Assignment 2

February 9, 2025

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

[2]:
```
df=pd.read_csv("Cancer_data.csv")
```

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

[3]:

	mean_radius	mean_texture	mean_perimeter	mean_area	mean_smoothness	\
0	17.99	10.38	122.80	1001.0	0.11840	
1	20.57	17.77	132.90	1326.0	0.08474	
2	19.69	21.25	130.00	1203.0	0.10960	
3	11.42	20.38	77.58	386.1	0.14250	
4	20.29	14.34	135.10	1297.0	0.10030	

	diagnosis
0	0
1	0
2	0
3	0
4	0

[4]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 6 columns):
 #   Column           Non-Null Count  Dtype  
---  ------           --------------  -----  
 0   mean_radius      564 non-null    float64
 1   mean_texture     562 non-null    float64
 2   mean_perimeter   563 non-null    float64
 3   mean_area        562 non-null    float64
 4   mean_smoothness  566 non-null    float64
 5   diagnosis        569 non-null    int64  
dtypes: float64(5), int64(1)
memory usage: 26.8 KB
```

[5]:
```
df.describe()
```

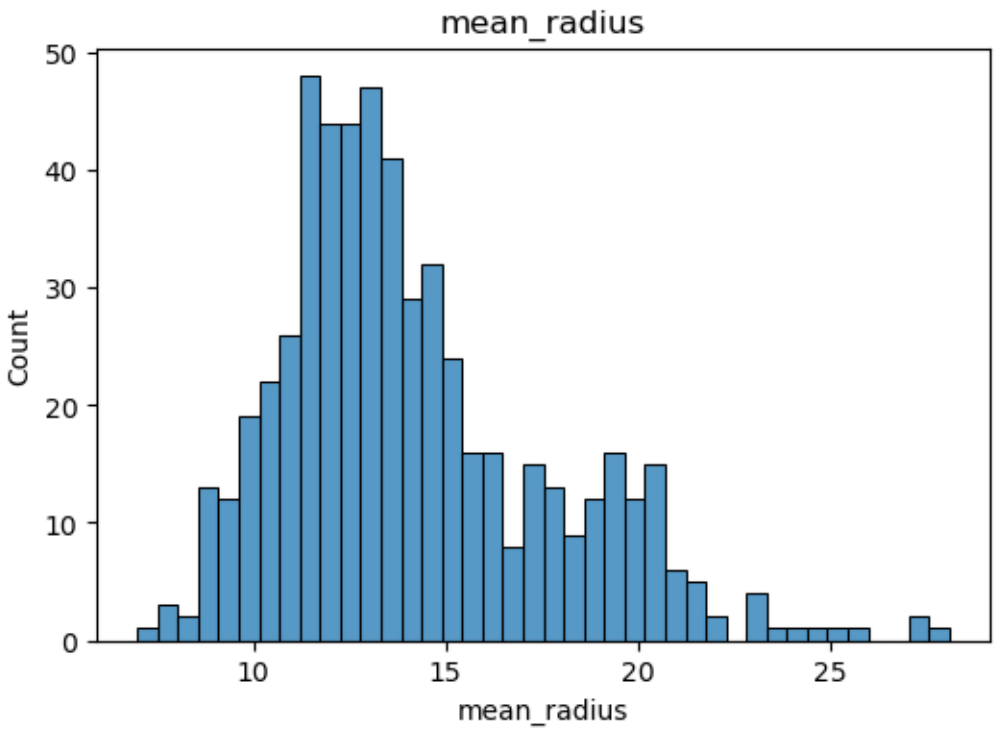
[5]:

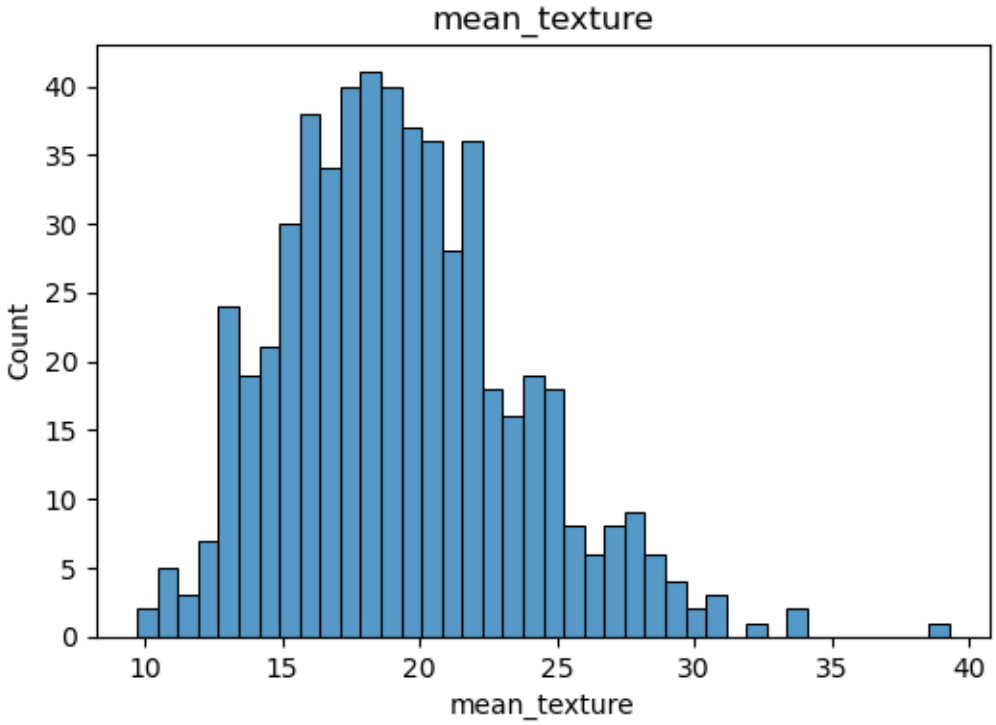
	mean_radius	mean_texture	mean_perimeter	mean_area	\
