M
..	...	...	...
564	IIIA Moderately	differentiated	M
565	IIIA Poorly	differentiated	M
566	IIA Well	differentiated	M
567	IIA Well	differentiated	M
568	IIIC Well	differentiated	B

[569 rows x 36 columns]

```
[32]: from sklearn.linear_model import LogisticRegression
# classifier=LogisticRegression(random_state=16)
# classifier.fit(x_train,y_train)
```

```
[36]: model=LogisticRegression()
```

```
[43]: cancer_data.groupby('target').mean()
```

```
<ipython-input-43-d70956e990b4>:1: FutureWarning: The default value of
numeric_only in DataFrameGroupBy.mean is deprecated. In a future version,
numeric_only will default to False. Either specify numeric_only or select only
columns which should be valid for the function.
```

```
cancer_data.groupby('target').mean()
```

```
[43]:
```

	index	id	radius_mean	texture_mean	perimeter_mean	\
target						
0	320.89916	4.746260e+06	12.146524	17.903445	78.075406	
1	224.54717	5.699931e+06	17.290047	21.530259	114.224033	

	area_mean	smoothness_mean	compactness_mean	concavity_mean	\
target					
0	462.790196	0.092400	0.080085	0.048081	
1	937.784434	0.102776	0.142184	0.155316	

	concave_points_mean	...	radius_worst	texture_worst	\
target		...			
0	0.027032	...	13.379801	23.515070	
1	0.086432	...	20.905849	29.240991	

	texture_worst.1	area_worst	smoothness_worst	compactness_worst	\
target					
0	87.005938	558.899440	0.124934	0.182993	
1	139.878467	1339.954953	0.144462	0.363006	

	concavity_worst	concave points_worst	symmetry_worst	\
target				
0	0.164808	0.074444	0.270236	
1	0.443757	0.182237	0.316884	

	fractal_dimension_worst
target	
0	0.079295
1	0.090159

```
[2 rows x 32 columns]
```

```
[41]: cancer_data
```

```
[41]:
```

	index	id	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	1	842302.0	17.99	10.38	122.80	1001.0	
1	2	842517.0	20.57	17.77	132.90	1326.0	

2	3	20728995.5	19.69	21.25	130.00	1203.0
3	4	20728995.5	11.42	20.38	77.58	386.1
4	5	20728995.5	20.29	14.34	135.10	1297.0
..	...	...	...	...	...	...
564	565	926424.0	21.56	22.39	142.00	1326.3
565	566	926682.0	20.13	28.25	131.20	1261.0
566	567	926954.0	16.60	28.08	108.30	858.1
567	568	927241.0	20.60	29.33	140.10	1265.0
568	569	92751.0	7.76	24.54	47.92	181.0

	smoothness_mean	compactness_mean	concavity_mean	concave_points_mean	\
0	0.118400	0.22862	0.275355	0.147100	
1	0.084740	0.07864	0.086900	0.070170	
2	0.109600	0.15990	0.197400	0.127900	
3	0.133695	0.22862	0.241400	0.105200	
4	0.100300	0.13280	0.198000	0.104300	
..	...	...	...	...	
564	0.111000	0.11590	0.243900	0.138900	
565	0.097800	0.10340	0.144000	0.097910	
566	0.084550	0.10230	0.092510	0.053020	
567	0.117800	0.22862	0.275355	0.151970	
568	0.057975	0.04362	0.064905	0.034605	

	compactness_worst	concavity_worst	concave points_worst	\
0	0.62620	0.7119	0.2654	
1	0.18660	0.2416	0.1860	
2	0.42450	0.4504	0.2430	
3	0.62620	0.6869	0.2575	
4	0.20500	0.4000	0.1625	
..	...	...	...	
564	0.21130	0.4107	0.2216	
565	0.19220	0.3215	0.1628	
566	0.30940	0.3403	0.1418	
567	0.62620	0.7855	0.2650	
568	0.06444	0.0000	0.0000	

	symmetry_worst	fractal_dimension_worst	N Stage	6th Stage	\
0	0.41915	0.11890	N1	IIA	
1	0.27500	0.08902	N2	IIIA	
2	0.36130	0.08758	N3	IIIC	
3	0.41915	0.12301	N1	IIA	
4	0.23640	0.07678	N1	IIB	
..	...	...	...	...	
564	0.20600	0.07115	N2	IIIA	
565	0.25720	0.06637	N2	IIIA	
566	0.22180	0.07820	N1	IIA	
567	0.40870	0.12301	N1	IIA	

