STATS 3DA3

Homework Assignment 6

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2024-04-16

Question 1

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.preprocessing import StandardScaler
```

```
kidney = pd.read_csv("/Users/echo/Desktop/Stats 3DA3 desktop/3da_ass_6/kidney_disease.csv")
kidney.head()
```

	id	age	bp	sg	al	su	rbc	pc	pcc	ba	...	pcv	wc	rc	h
0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	...	44	7800	5.2	y
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	...	38	6000	NaN	n
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	...	31	7500	NaN	n
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32	6700	3.9	y
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	...	35	7300	4.6	n

```
#kidney = pd.read_csv("/Users/cassie/Library/Mobile Documents/com~apple~CloudDocs/Document/202
#kidney.head()
```

The dataset is from Rubini and Eswaran (2015). The classification problem based on this dataset is to predict whether a patient will develop chronic kidney disease or not, using health-related attributes such as age, blood presure, red blood cells and so on.

Question 2

```
kidney = kidney.drop('id', axis=1)
```

```
kidney.describe()
```

	age	bp	sg	al	su	bgr	bu	sc
count	391.000000	388.000000	353.000000	354.000000	351.000000	356.000000	381.000000	383.000000
mean	51.483376	76.469072	1.017408	1.016949	0.450142	148.036517	57.425722	3.072454
std	17.169714	13.683637	0.005717	1.352679	1.099191	79.281714	50.503006	5.741126
min	2.000000	50.000000	1.005000	0.000000	0.000000	22.000000	1.500000	0.400000
25%	42.000000	70.000000	1.010000	0.000000	0.000000	99.000000	27.000000	0.900000
50%	55.000000	80.000000	1.020000	0.000000	0.000000	121.000000	42.000000	1.300000
75%	64.500000	80.000000	1.020000	2.000000	0.000000	163.000000	66.000000	2.800000
max	90.000000	180.000000	1.025000	5.000000	5.000000	490.000000	391.000000	76.000000

```
kidney.dtypes
```

```
age              float64
bp               float64
sg               float64
al               float64
su               float64
rbc               object
pc                object
pcc               object
ba                object
bgr              float64
bu               float64
sc               float64
sod              float64
pot              float64
hemo             float64
pcv               object
wc                object
```

```
rc                object
htn               object
dm                object
cad               object
appet             object
pe                object
ane               object
classification    object
dtype: object
```

```
kidney['rbc'] = kidney['rbc'].replace({'normal': 1, 'abnormal': 0})
kidney['pc'] = kidney['pc'].replace({'normal': 1, 'abnormal': 0})
kidney['pcc'] = kidney['pcc'].replace({'present': 1, 'notpresent': 0})
kidney['ba'] = kidney['ba'].replace({'present': 1, 'notpresent': 0})
kidney['htn'] = kidney['htn'].replace({'yes': 1, 'no': 0})
kidney['dm'] = kidney['dm'].replace({'yes': 1, 'no': 0})
kidney['cad'] = kidney['cad'].replace({'yes': 1, 'no': 0})
kidney['appet'] = kidney['appet'].replace({'good': 1, 'poor': 0})
kidney['pe'] = kidney['pe'].replace({'yes': 1, 'no': 0})
kidney['ane'] = kidney['ane'].replace({'yes': 1, 'no': 0})
kidney['classification'] = kidney['classification'].replace({'ckd': 1, 'notckd': 0})
```

```
kidney['pcv'] = pd.to_numeric(kidney['pcv'], errors='coerce')
kidney['wc'] = pd.to_numeric(kidney['wc'], errors='coerce')
kidney['rc'] = pd.to_numeric(kidney['rc'], errors='coerce')
```

```
num_col = ['age', 'bp', 'sg', 'al', 'su', 'bgr', 'bu', 'sc', 'sod', 'pot', 'hemo', 'pcv', 'wc'
bi_col = ['rbc', 'pc', 'pcc', 'ba', 'htn', 'dm', 'cad', 'appet', 'pe', 'ane']
```

```
scaler = StandardScaler()
kidney[num_col] = scaler.fit_transform(kidney[num_col])
kidney
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv
0	-0.203139	0.258373	0.454071	-0.012548	-0.410106	NaN	1.0	0.0	0.0	-0.341498	...	0.56988
1	-2.594124	-1.936857	0.454071	2.208413	-0.410106	NaN	1.0	0.0	0.0	NaN	...	-0.09853
2	0.613295	0.258373	-1.297699	0.727772	2.323069	1.0	1.0	0.0	0.0	3.473064	...	-0.87835
3	-0.203139	-0.473370	-2.173584	2.208413	-0.410106	1.0	0.0	1.0	0.0	-0.392022	...	-0.76695
4	-0.028189	0.258373	-1.297699	0.727772	-0.410106	1.0	1.0	0.0	0.0	-0.530963	...	-0.43274
...	...	...	...	...	...	...	...	...	...	...	...	...
395	0.205078	0.258373	0.454071	-0.752868	-0.410106	1.0	1.0	0.0	0.0	-0.101509	...	0.90409
396	-0.553039	-0.473370	1.329955	-0.752868	-0.410106	1.0	1.0	0.0	0.0	-0.922524	...	1.68391
397	-2.302541	0.258373	0.454071	-0.752868	-0.410106	1.0	1.0	0.0	0.0	-0.606749	...	1.12689
398	-2.010957	-1.205114	1.329955	-0.752868	-0.410106	1.0	1.0	0.0	0.0	-0.429915	...	1.34970
399	0.380028	0.258373	1.329955	-0.752868	-0.410106	1.0	1.0	0.0	0.0	-0.215188	...	1.57250

First, we choose to drop vairable `id` from the dataset, because this column doesn't provide any useful informartion for our analysis or modeling.

Also, from the output we see that there are both numerical and categorical features, and we observe that most of the categorical features are binary. Therefore, to simplify the data representation and analysis, we consider transforming the bianry features into numeric representations, using 0 and 1. The numeric transformation is performed taking careful consideration of the original meaning of each categories for different binary features. For instance, in the `rbc` variable, we transform category 'normal' as 1 and 'abnormal' as 0.

Moreover, we transformed `pcv`, `wc`, `rc` to numeric variables, because they are all in ordinal form.

Lastly, we want to ensure that all the features have the same scale, so we standardized all the numerical features.

Question 3

```
import warnings
warnings.simplefilter(action='ignore', category=FutureWarning)
```

```
warnings.filterwarnings('ignore', category=UserWarning, module='seaborn')
warnings.filterwarnings('ignore')
```

```
kidney.shape
```

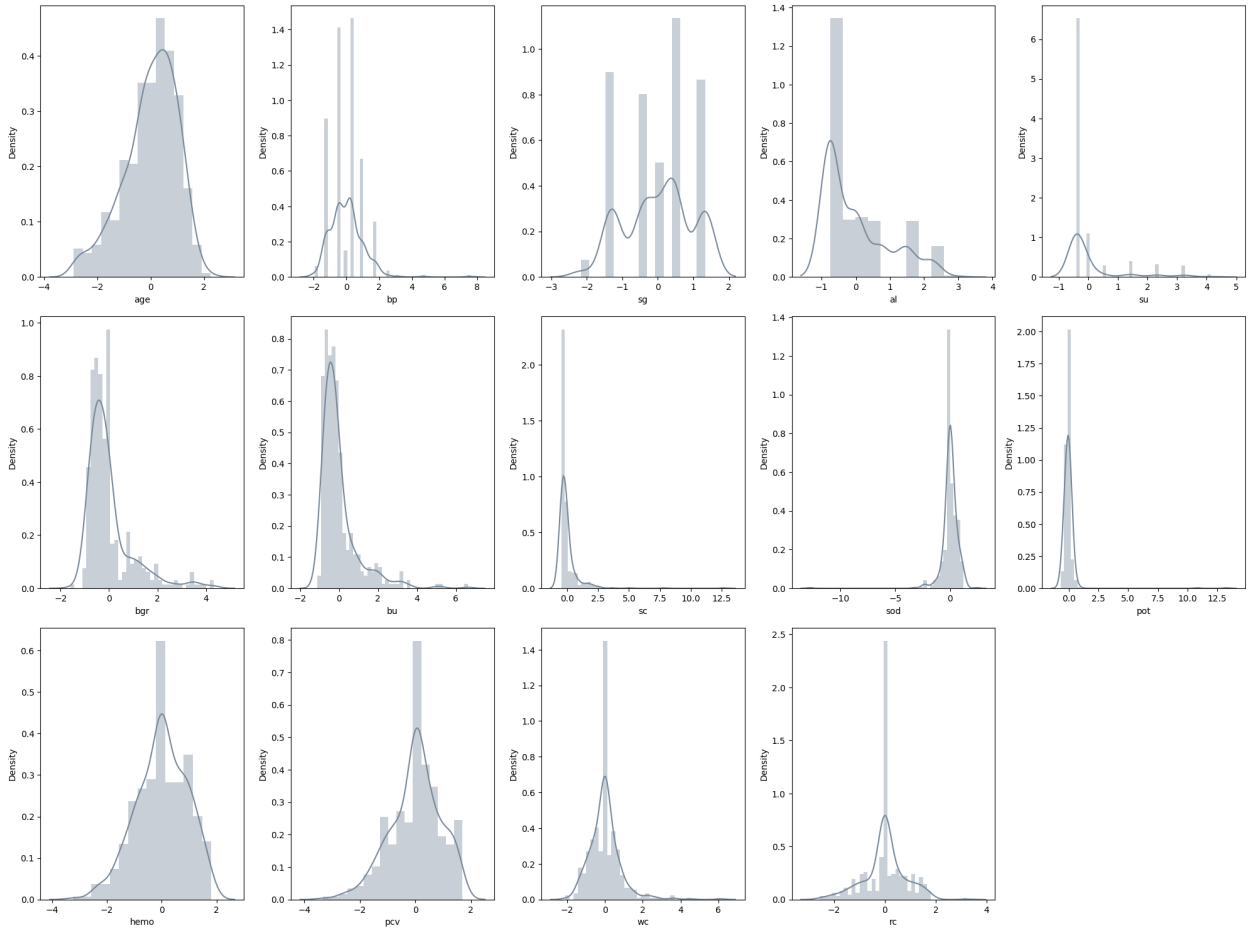
```
(400, 25)
```

```
kidney.dtypes
```