count	564.000000	562.000000	563.000000	562.000000	
mean	14.131346	19.305534	92.098934	655.263345	
std	3.538116	4.318572	24.347809	352.660038	
min	6.981000	9.710000	43.790000	143.500000	
25%	11.687500	16.172500	75.190000	419.925000	
50%	13.355000	18.880000	86.240000	548.750000	
75%	15.892500	21.817500	104.500000	787.050000	
max	28.110000	39.280000	188.500000	2501.000000	

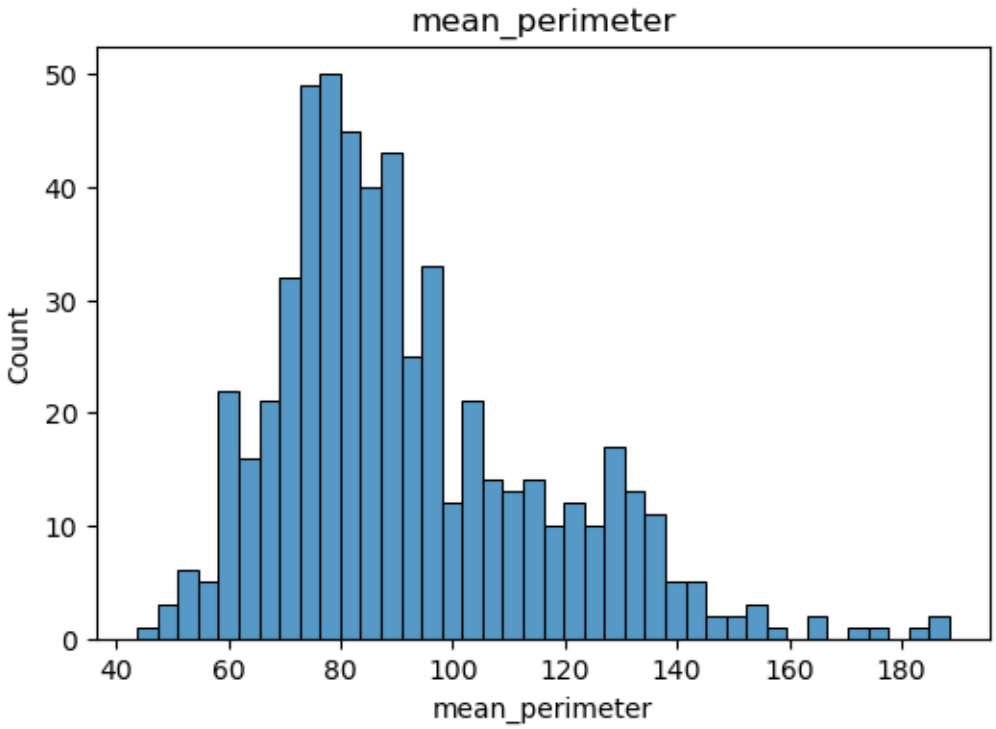
	mean_smoothness	diagnosis
count	566.000000	569.000000
mean	0.096296	0.627417
std	0.014035	0.483918
min	0.052630	0.000000
25%	0.086130	0.000000