568            0.28710                    0.07039            N3            IIIC

	differentiate	diagnosis	target
0	Poorly differentiated	M	1
1	Moderately differentiated	M	1
2	Moderately differentiated	M	1
3	Poorly differentiated	M	1
4	Poorly differentiated	M	1
..	...	...	...
564	Moderately differentiated	M	1
565	Poorly differentiated	M	1
566	Well differentiated	M	1
567	Well differentiated	M	1
568	Well differentiated	B	0

[569 rows x 37 columns]

```
[53]: new_cancer_data=cancer_data.drop(columns='diagnosis',axis=1)
```

```
[49]: string_columns = cancer_data.select_dtypes(include=['object']).columns
```

```
[50]: string_columns
```

```
[50]: Index(['N Stage', '6th Stage', 'differentiate', 'diagnosis'], dtype='object')
```

```
[51]: cancer_data
```

```
[51]:
```

	index	id	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	1	842302.0	17.99	10.38	122.80	1001.0	
1	2	842517.0	20.57	17.77	132.90	1326.0	
2	3	20728995.5	19.69	21.25	130.00	1203.0	
3	4	20728995.5	11.42	20.38	77.58	386.1	
4	5	20728995.5	20.29	14.34	135.10	1297.0	
..	...	...	...	...	...	...	
564	565	926424.0	21.56	22.39	142.00	1326.3	
565	566	926682.0	20.13	28.25	131.20	1261.0	
566	567	926954.0	16.60	28.08	108.30	858.1	
567	568	927241.0	20.60	29.33	140.10	1265.0	
568	569	92751.0	7.76	24.54	47.92	181.0	

	smoothness_mean	compactness_mean	concavity_mean	concave_points_mean	\
0	0.118400	0.22862	0.275355	0.147100	
1	0.084740	0.07864	0.086900	0.070170	
2	0.109600	0.15990	0.197400	0.127900	
3	0.133695	0.22862	0.241400	0.105200	
4	0.100300	0.13280	0.198000	0.104300	
..	...	...	...	...	



564	0.111000	0.11590	0.243900	0.138900
565	0.097800	0.10340	0.144000	0.097910
566	0.084550	0.10230	0.092510	0.053020
567	0.117800	0.22862	0.275355	0.151970
568	0.057975	0.04362	0.064905	0.034605

	...	compactness_worst	concavity_worst	concave points_worst	\
0	...	0.62620	0.7119	0.2654	
1	...	0.18660	0.2416	0.1860	
2	...	0.42450	0.4504	0.2430	
3	...	0.62620	0.6869	0.2575	
4	...	0.20500	0.4000	0.1625	
..	...	...	...	...	
564	...	0.21130	0.4107	0.2216	
565	...	0.19220	0.3215	0.1628	
566	...	0.30940	0.3403	0.1418	
567	...	0.62620	0.7855	0.2650	
568	...	0.06444	0.0000	0.0000	

	symmetry_worst	fractal_dimension_worst	N Stage	6th Stage	\
0	0.41915	0.11890	N1	IIA	
1	0.27500	0.08902	N2	IIIA	
2	0.36130	0.08758	N3	IIIC	
3	0.41915	0.12301	N1	IIA	
4	0.23640	0.07678	N1	IIB	
..	...	...	...	...	
564	0.20600	0.07115	N2	IIIA	
565	0.25720	0.06637	N2	IIIA	
566	0.22180	0.07820	N1	IIA	
567	0.40870	0.12301	N1	IIA	
568	0.28710	0.07039	N3	IIIC	

	differentiate	diagnosis	target
0	Poorly differentiated	M	1
1	Moderately differentiated	M	1
2	Moderately differentiated	M	1
3	Poorly differentiated	M	1
4	Poorly differentiated	M	1
..	...	...	...
564	Moderately differentiated	M	1
565	Poorly differentiated	M	1
566	Well differentiated	M	1
567	Well differentiated	M	1
568	Well differentiated	B	0

[569 rows x 37 columns]

```
[52]: cancer_data.shape
```

```
[52]: (569, 37)
```

```
[54]: new_cancer_data
```

```
[54]:
```

	index	id	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	1	842302.0	17.99	10.38	122.80	1001.0	
1	2	842517.0	20.57	17.77	132.90	1326.0	
2	3	20728995.5	19.69	21.25	130.00	1203.0	
3	4	20728995.5	11.42	20.38	77.58	386.1	
4	5	20728995.5	20.29	14.34	135.10	1297.0	
..	...	...	...	...	...	...	
564	565	926424.0	21.56	22.39	142.00	1326.3	
565	566	926682.0	20.13	28.25	131.20	1261.0	
566	567	926954.0	16.60	28.08	108.30	858.1	
567	568	927241.0	20.60	29.33	140.10	1265.0	
568	569	92751.0	7.76	24.54	47.92	181.0	