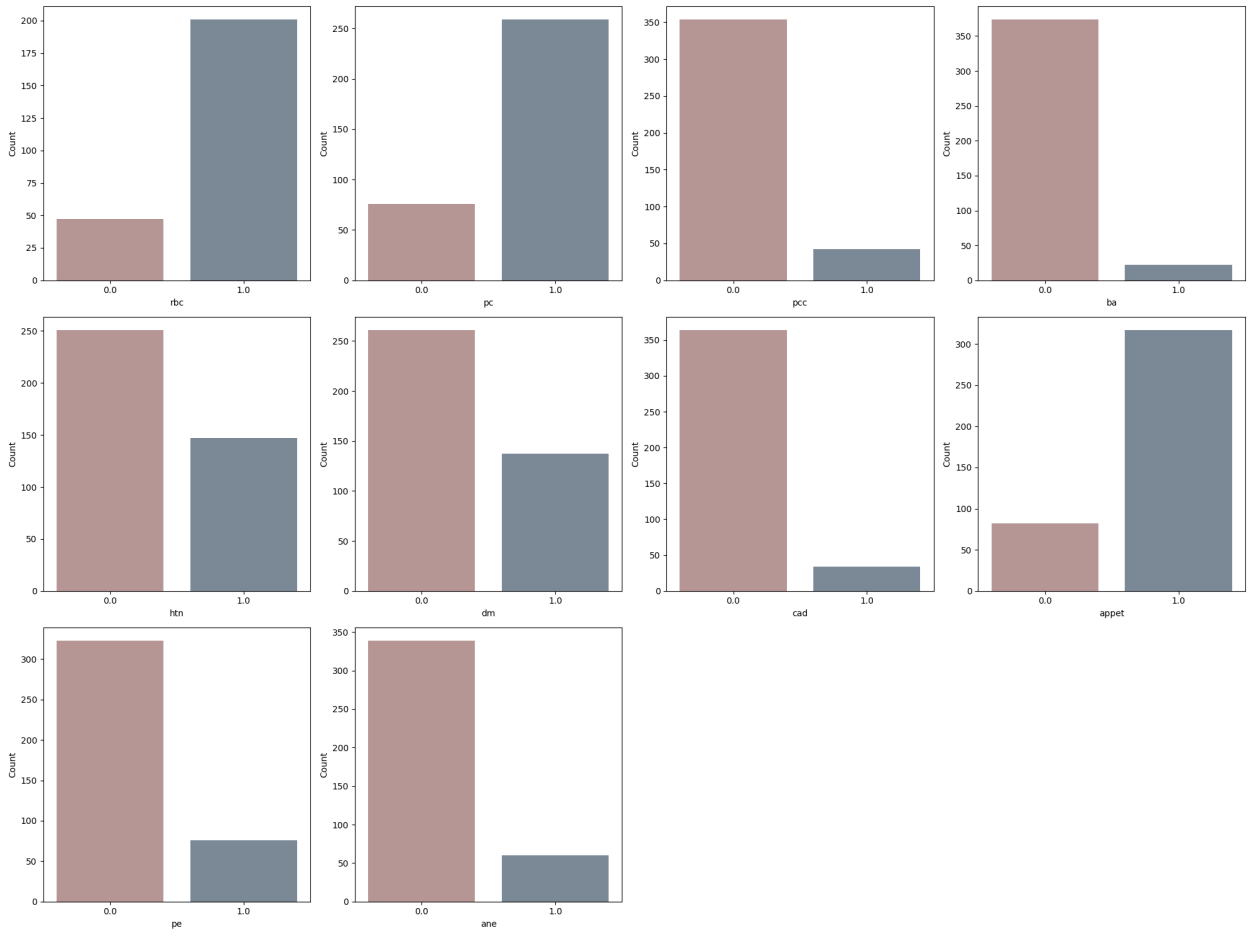
```
age             float64
bp              float64
sg              float64
al              float64
su              float64
rbc             float64
pc              float64
pcc             float64
ba              float64
bgr             float64
bu              float64
sc              float64
sod             float64
pot             float64
hemo            float64
pcv             float64
wc              float64
rc              float64
htn             float64
dm              float64
cad             float64
appet           float64
pe              float64
```

```
ane                 float64
classification        int64
dtype: object
```

```
plt.figure(figsize=(20, 15))
for i, col in enumerate(num_col, 1):
    plt.subplot(3, 5, i)
    sns.distplot(kidney[col], color='#778899')
    plt.xlabel(col)

plt.tight_layout()
plt.show()
```

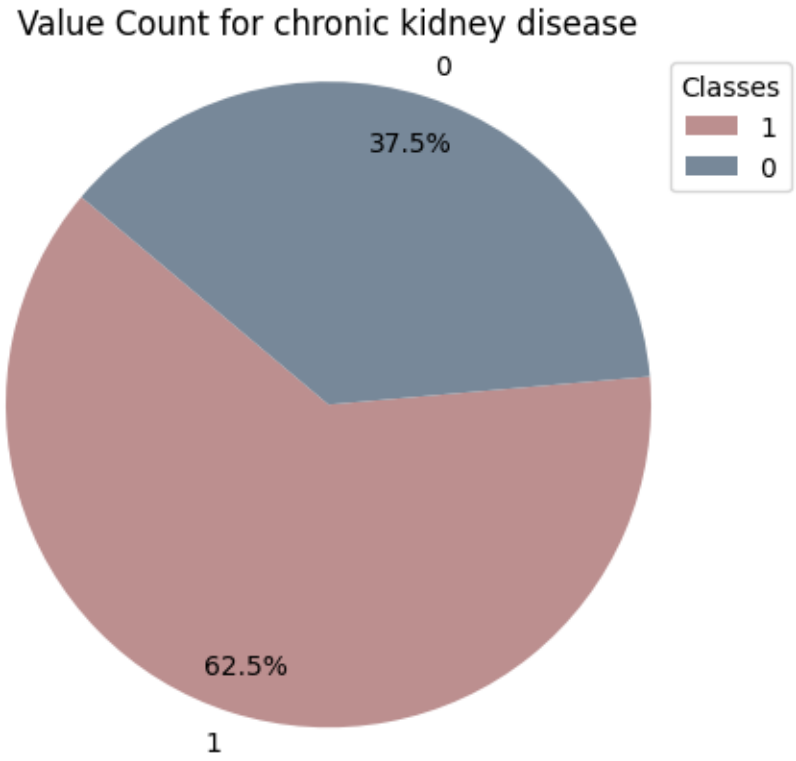


```
plt.figure(figsize=(20, 15))
for i, column in enumerate(bi_col, 1):
    plt.subplot(3, 4, i)
    sns.countplot(data=kidney, x=column, palette=['rosybrown','#778899'])
    plt.xlabel(column)
    plt.ylabel('Count')

plt.tight_layout()
plt.show()
```




```
value_counts = kidney['classification'].value_counts()
categories = value_counts.index
counts = value_counts.values
```

```
colors = ['rosybrown', '#778899']
plt.pie(counts, labels=categories, autopct='%1.1f%%', startangle=140, pctdistance=0.85, colors=
plt.axis('equal')
plt.title('Value Count for chronic kidney disease')
plt.legend(categories, title='Classes', loc='best')
plt.show()
```



After the variable transformation done in Question2...

The dataset contains 400 observations and 25 columns, with 24 features and one target variable, `class`, which indicates the presence or absence of chronoic kidney disease.

There are the features in the datased are: Age (age), Blood Pressure (bp), Specific Gravity (sg), Albumin (al), Sugar (su), Red Blood Cells (rbc), Pus Cell (pc), Pus Cell Clumps (pcc), Bacteria (ba), Blood Glucose Random (bgr), Blood Urea (bu), Serum Creatinine (sc), Sodium (sod), Potassium (pot), Hemoglobin (hemo), Packed Cell Volume (pcv), White Blood Cell Count (wc), Red Blood Cell Count (rc), Hypertension (htn), Diabetes Mellitus (dm), Coronary Artery Disease (cad), Appetite (appet), Pedal Edema (pe), Anemia (ane).

From the plots we can see that the distribution for variable `bu` is right-skewed, which indicates that there are more patients with high blood urea levels and fewer patients with low levels.

Also, it's clear from the count plot that around 200 patients have normal red blood cell.

What's more, the pie chart shows that approximately 62.5% of the observations have chronic kidney disease.

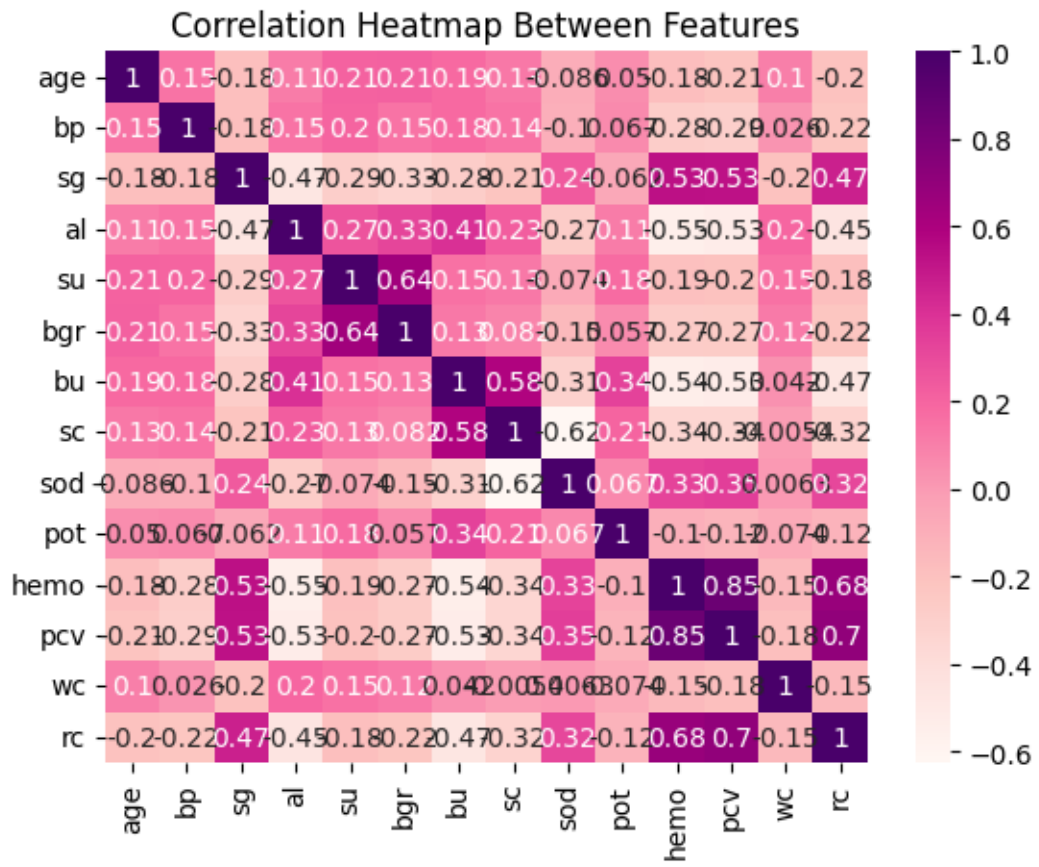
Question 4

```
df_num = kidney[num_col].apply(lambda x: x.fillna(x.mean()), axis=0)
df_num
```

	age	bp	sg	al	su	bgr	bu	sc	sod
0	-0.203139	0.258373	0.454071	-0.012548	-0.410106	-3.414983e-01	-0.424804	-0.326574	2.27010
1	-2.594124	-1.936857	0.454071	2.208413	-0.410106	-1.796316e-16	-0.781687	-0.396338	2.27010
2	0.613295	0.258373	-1.297699	0.727772	2.323069	3.473064e+00	-0.087748	-0.221928	2.27010
3	-0.203139	-0.473370	-2.173584	2.208413	-0.410106	-3.920223e-01	-0.028268	0.126891	-2.55277
4	-0.028189	0.258373	-1.297699	0.727772	-0.410106	-5.309633e-01	-0.623073	-0.291692	2.27010
...	...	...	...	...	...	...	...	...	...
395	0.205078	0.258373	0.454071	-0.752868	-0.410106	-1.015093e-01	-0.167055	-0.448661	1.20006
396	-0.553039	-0.473370	1.329955	-0.752868	-0.410106	-9.225244e-01	-0.523939	-0.326574	3.34027
397	-2.302541	0.258373	0.454071	-0.752868	-0.410106	-6.067493e-01	-0.623073	-0.431220	-5.08803
398	-2.010957	-1.205114	1.329955	-0.752868	-0.410106	-4.299153e-01	-0.147229	-0.361456	-2.43334
399	0.380028	0.258373	1.329955	-0.752868	-0.410106	-2.151883e-01	-0.781687	-0.344015	3.34027

```
correlation_matrix = df_num.corr()
sns.heatmap(correlation_matrix, annot=True, cmap='RdPu')
plt.title('Correlation Heatmap Between Features')
```

```
Text(0.5, 1.0, 'Correlation Heatmap Between Features')
```



From the heatmap we can observe that variables `bgr` and `su` have strong positive correlation (0.64), which suggests that as the amount of sugar increases, there is a tendency for the level of blood glucose random to increase as well.

Also, we find that `sc` and `bu` are positively correlated as well, with correlation of 0.58, which implies that pateints with higher blood urea may have a higher level of serum creatinine.