50%	0.095825	1.000000
75%	0.105300	1.000000
max	0.163400	1.000000

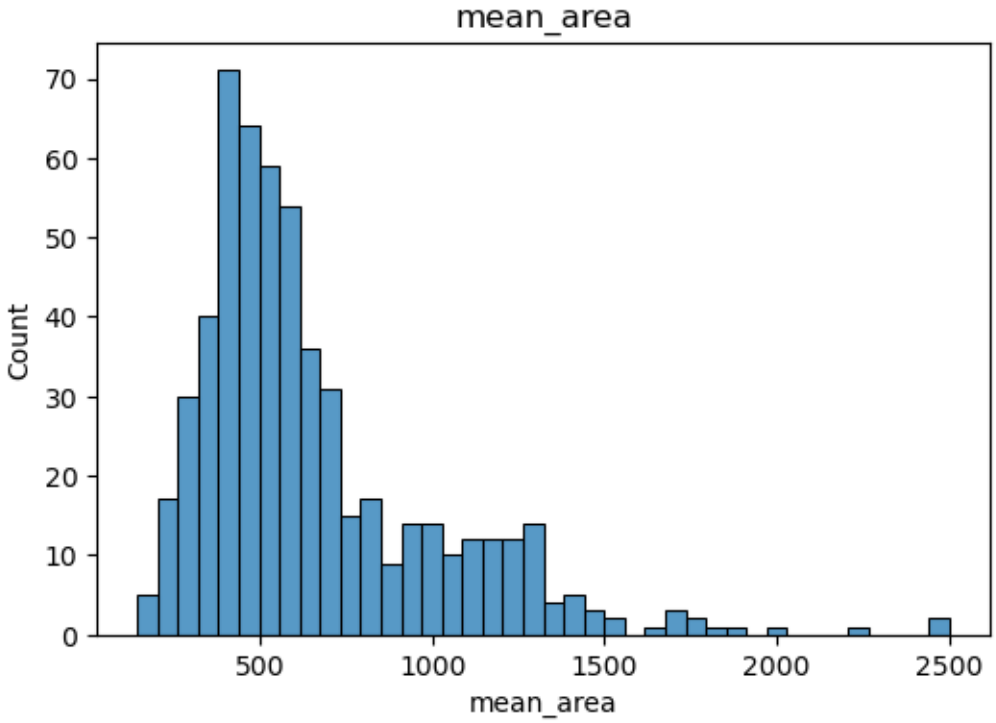
There are a total of 5 features of 569 entries. Every single feature has null values in it. One label column with the values of 0's and 1's. 1 saying Yes and 0 saying No. Every rest feature is continous in nature. mean_smoothness looks normalized with a max value of 0.163400

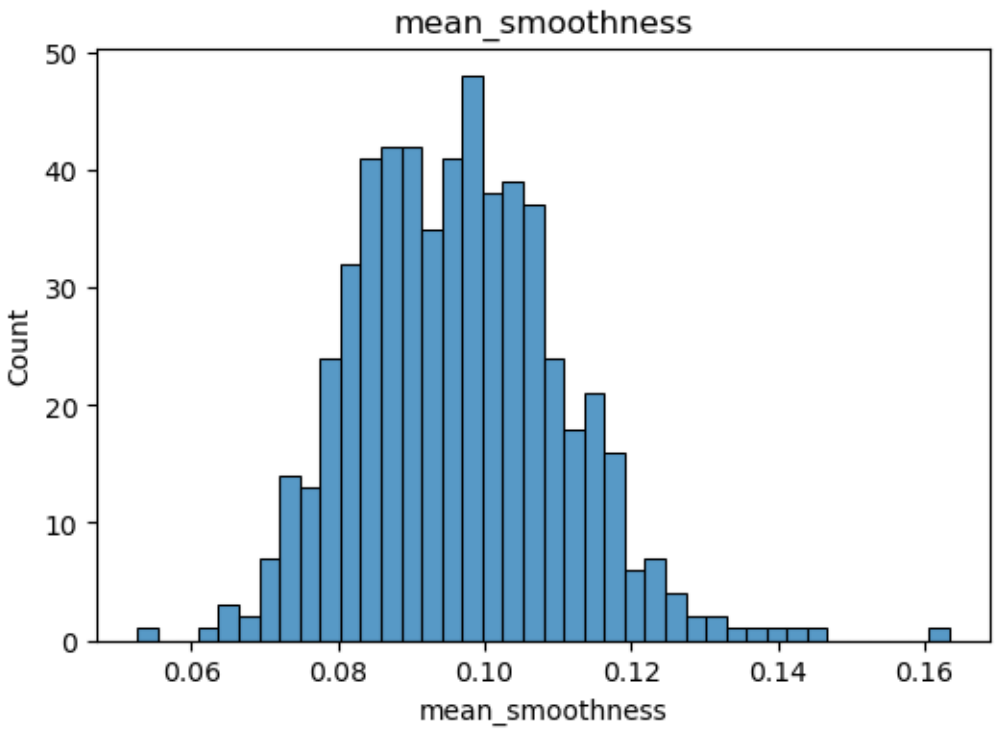
[6]:
```
for column in df.columns:
    if df[column].dtype=='float64':
        plt.figure(figsize=(6,4))
        sns.histplot(df[column],bins=40)