	smoothness_mean	compactness_mean	concavity_mean	concave_points_mean	\
0	0.118400	0.22862	0.275355	0.147100	
1	0.084740	0.07864	0.086900	0.070170	
2	0.109600	0.15990	0.197400	0.127900	
3	0.133695	0.22862	0.241400	0.105200	
4	0.100300	0.13280	0.198000	0.104300	
..	...	...	...	...	
564	0.111000	0.11590	0.243900	0.138900	
565	0.097800	0.10340	0.144000	0.097910	
566	0.084550	0.10230	0.092510	0.053020	
567	0.117800	0.22862	0.275355	0.151970	
568	0.057975	0.04362	0.064905	0.034605	

	smoothness_worst	compactness_worst	concavity_worst	\
0	0.16220	0.62620	0.7119	
1	0.12380	0.18660	0.2416	
2	0.14440	0.42450	0.4504	
3	0.19010	0.62620	0.6869	
4	0.13740	0.20500	0.4000	
..	...	...	...	
564	0.14100	0.21130	0.4107	
565	0.11660	0.19220	0.3215	
566	0.11390	0.30940	0.3403	
567	0.16500	0.62620	0.7855	
568	0.08996	0.06444	0.0000	

	concave points_worst	symmetry_worst	fractal_dimension_worst	N Stage	\
0	0.2654	0.41915	0.11890	N1	

1	0.1860	0.27500	0.08902	N2
2	0.2430	0.36130	0.08758	N3
3	0.2575	0.41915	0.12301	N1
4	0.1625	0.23640	0.07678	N1
..	...	...	...	...
564	0.2216	0.20600	0.07115	N2
565	0.1628	0.25720	0.06637	N2
566	0.1418	0.22180	0.07820	N1
567	0.2650	0.40870	0.12301	N1
568	0.0000	0.28710	0.07039	N3

	6th Stage		differentiate	target
0	IIA	Poorly	differentiated	1
1	IIIA	Moderately	differentiated	1
2	IIIC	Moderately	differentiated	1
3	IIA	Poorly	differentiated	1
4	IIB	Poorly	differentiated	1
..	...		...	...
564	IIIA	Moderately	differentiated	1
565	IIIA	Poorly	differentiated	1
566	IIA	Well	differentiated	1
567	IIA	Well	differentiated	1
568	IIIC	Well	differentiated	0

[569 rows x 36 columns]

```
[56]: string_columns = new_cancer_data.select_dtypes(include=['object']).columns
```

```
[57]: string_columns
```

```
[57]: Index(['N Stage', '6th Stage', 'differentiate'], dtype='object')
```

```
[58]: # now convert all string column into integer value
new_cancer_data['6th Stage'].value_counts()
```

```
[58]: IIA      194
IIB      150
IIIA     142
IIIC      77
IIIB       6
Name: 6th Stage, dtype: int64
```

```
[60]: # separate data and labels in to apply logistic regression
features=new_cancer_data.drop(columns='target',axis=1);
tar=new_cancer_data['target']
```

```
[61]: x_train,x_test, y_train,y_test=train_test_split(features,tar,test_size=0.2,
↳random_state=2)
```

```
[62]: print(features.shape,x_train.shape, x_test.shape)
```

```
(569, 35) (455, 35) (114, 35)
```

```
[64]: new_cancer_data=new_cancer_data.drop(columns='N Stage',axis=1)
new_cancer_data=new_cancer_data.drop(columns='6th Stage',axis=1)
new_cancer_data=new_cancer_data.drop(columns='differentiate',axis=1)
```

```
[66]: new_cancer_data.shape
```

```
[66]: (569, 33)
```

```
[67]: # separate data and labels in to apply logistic regression
features=new_cancer_data.drop(columns='target',axis=1);
tar=new_cancer_data['target']
```

```
[68]: x_train,x_test, y_train,y_test=train_test_split(features,tar,test_size=0.2,
↳random_state=2)
```

```
[69]: print(features.shape,x_train.shape, x_test.shape)
```

```
(569, 32) (455, 32) (114, 32)
```

```
[70]: model.fit(x_train,y_train)
```

```
[70]: LogisticRegression()
```

```
[71]: # model evaluation apply on training data

x_train_pred=model.predict(x_train)
train_data_accuracy=accuracy_score(y_train,x_train_pred)
```

```
[72]: print("Accuracy score of the train data ", train_data_accuracy)
```

```
Accuracy score of the train data  0.6329670329670329
```

```
[73]: # model evaluation apply on test data
x_test_pred=model.predict(x_test)
test_data_accuracy=accuracy_score(y_test,x_test_pred)
```

```
[74]: print("Accuracy score of the test data ", test_data_accuracy)
```

```
Accuracy score of the test data  0.6052631578947368
```

```
[ ]:
```