Also, with the correlation of -0.62, the variables `sod` and `sc` are the most negtively correlated, so we can say that as serum creatinine decreases, there is a strong tendency for the level of sodium to increase.

Question 5

```
missings = kidney.isnull().sum()
missings
```

```
age                9
bp                12
sg                47
al                46
su                49
rbc              152
pc                65
pcc                4
ba                 4
bgr               44
bu                19
sc                17
sod               87
pot               88
hemo              52
pcv               71
wc               106
rc               131
htn                2
dm                 2
cad                2
appet              1
pe                 1
ane                1
classification     0
dtype: int64
```

```
mean = kidney[num_col].mean()
kidney[num_col] = kidney[num_col].fillna(mean)


mode = kidney.mode().iloc[0]
kidney[bi_col] = kidney[bi_col].fillna(mode)
```

```
kidney.head()
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv
0	-0.203139	0.258373	0.454071	-0.012548	-0.410106	1.0	1.0	0.0	0.0	-3.414983e-01	...	0.56988
1	-2.594124	-1.936857	0.454071	2.208413	-0.410106	1.0	1.0	0.0	0.0	-1.796316e-16	...	-0.0985
2	0.613295	0.258373	-1.297699	0.727772	2.323069	1.0	1.0	0.0	0.0	3.473064e+00	...	-0.8783
3	-0.203139	-0.473370	-2.173584	2.208413	-0.410106	1.0	0.0	1.0	0.0	-3.920223e-01	...	-0.7669
4	-0.028189	0.258373	-1.297699	0.727772	-0.410106	1.0	1.0	0.0	0.0	-5.309633e-01	...	-0.4327

```
missings = kidney.isnull().sum()
missings
```

```
age     0
bp      0
sg      0
al      0
su      0
rbc     0
pc      0
pcc     0
ba      0
bgr     0
bu      0
sc      0
sod     0
pot     0
hemo    0
pcv     0
wc      0
rc      0
htn     0
```

```
dm                0
cad               0
appet             0
pe                0
ane               0
classification    0
dtype: int64
```

To address missing values, we filled missing values in numerical variables with their means, and we filled missing values in binary variables with their most frequent level.

Also, for categorical variables that have multiple levels, we transformed them into numerical form and then filled the missing values with their means.

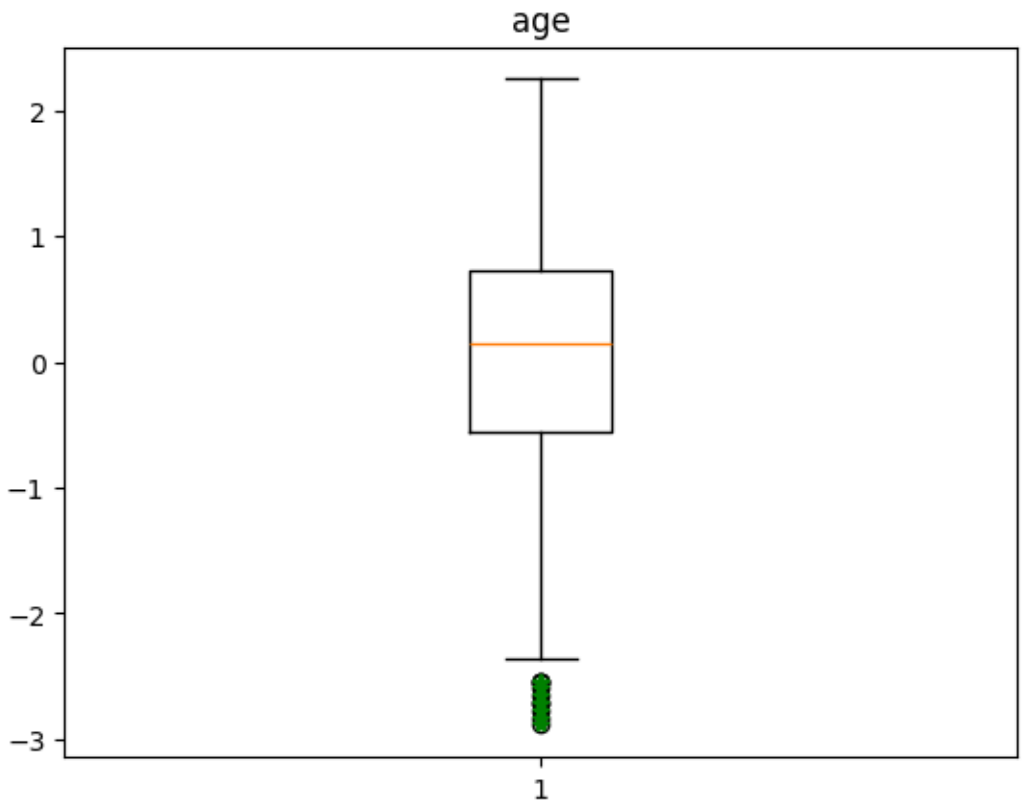
Question 6

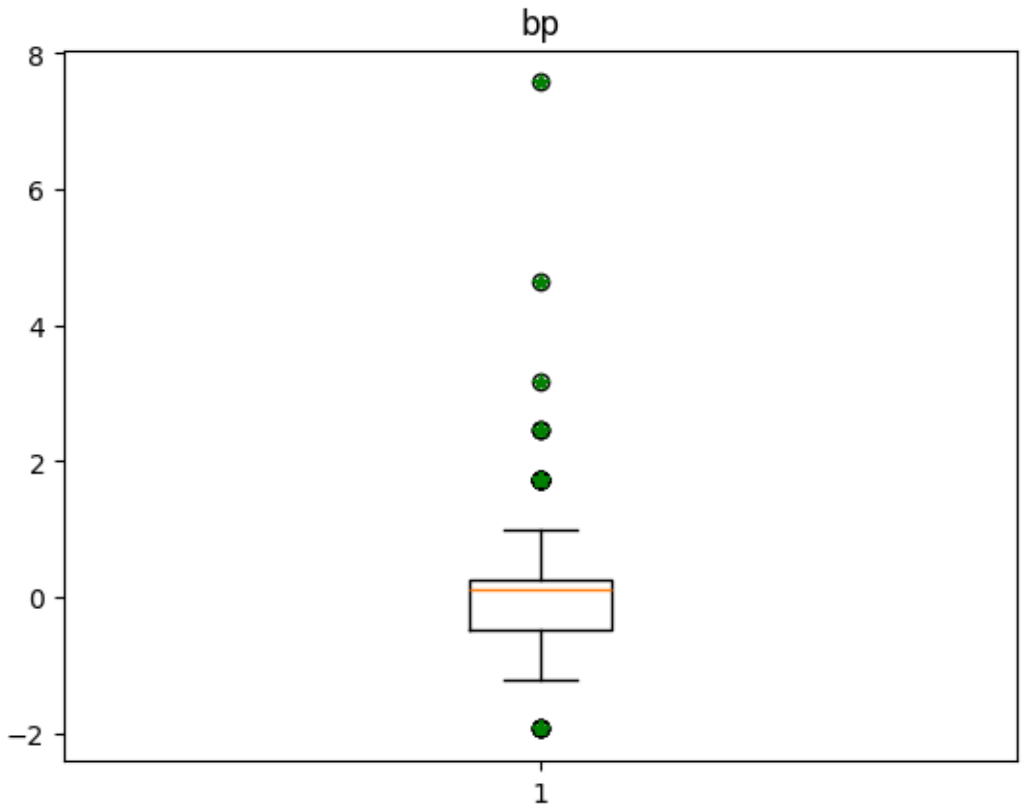
```
x = kidney.drop('classification',axis=1)
y = kidney['classification']
```

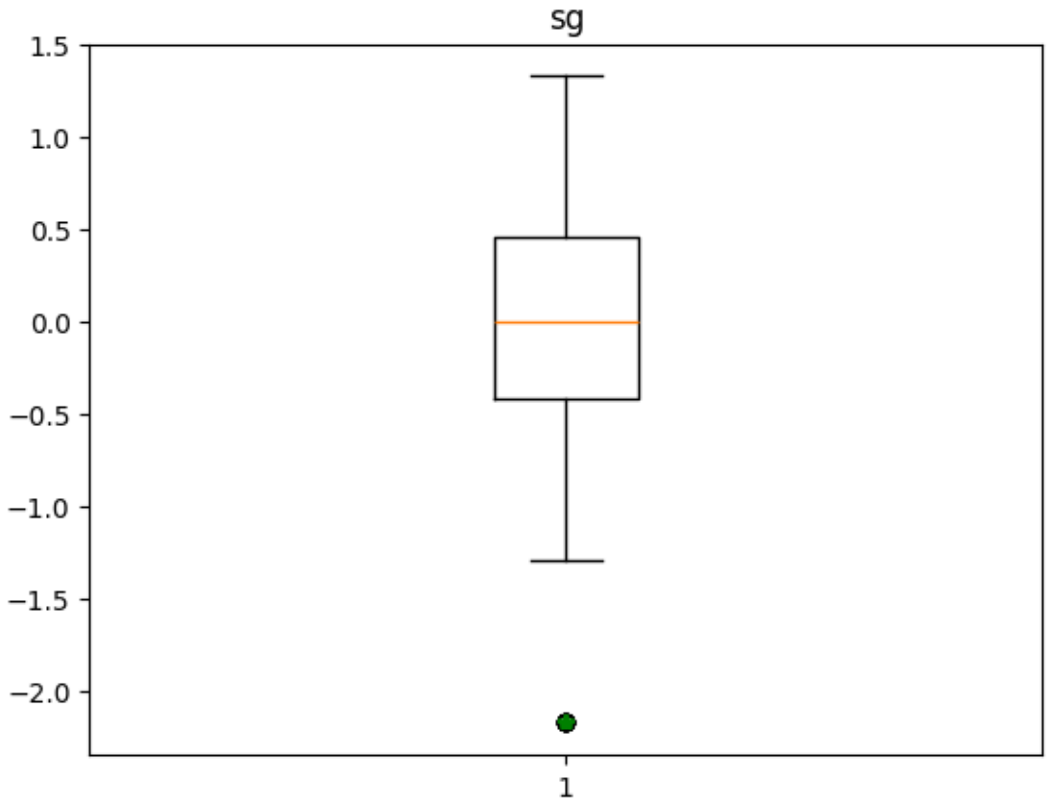
```
def detect_outliers(data, col):
    q1, q3 = np.percentile(data[col], [25, 75])
    iqr = q3 - q1

    upper_bound = q3 + 1.5 * iqr
    lower_bound = q1 - 1.5 * iqr

    outliers = data[(data[col] > upper_bound) | (data[col] < lower_bound)]