        plt.title(column)
        plt.show()
```


mean_radius
Count
mean_radius
0
10
20
30
40
50
10
15
20
25


mean_texture
Count
mean_texture
0
5
10
15
20
25
30
35
40
10
15
20
25
30
35
40


mean_perimeter
Count
mean_perimeter
0
10
20
30
40
50
40
60
80
100
120
140
160
180

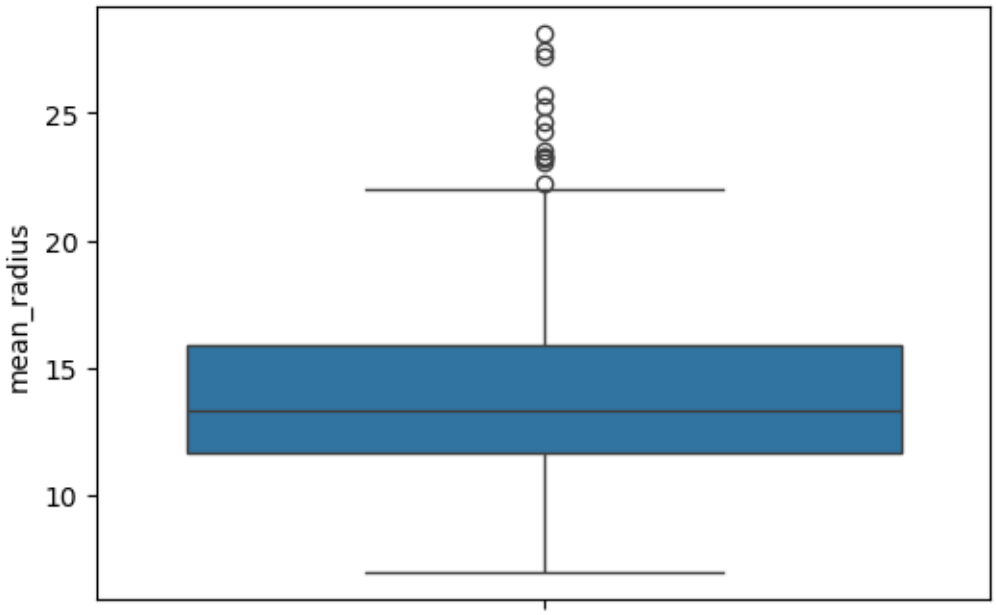

mean_area
Count
mean_area
0
10
20
30
40
50
60
70
500
1000
1500
2000
2500



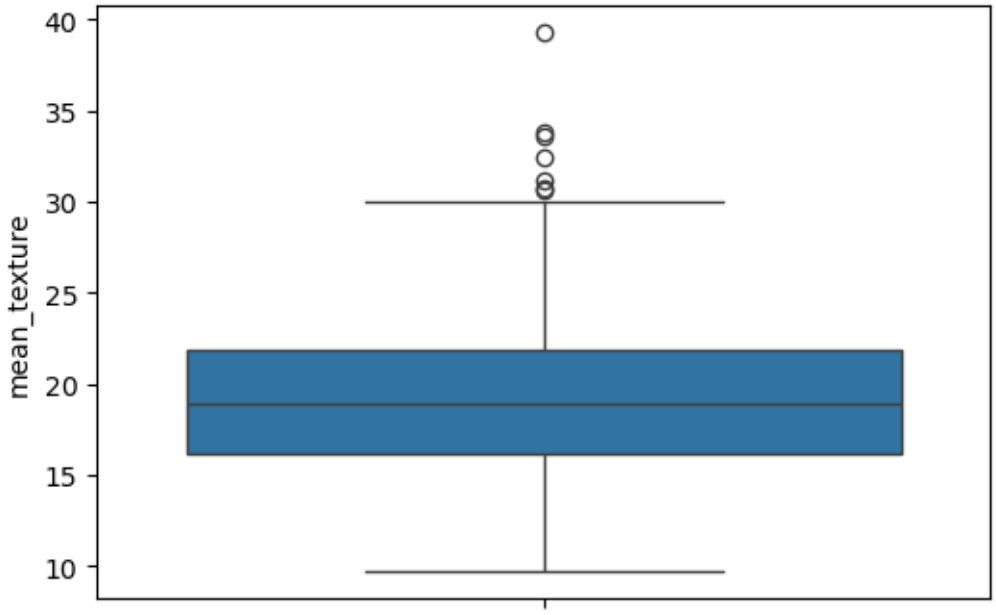
All the features except mean_smoothness are left skewed and all of them might probably have outliers. All have single peak.