    return outliers
```

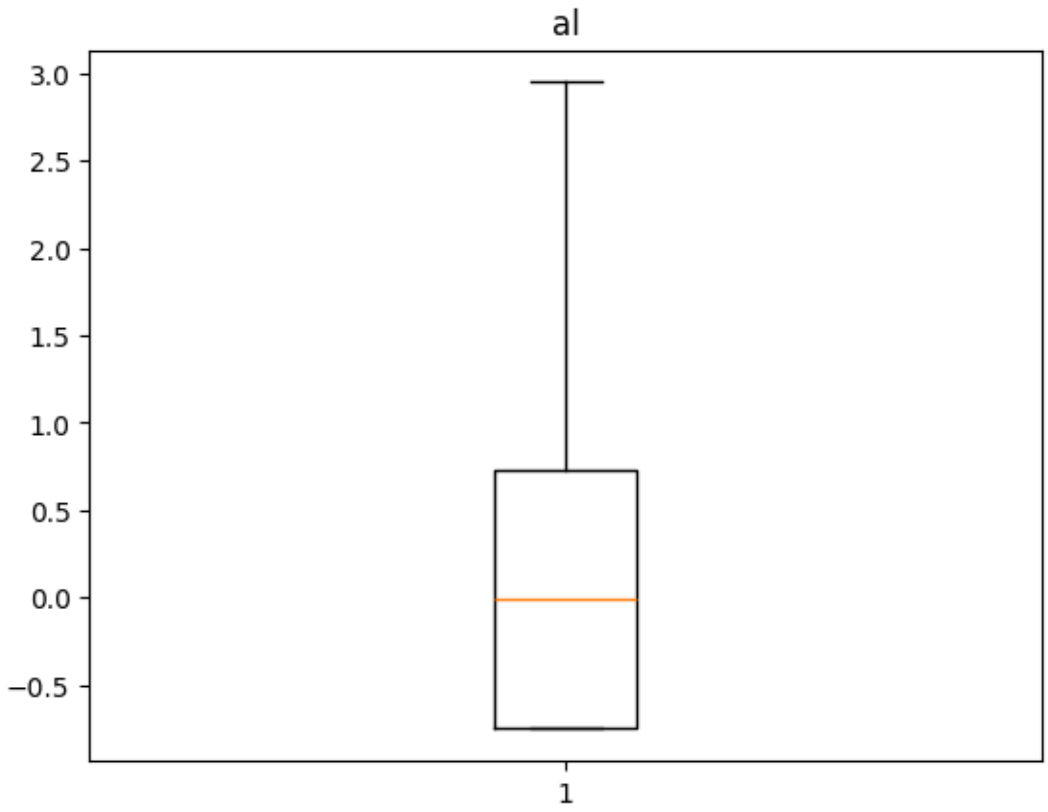
```
for col in num_col:
    # detect outliers
    outliers = detect_outliers(x, col)
```

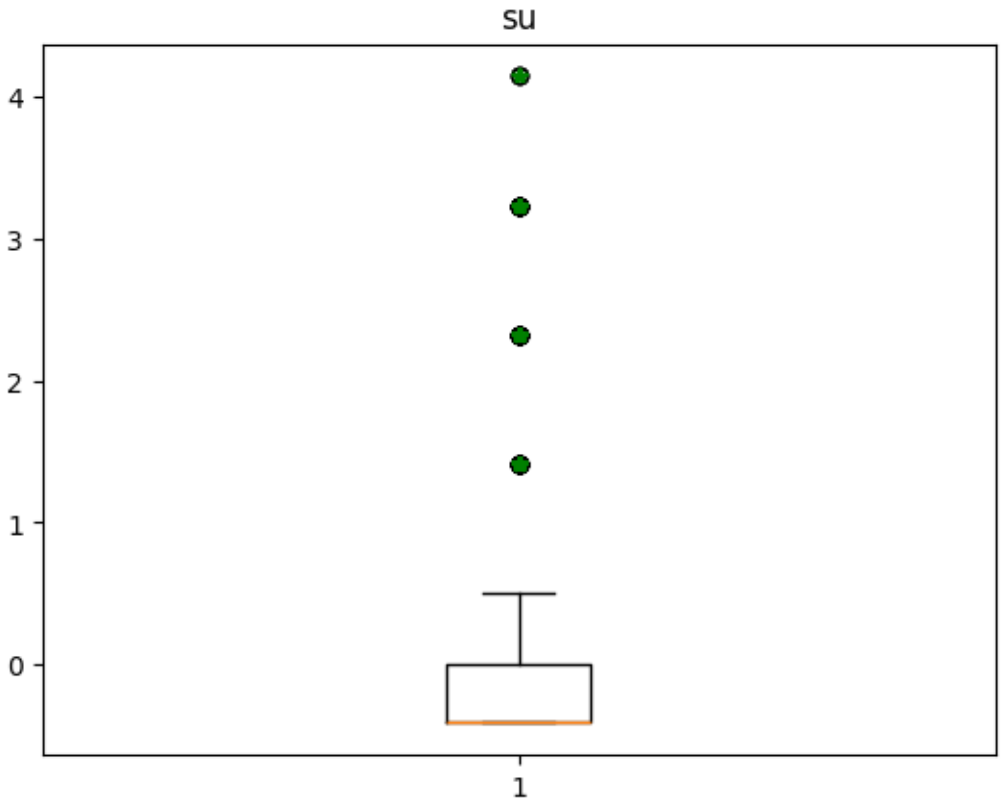
```
# create the boxplot
fig, ax = plt.subplots()
ax.boxplot(x[col])
ax.set_title(col)

# mark the outliers
for index, row in outliers.iterrows():
    ax.plot(1, row[col], 'g*')

# show the plot
plt.show()
```

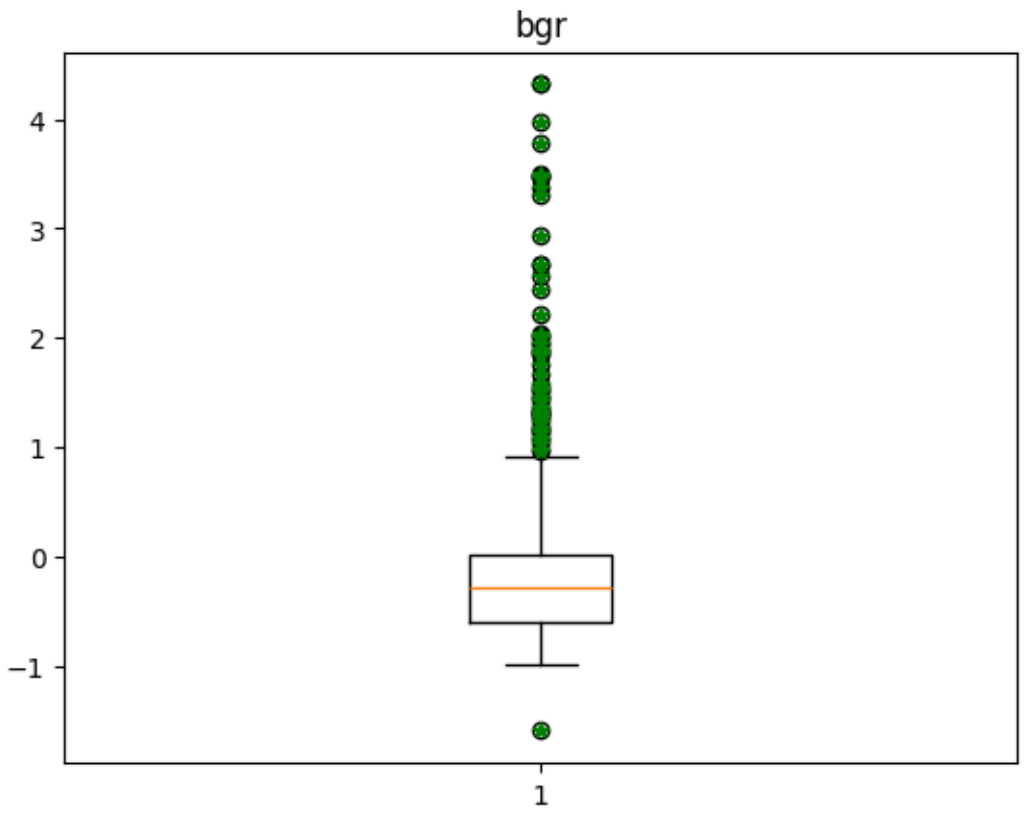


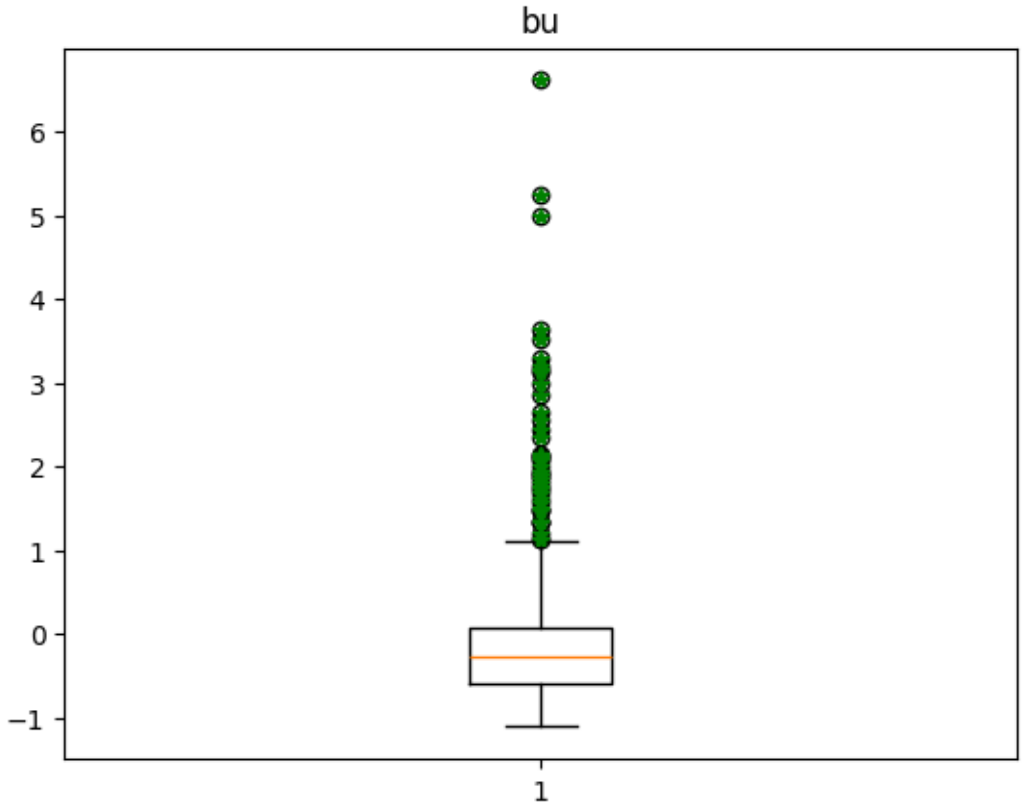

bp
8
6
4
2
0
−2
1

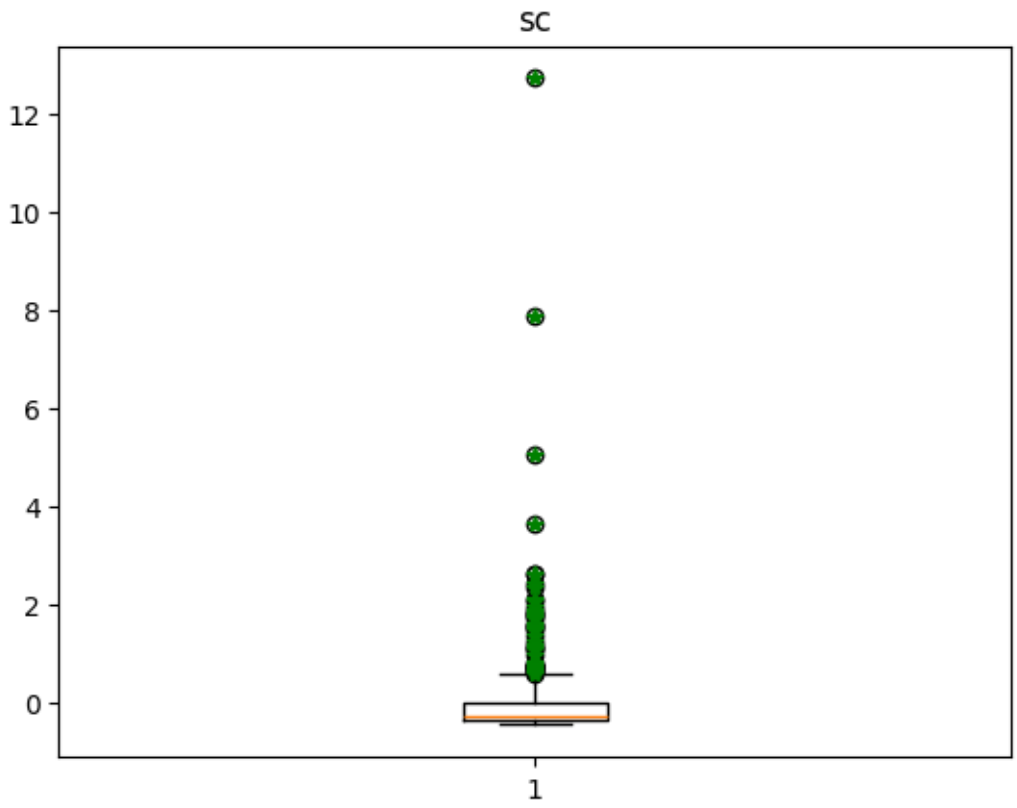

sg
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2.0
1

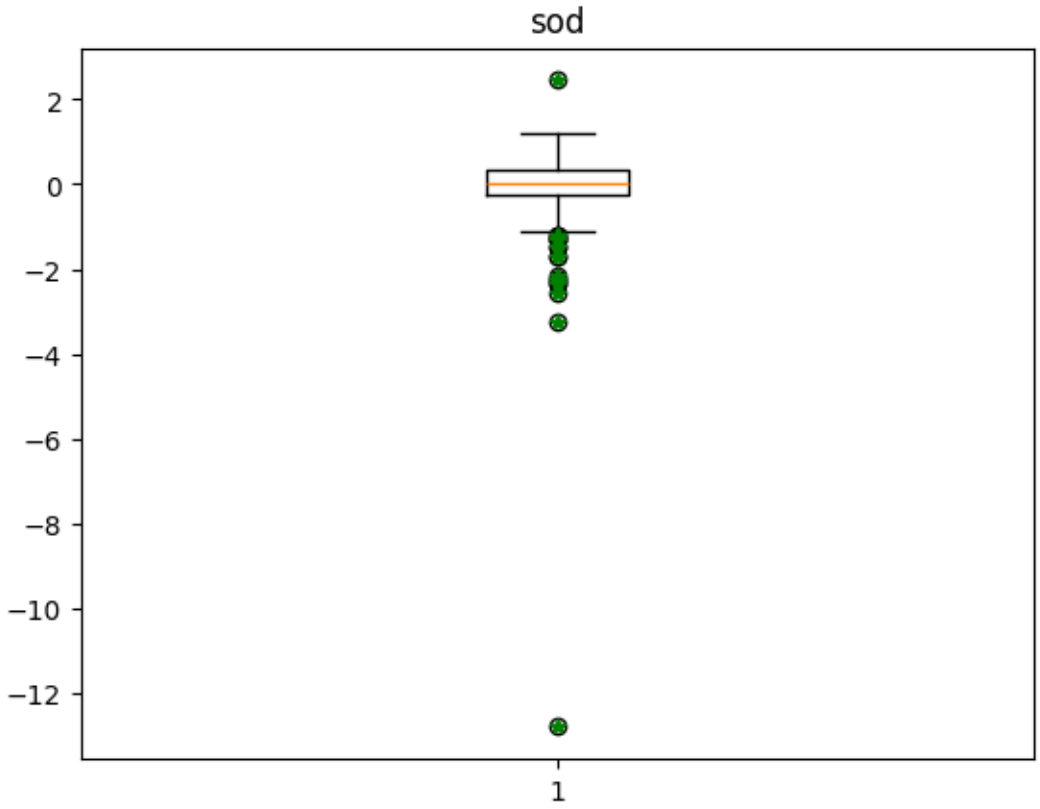

al
3.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
1

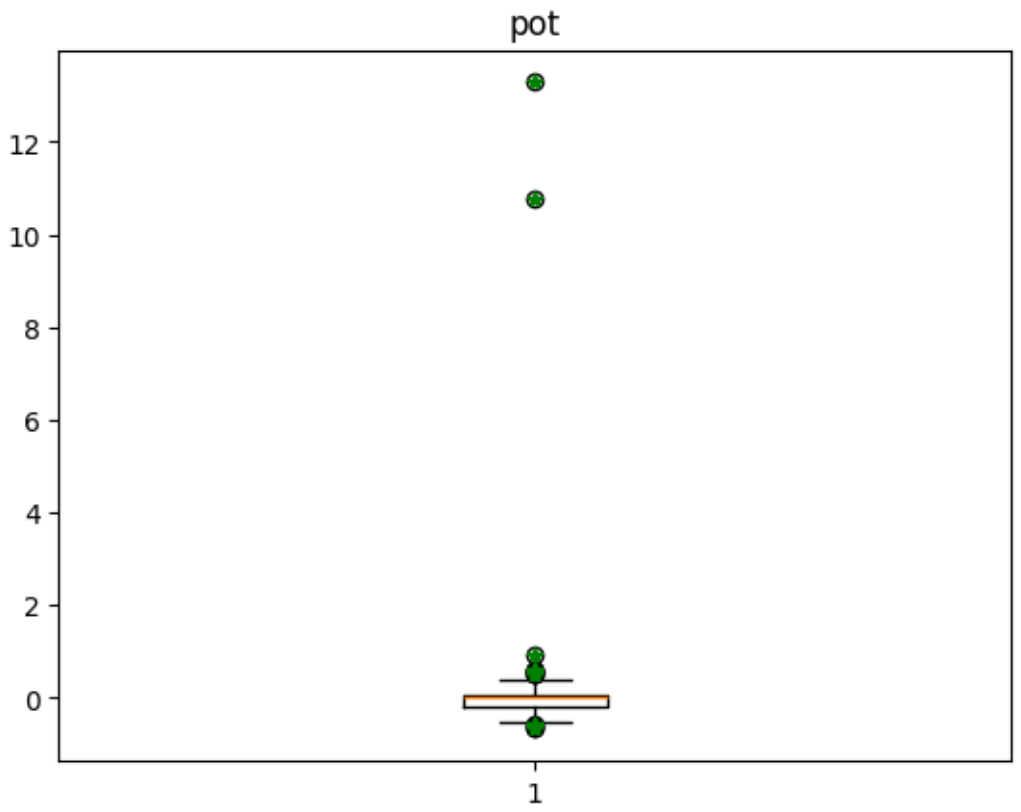

su
4
3
2
1
0
1

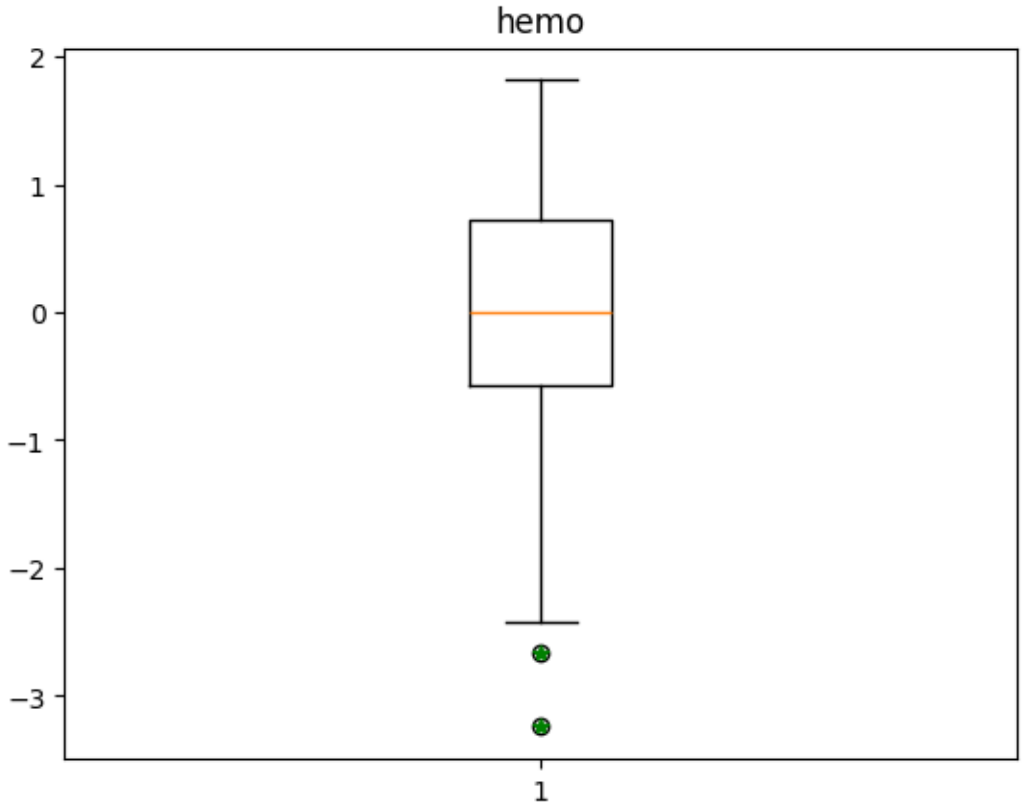

bgr
4
3
2
1
0
−1
1

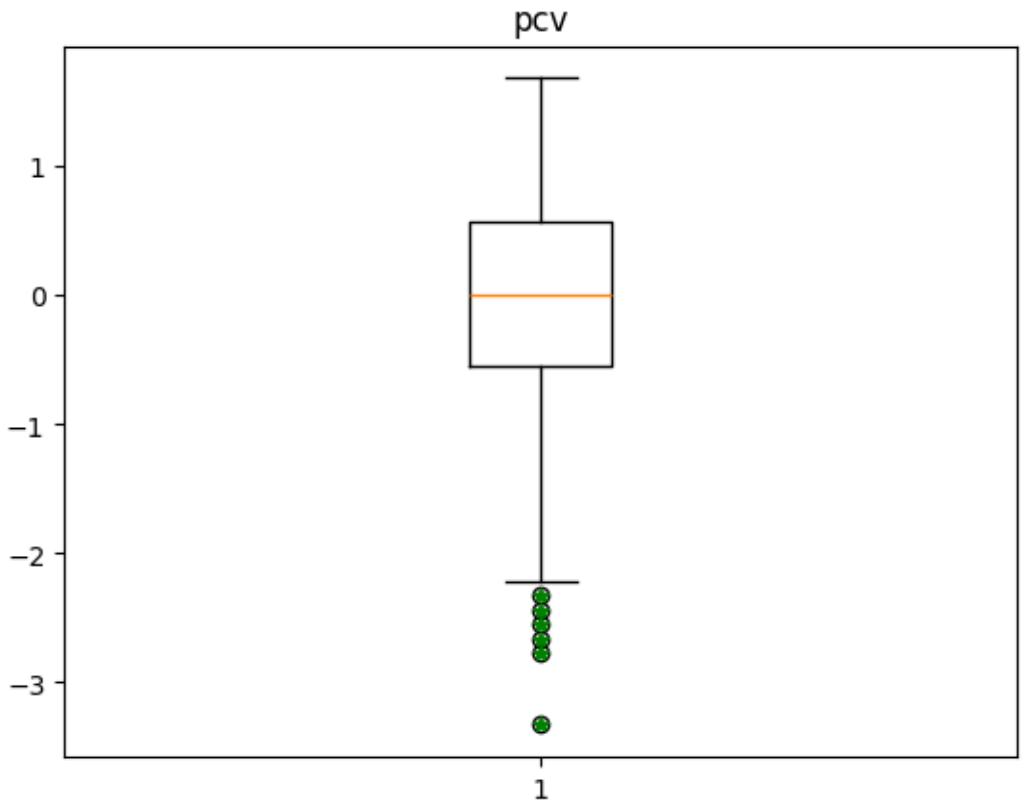

bu
6
5
4
3
2
1
0
−1
1

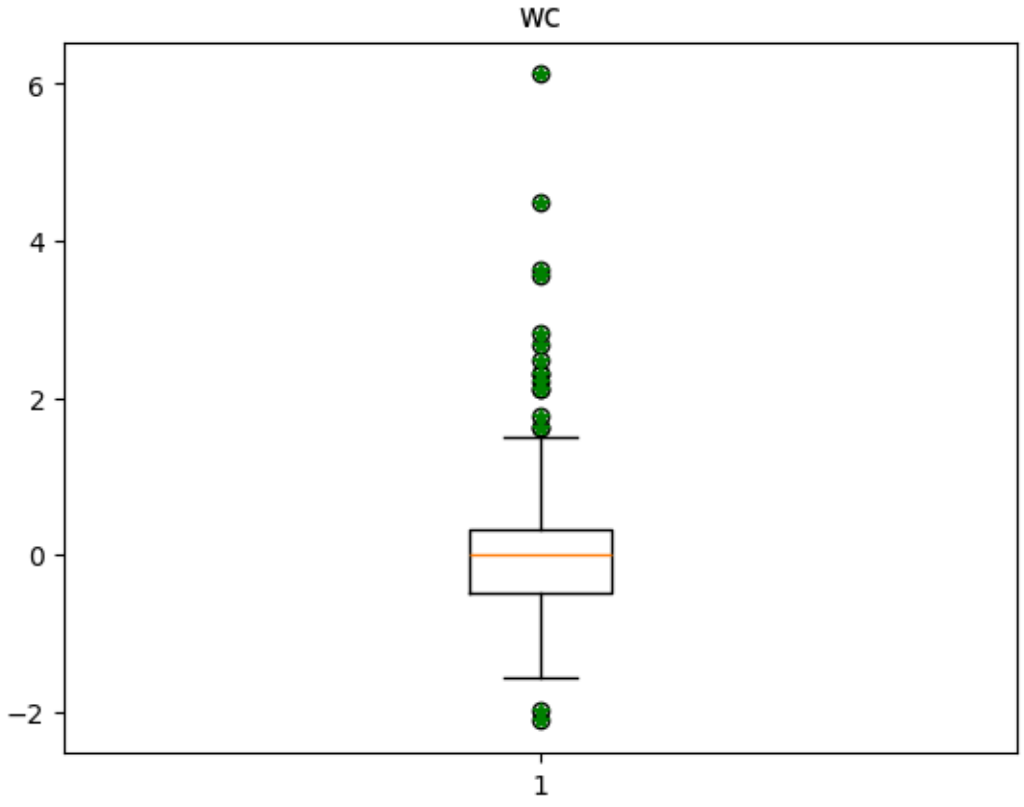

sc
12
10
8
6
4
2
0
1

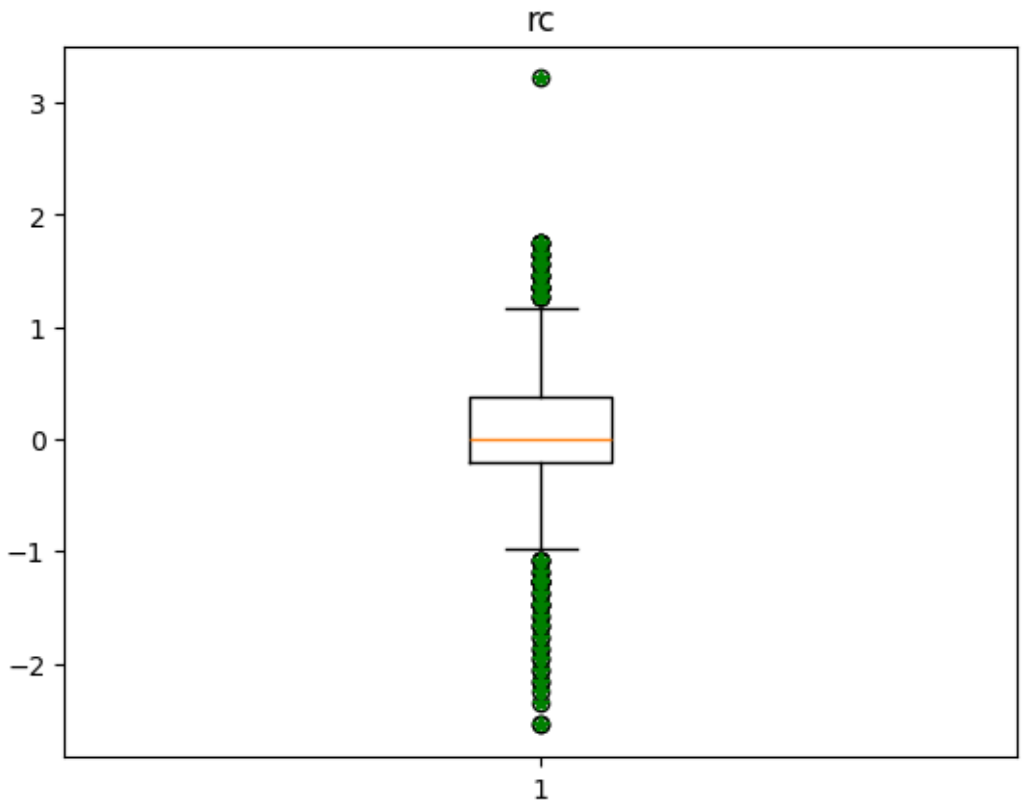

sod
2
0
−2
−4
−6
−8
−10
−12
1


pot
12
10
8
6
4
2
0
1


hemo
2
1
0
−1
−2
−3
1


pcv
1
0
−1
−2
−3
1


wc
6
4
2
0
−2
1