0.1 Outlier Handling

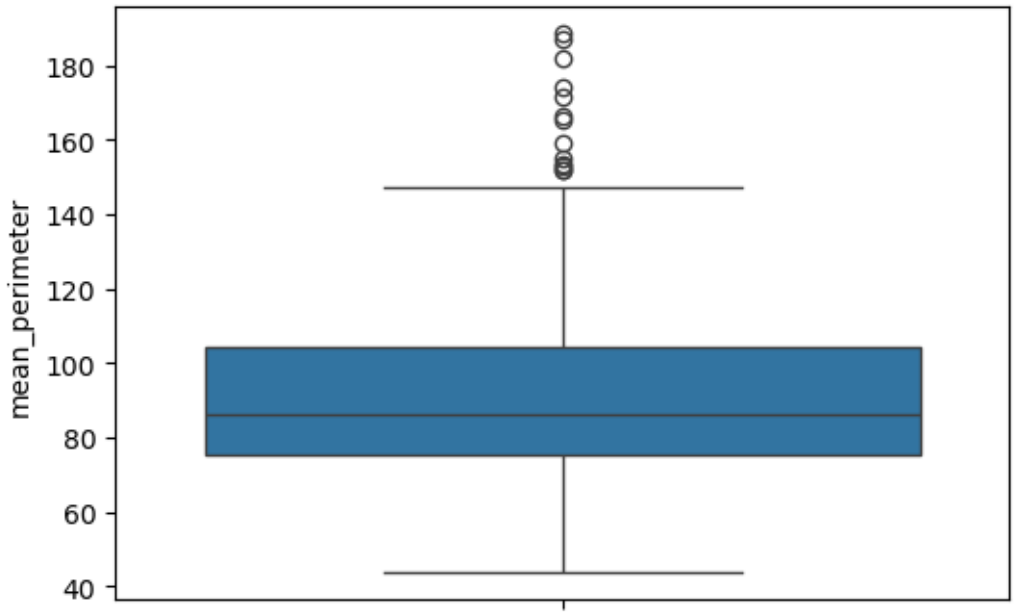
[7]:
```
for column in df.columns:
    if df[column].dtype=='float64':
        plt.figure(figsize=(6,4))
        sns.boxplot(df[column])
        plt.show()
        print("95%:",df[column].quantile(0.95))
        print("5%:",df[column].quantile(0.05))
```



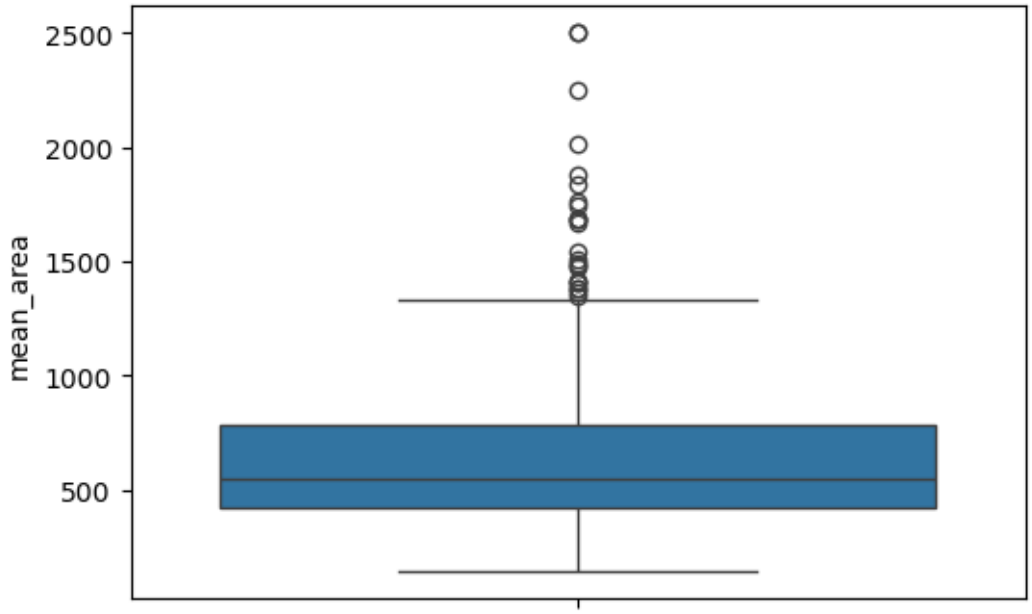
95%: 20.5785
5%: 9.51345



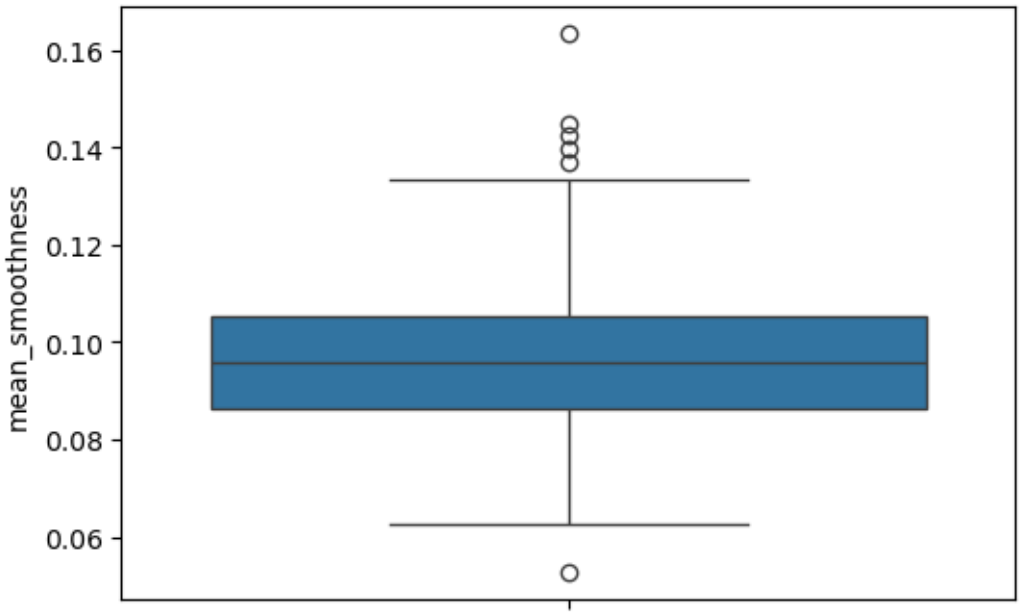
95%: 27.15
5%: 13.081



95%: 135.88
5%: 60.762



95%: 1310.85
5%: 278.65000000000003




```
95%: 0.1186
5%: 0.075015
```

[8]:
```
df['mean_radius']=np.where(df['mean_radius']>20.5785,20.5785,df['mean_radius'])
df['mean_texture']=np.where(df['mean_texture']>27.15,27.15,df['mean_texture'])
df['mean_perimeter']=np.where(df['mean_perimeter']>135.88,135.
 ↪88,df['mean_perimeter'])
df['mean_area']=np.where(df['mean_area']>1310.85,1310.85,df['mean_area'])
df['mean_smoothness']=np.where(df['mean_smoothness']>0.1186,0.
 ↪1186,df['mean_smoothness'])
df['mean_smoothness']=np.where(df['mean_smoothness']<0.075015,0.