```
detect_outliers(kidney, num_col).drop(bi_col, axis=1)
```

	age	bp	sg	al	su	bgr	bu	sc	sod	pot	hemo
0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1	-2.594124	-1.936857	NaN	2.208413	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2	NaN	NaN	NaN	NaN	2.323069	3.473064	NaN	NaN	NaN	NaN	NaN
3	NaN	NaN	-2.173584	2.208413	NaN	NaN	NaN	NaN	-2.552778	NaN	NaN
4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
...	...	...	...	...	...	...	...	...	...	...	...
395	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
396	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
397	-2.302541	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
398	-2.010957	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
399	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

Question 7

```
from sklearn.preprocessing import scale
from sklearn.decomposition import PCA, TruncatedSVD, FactorAnalysis
```

```
pca_X = PCA()
pca_loadings = pd.DataFrame(pca_X.fit(x).components_.T,
                            index=x.columns,
                            columns=['PC1', 'PC2', 'PC3', 'PC4', 'PC5', 'PC6', 'PC7', 'PC8', '
                                     'PC13', 'PC14', 'PC15', 'PC16', 'PC17', 'PC18', 'PC19', '
pca_loadings
```

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
age	0.163744	-0.223728	0.277279	-0.412386	-0.465199	-0.617097	-0.112038	0.050562	0.157896
bp	0.177148	-0.091818	0.108974	-0.676162	-0.053237	0.629353	0.215219	0.026419	0.179897
sg	-0.295206	0.141609	0.234392	-0.103098	0.003571	-0.005508	0.056622	-0.829606	-0.067198
al	0.311991	-0.063509	-0.224997	0.196243	0.167188	-0.032332	-0.017493	-0.204262	0.762125
su	0.195823	-0.483840	0.356545	0.199517	0.125096	0.138751	0.079477	-0.042238	-0.151181
rbc	-0.050890	-0.006686	0.038103	-0.012677	-0.017115	-0.037722	0.030202	0.030181	-0.110461
pc	-0.096472	0.011941	0.053289	-0.018397	-0.071838	0.009624	0.021986	0.038118	-0.154659
pcc	0.052590	-0.030283	-0.048973	0.021640	-0.002267	-0.030192	-0.002666	-0.011322	0.091617
ba	0.028661	-0.009118	-0.032156	0.006842	0.013572	0.004777	0.009469	-0.005858	0.086139
bgr	0.215403	-0.495017	0.219446	0.284253	-0.005181	0.148472	-0.169923	-0.184750	-0.124162
bu	0.321439	0.317964	0.207412	-0.056929	0.225238	-0.179453	0.099100	-0.269756	0.006332
sc	0.257954	0.422799	0.416892	0.208251	-0.193333	0.075203	0.222308	0.106880	-0.015626
sod	-0.209245	-0.275766	-0.152954	-0.319521	0.444147	-0.218248	0.011102	-0.082847	-0.073592
pot	0.092670	0.082245	0.376384	-0.116766	0.648244	-0.206929	0.079067	0.283717	0.008128
hemo	-0.374006	-0.085146	0.267066	0.091364	-0.056588	-0.011472	0.147553	0.106960	0.263812
pcv	-0.364708	-0.072185	0.242535	0.113128	-0.035284	0.011364	0.104053	0.069913	0.286020
wc	0.089577	-0.192568	-0.255799	0.086716	-0.087385	-0.203044	0.884097	-0.051837	-0.120069
rc	-0.292720	-0.069339	0.179709	0.071022	-0.015646	0.056233	0.101908	0.023917	0.279508

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
htn	0.158066	-0.046131	-0.009124	-0.053026	-0.072389	-0.043459	-0.074701	-0.107894	0.007896
dm	0.140228	-0.121243	0.043347	0.005572	-0.061366	-0.018920	-0.050017	-0.051228	-0.052768
cad	0.048481	-0.013770	0.020686	0.006934	-0.034236	-0.016786	-0.038883	-0.046294	-0.005030
appet	-0.085034	0.000327	0.066908	0.031611	0.023304	0.014346	0.000968	0.085127	-0.013733
pe	0.083930	0.015474	-0.065265	0.021941	0.035216	-0.048617	0.001141	-0.073889	0.083457
ane	0.083565	0.053091	-0.042330	-0.039537	0.039819	0.015069	-0.033298	-0.089891	-0.086095

```
pc_scores = pd.DataFrame(
    pca_X.transform(x),
    columns=['PC1', 'PC2', 'PC3', 'PC4', 'PC5', 'PC6', 'PC7', 'PC8', 'PC9', 'PC10', 'PC11', 'PC
                                        'PC13', 'PC14', 'PC15', 'PC16', 'PC17', 'PC18', 'PC19', '
    index=x.index
)
pc_scores
```

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
0	-1.126096	-0.051177	0.251939	-0.221743	-0.174617	0.265732	0.022493	-0.090474	0.572326
1	-0.713965	0.719191	-1.680807	2.543062	1.655340	0.565545	-1.073108	-0.715460	0.869754
2	2.664229	-3.161935	0.781938	0.992487	0.210229	0.684855	-1.099201	-0.034956	-0.646016
3	2.546107	1.021639	-1.706398	1.510268	-0.973943	0.335632	-1.075256	1.083483	1.730742
4	0.267522	0.084497	-1.033060	-0.245040	0.078197	0.221100	-0.471471	1.256718	0.573576
...	...	...	...	...	...	...	...	...	...
395	-1.836831	-0.281001	0.552994	-0.859268	0.333991	-0.137166	-0.218589	0.085222	0.089361
396	-3.194296	0.387253	0.627411	0.234210	-0.135894	0.097661	0.427437	-0.395969	0.542821
397	-2.491306	0.678241	-0.048461	0.538923	0.725338	1.760391	0.128581	0.268506	0.057213
398	-2.697773	0.988218	0.275947	1.426162	0.777462	0.605120	0.045674	-0.617359	-0.192834
399	-2.718098	-0.227338	1.038529	-0.504280	-0.618452	0.197430	-0.027061	-0.410708	0.650781

```
pc_scores.var()
```

```
PC1     4.392111
PC2     1.473818
PC3     1.110992
PC4     0.928267
PC5     0.909305
PC6     0.841049
PC7     0.648943
PC8     0.511006
PC9     0.493134
PC10    0.381556
PC11    0.302385
PC12    0.255862
PC13    0.216661
PC14    0.174726
PC15    0.144494
PC16    0.119038
PC17    0.100446
PC18    0.097069
PC19    0.088544
PC20    0.077189
PC21    0.071419
PC22    0.054153
PC23    0.041617
PC24    0.038226
dtype: float64
```

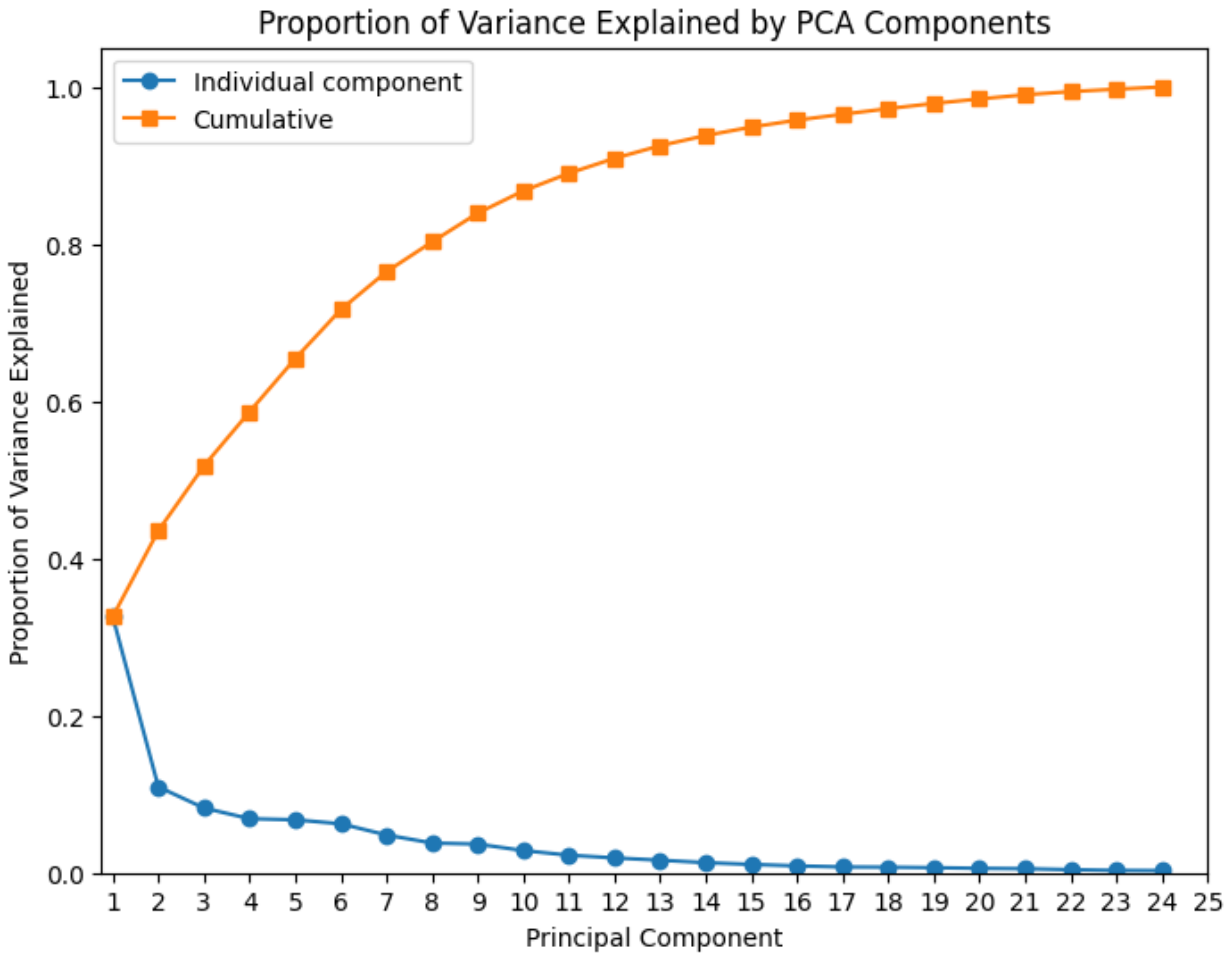
```
np.sum(pc_scores.var())
```

```
13.472011278195481
```

```
print(pca_X.explained_variance_)
print(pca_X.explained_variance_ratio_)
```

```
[4.39211094 1.47381819 1.1109917  0.928267   0.90930501 0.84104926
 0.64894312 0.5110063  0.49313447 0.38155552 0.30238527 0.25586249
 0.21666067 0.17472602 0.14449442 0.11903755 0.10044645 0.09706937
 0.08854397 0.07718852 0.07141898 0.05415326 0.04161668 0.03822612]
[0.32601746 0.10939853 0.08246665 0.06890337 0.06749586 0.06242938
 0.04816973 0.03793096 0.03660437 0.02832209 0.02244544 0.01899215
 0.01608228 0.01296956 0.01072553 0.00883592 0.00745594 0.00720526
 0.00657244 0.00572955 0.00530129 0.00401969 0.00308912 0.00283745]
```

```
plt.figure(figsize=(8, 6))
plt.plot([1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24], pca_X.explained_vari
plt.plot([1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24], np.cumsum(pca_X.expl
plt.ylabel('Proportion of Variance Explained')
plt.xlabel('Principal Component')
plt.xlim(0.75,4.25)
plt.ylim(0,1.05)
plt.xticks([1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25])
plt.legend(loc=2)
plt.title('Proportion of Variance Explained by PCA Components')
plt.show()
```




```
from sklearn.cluster import KMeans
```

```
km=KMeans(n_clusters=2,n_init=20,random_state=0)
km.fit(x)
km.labels_
```

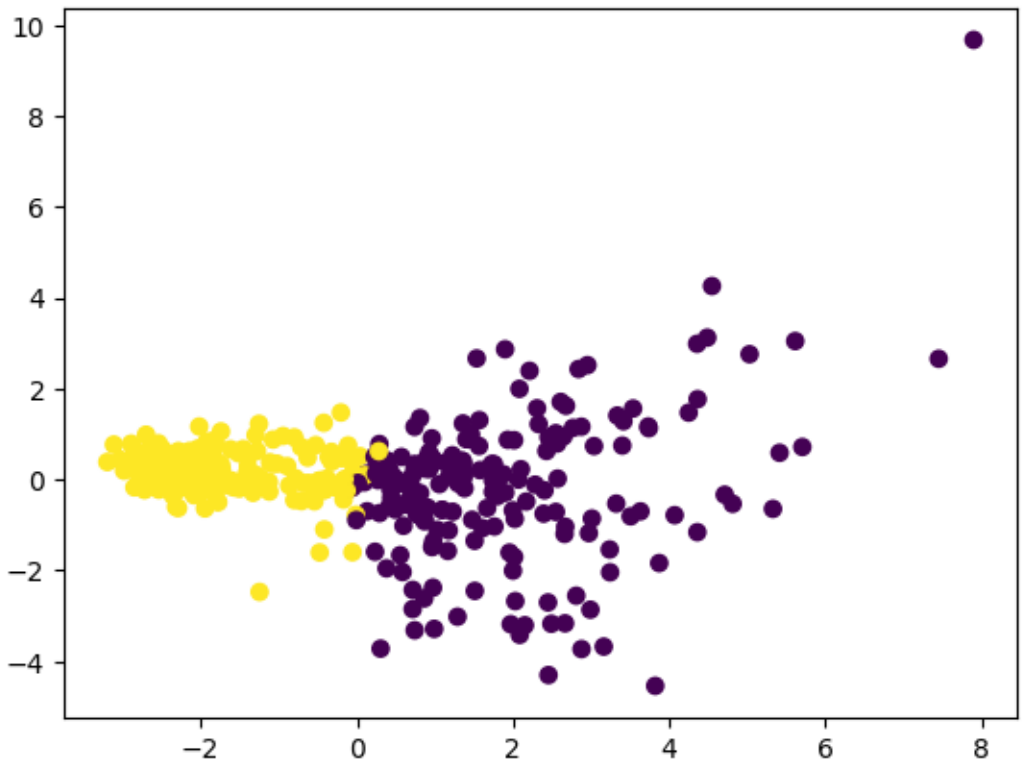
```
array([1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0,
       0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0,
       0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1,
       0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0,
       0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 1, 0,
       1, 0, 0, 0, 1, 1, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1,
       0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0,
```

```
       0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 1, 0, 0,
       0, 0, 0, 0, 0, 0, 1, 1, 0, 1, 1, 1, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 1, 0,
       1, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0,
       0, 1, 0, 0, 0, 1, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1], dtype=int32)
```

```python
pd.Series(km.labels_).value_counts()
```

```
1    206
0    194
Name: count, dtype: int64
```

```python
plt.scatter(pc_scores['PC1'],pc_scores['PC2'],c=km.labels_)
```




```
pca = PCA(n_components=2)
pca.fit(x)
print("Data before PCA")
display(x)
x_pca = pca.transform(x)
print("Data after PCA")
df_x_pca = pd.DataFrame(x_pca, columns=['PC1', 'PC2'])
display(df_x_pca)
```

```
Data before PCA
Data after PCA
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	hemo
0	-0.203139	0.258373	0.454071	-0.012548	-0.410106	1.0	1.0	0.0	0.0	-3.414983e-01	...	0.988
1	-2.594124	-1.936857	0.454071	2.208413	-0.410106	1.0	1.0	0.0	0.0	-1.796316e-16	...	-0.42
2	0.613295	0.258373	-1.297699	0.727772	2.323069	1.0	1.0	0.0	0.0	3.473064e+00	...	-1.00

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	hemo
3	-0.203139	-0.473370	-2.173584	2.208413	-0.410106	1.0	0.0	1.0	0.0	-3.920223e-01	...	-0.45
4	-0.028189	0.258373	-1.297699	0.727772	-0.410106	1.0	1.0	0.0	0.0	-5.309633e-01	...	-0.31
...	...	...	...	...	...	...	...	...	...	...	...	...
395	0.205078	0.258373	0.454071	-0.752868	-0.410106	1.0	1.0	0.0	0.0	-1.015093e-01	...	1.091
396	-0.553039	-0.473370	1.329955	-0.752868	-0.410106	1.0	1.0	0.0	0.0	-9.225244e-01	...	1.366
397	-2.302541	0.258373	0.454071	-0.752868	-0.410106	1.0	1.0	0.0	0.0	-6.067493e-01	...	1.125
398	-2.010957	-1.205114	1.329955	-0.752868	-0.410106	1.0	1.0	0.0	0.0	-4.299153e-01	...	0.575
399	0.380028	0.258373	1.329955	-0.752868	-0.410106	1.0	1.0	0.0	0.0	-2.151883e-01	...	1.125

	PC1	PC2
0	-1.126096	-0.051177
1	-0.713965	0.719191
2	2.664229	-3.161935
3	2.546107	1.021639
4	0.267522	0.084497
...	...	...
395	-1.836831	-0.281001
396	-3.194296	0.387253
397	-2.491306	0.678241
398	-2.697773	0.988218
399	-2.718098	-0.227338

Question 8

```
from sklearn.model_selection import train_test_split
```

```
X_train, X_test, y_test, y_train=train_test_split(
    x,
    y,
```

```
    test_size=0.3,
    random_state=1)
```

Question 9

We decide to choose **logistic regression classifier** and **decision tree classifier**.

For logistic regression: Logistic Regression is a simple and efficient linear model suitable for binary classification problems,(presence or absence of kidney disease). It provides interpretable coefficients that can help in understanding feature importance.

For decision tree: Decision Trees are flexible, can model complex relationships, and are intuitive to interpret. They can fit non-linear patterns without the need for data transformation. However, they are moreprone to overfitting in some case.

Question 10

The evaluation metrics that summarize the performance of the model. There four different kinds of metrics, Precision, Recall, F1-score and Accuracy. Precision measures the proportion of predicted positive cases that are actually positive. Recall measures the proportion of actual positive cases that are predicted correctly. F1-score is the harmonic mean of precision and recall, and it is a way to balance the trade-off between the two metrics. Accuracy is the proportion of instances in the dataset that were classified correctly. In the project, we are using F1-score and accuracy.