 ↪075015,df['mean_smoothness'])
```

0.1.1 Handling missing values

[9]:
```
df.isna().sum()
```

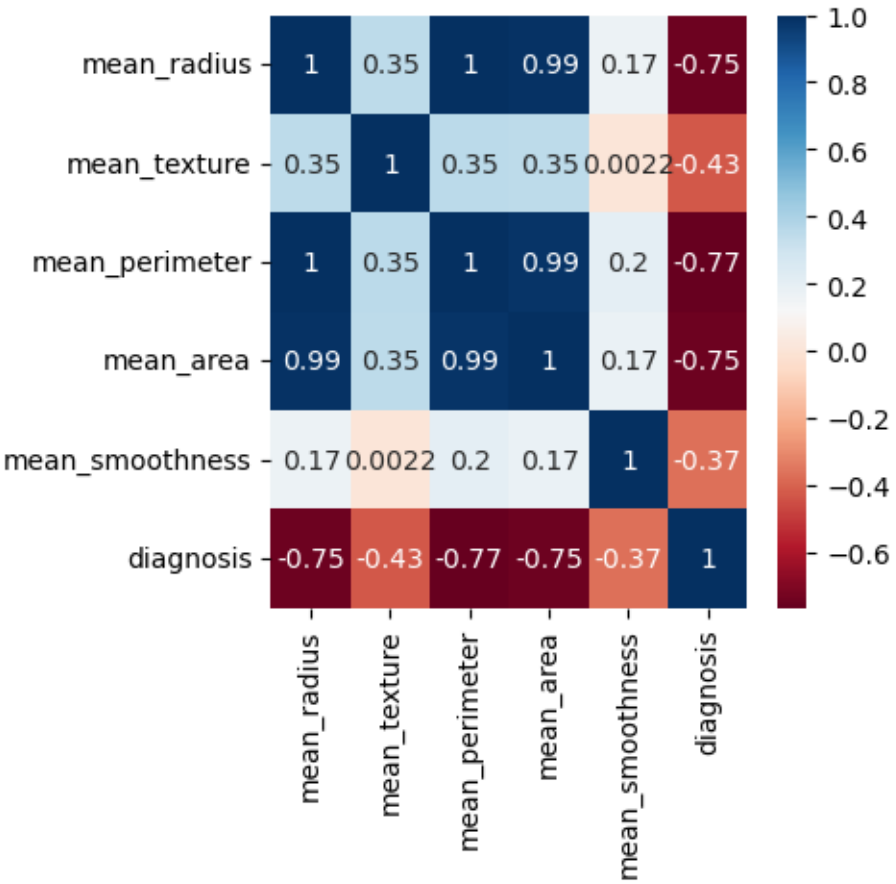
[9]:
```
mean_radius         5
mean_texture        7
mean_perimeter      6
mean_area           7
mean_smoothness     3
diagnosis           0
dtype: int64
```

[10]:
```
for column in df.columns:
    if df[column].dtype=='float64':
        df[column]=df[column].fillna(df[column].median())
```

0.1.2 Standardization

[11]:
```
 for column in df.columns:
     if df[column].dtype=='float64':
         df[column]=((df[column]-df[column].mean())/df[column].std())
```

[12]:
```
fig,ax=plt.subplots(figsize=(4,4))
sns.heatmap(df.corr(numeric_only=True),annot=True,cmap="RdBu")
plt.show()
```



As we can see that mean_perimeter, mean_area and mean_radius are highly correlated, using all of them would probably cause multicollinearity. Hence, we would be using only mean_radius and dropping mean_perimeter and mean_area

[13]:
```
df=df.drop(['mean_perimeter','mean_area'],axis=1)
```

0.1.3 Logistic Regression Model

[14]:
```
y=df['diagnosis']
X=df.drop('diagnosis',axis=1)
```

[15]:
```
from sklearn.model_selection import train_test_split
X_train,X_test,y_train,y_test=train_test_split(X,y,test_size=0.
 ↪2,random_state=42)
```

[16]:
```
from sklearn.linear_model import LogisticRegression

logreg=LogisticRegression(solver='lbfgs',max_iter=1000)
logreg.fit(X_train,y_train)
```

[16]:
```
LogisticRegression(max_iter=1000)
```

[17]:
```
y_pred=logreg.predict(X_test)
```

[18]:
```
from sklearn.metrics import confusion_matrix,classification_report
cnf_mx=confusion_matrix(y_test,y_pred)
cnf_mx
```

[18]:
```
array([[41,  2],
       [ 2, 69]])
```

[19]:
```
print(classification_report(y_test,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.95      0.95      0.95        43
           1       0.97      0.97      0.97        71

    accuracy                           0.96       114
   macro avg       0.96      0.96      0.96       114
weighted avg       0.96      0.96      0.96       114
```

The model has 96% accuracy

[20]:
```
import pickle
model_pickle_file="Cancer_pkl"
with open(model_pickle_file,'wb') as file:
    pickle.dump(logreg,file)
```