Question 11&12

```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(x, y, test_size=0.3, random_state=45)
```

```
#Build Decision Tree model on the dataset
from sklearn.tree import DecisionTreeClassifier
dt = DecisionTreeClassifier()
```

```
dt.fit(X_train, y_train)


#make prediction on test data
y_pred_dt = dt.predict(X_test)

#evaluating the algorithm
from sklearn.metrics import classification_report, confusion_matrix, accuracy_score, f1_score
print(confusion_matrix(y_test, y_pred_dt))
print(classification_report(y_test, y_pred_dt))
```

```
[[51  1]
 [ 4 64]]
              precision    recall  f1-score   support

           0       0.93      0.98      0.95        52
           1       0.98      0.94      0.96        68

    accuracy                           0.96       120
   macro avg       0.96      0.96      0.96       120
weighted avg       0.96      0.96      0.96       120
```

In this case, precision and recall are both high for class 0 and 1, indicating that the model is performing well in predicting these classes.

```
#Build logistic model on the dataset
from sklearn.linear_model import LogisticRegression
log = LogisticRegression()
log.fit(X_train,y_train)

#make prediction on test data
y_pred_log = log.predict(X_test)
```

```
#evaluating the algorithm
print(confusion_matrix(y_test, y_pred_log))
print(classification_report(y_test, y_pred_log))
```

```
[[51  1]
 [ 2 66]]
              precision    recall  f1-score   support

           0       0.96      0.98      0.97        52
           1       0.99      0.97      0.98        68

    accuracy                           0.97       120
   macro avg       0.97      0.98      0.97       120
weighted avg       0.98      0.97      0.98       120
```

```
dt_acc = accuracy_score(y_test, y_pred_dt)
dt_F1 = f1_score(y_test, y_pred_dt)
print("Decision tree accuracy:", dt_acc)
print("Decision tree F1 score:", dt_F1)

log_acc = accuracy_score(y_test, y_pred_log)
log_F1 = f1_score(y_test, y_pred_log)
print("Logistic regression accuracy:", log_acc)
print("Logistic F1 score:", log_F1)
```

```
Decision tree accuracy: 0.9583333333333334
Decision tree F1 score: 0.9624060150375939
Logistic regression accuracy: 0.975
Logistic F1 score: 0.9777777777777777
```

Comparison between two classifier:

In choosing between them, we should consider the complexity of the relationships in our dataset,the

importance of interpretability, the need for featuring, and the propensity of the model to overfit. For instance, if interpretability is key and our data includes complex, non-linearrelationships, a Decision Tree would be more suitable. Conversely, if we expect that a linear model could work well with the dataset or we are working with a very large, high-dimensional dataset. Logistic Regression could be more appropriate.

The **logistic regression model** displays exceptional predictive performance with an accuracy of 0.975 and F1-scores of 0.97 for class.
The **decision tree classifier** also shows high performance with an accuracy of 0.958 and F1-scores of 0.962 for class.
In summary, while both models are likely to be highly effective due to their high F1-scores and accuracy. The perfect precision and recall for class by the logistic regression model may be particularly valuable in clinical settings for CKD. However, decision trees offer a level of interpretability that can be important for clinical decision-making and understanding the model's predictions. Therefore, the final model choice might also consider the trade-off between the slight performance benefit of logistic regression and the interpretability of decision trees.

All in all, based on F1 score and accuracy, we choose the **Logistic Regression** as the better classifier.

```
from mlxtend.feature_selection import SequentialFeatureSelector as SFS
from mlxtend.plotting import plot_sequential_feature_selection as plot_sfs
from sklearn import metrics
```

```
np.sqrt(metrics.mean_squared_error(y_test, y_pred_log))
```

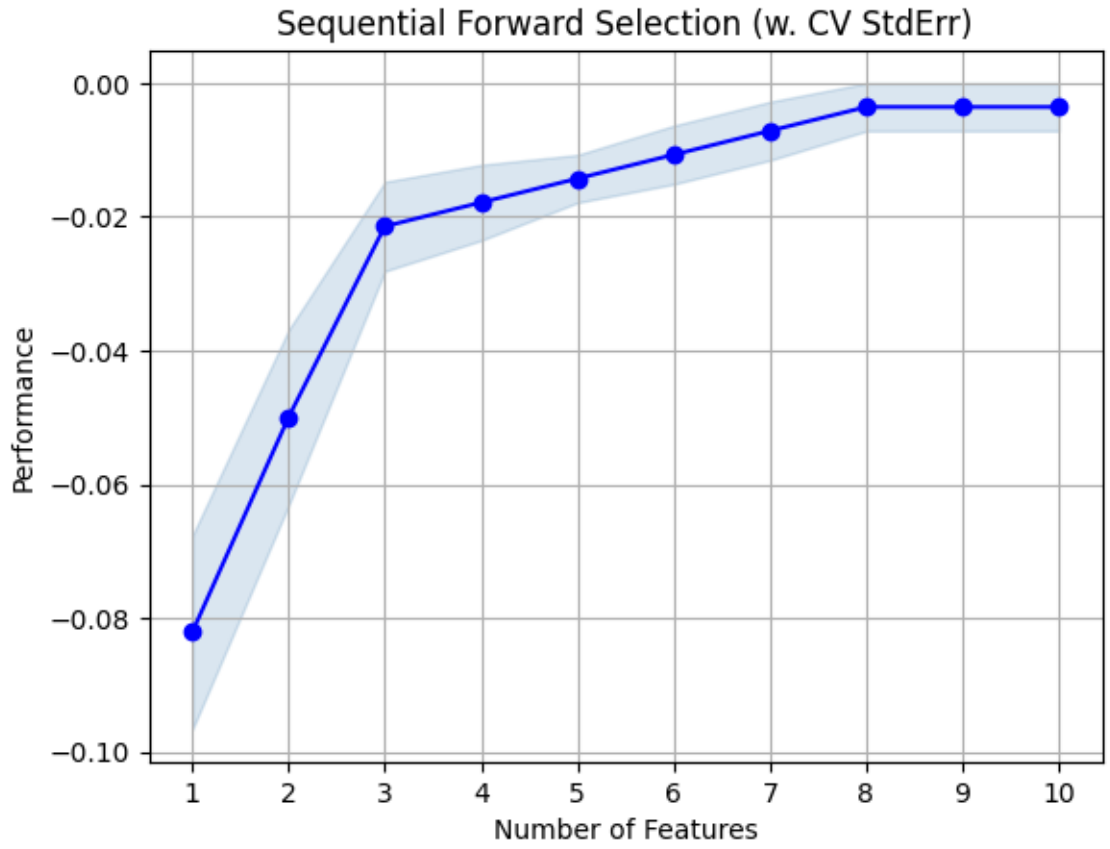
```
0.15811388300841897
```

```
sfs = SFS(
    log,
    k_features=(1,10),
    forward=True,
    floating=False,
    scoring='neg_mean_squared_error',
```

```
    cv=5
    )
```

```
sfs = sfs.fit(X_train, y_train)
```

```
fig = plot_sfs(sfs.get_metric_dict(), kind='std_err')

plt.title('Sequential Forward Selection (w. CV StdErr)')
plt.grid()
plt.show()
```




```
X_train.columns[list(sfs.k_feature_idx_)]
```

```
Index(['sg', 'al', 'bgr', 'sod', 'hemo', 'pcv', 'dm', 'appet'], dtype='object')
```

```
# Prediction on hold-out set
sel_col = X_train.columns[list(sfs.k_feature_idx_)]
X_train_sfs = X_train[sel_col]
X_test_sfs = X_test[sel_col]
sfs_m = LogisticRegression()
sfs_m.fit(X_train_sfs, y_train)
sfs_test = sfs_m.predict(X_test_sfs)
np.sqrt(metrics.mean_squared_error(y_test, sfs_test))
```

```
0.12909944487358055
```

We choose the stepwise selection method to improve logistic regression classifier. And, we verify that this method that will reduce MSE which means it could enhance the performance of this classifier. The specific code presentation is combined in Question11 and Question 12.

Question 13

```
y_pred_dt_all = dt.predict(x)
y_pred_dt_all
```

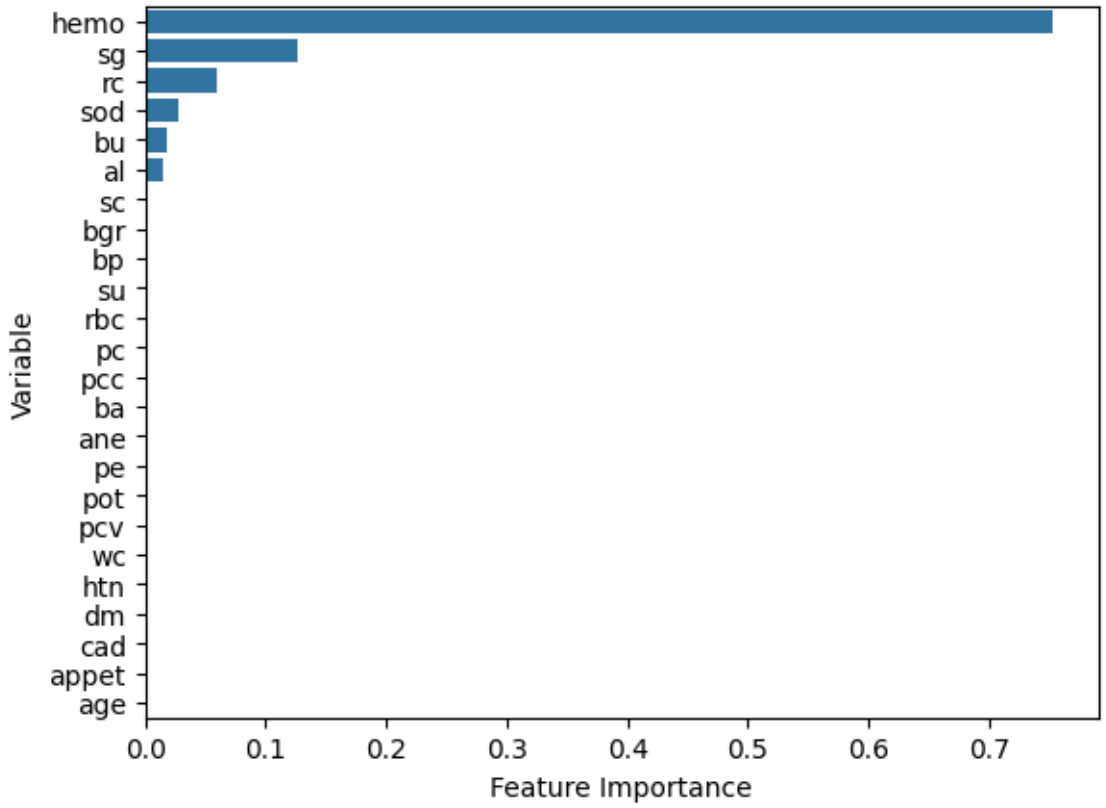
```
array([0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
```

```
       1, 0, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0])
```

```
y_pred_log_all = log.predict(x)
y_pred_log_all
```

```
array([0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0])
```

```
fea_imp = dt.feature_importances_
sorted_indices = fea_imp.argsort()[::-1]
sorted_feature_names = x.columns[sorted_indices]
sorted_importances = fea_imp[sorted_indices]


sns.barplot(x = sorted_importances, y = sorted_feature_names)
plt.xlabel("Feature Importance")
plt.ylabel("Variable")
plt.show()
```



Significance of Serum Creatinine (sc) in Logistic Regression:

If the logistic regression model shows a high positive coefficient for serum creatinine (sc), this indicates a strong association between elevated creatinine levels and the likelihood of having CKD. This insight highlights the importance of `sc` as a critical biomarker for diagnosing kidney disease, guiding clinical decisions regarding the need for further diagnostic testing or early intervention.

Significance of Hypertension (htn) in Decision Tree Analysis:

This suggests that hypertension is a primary factor in determining the presence of kidney disease. This finding emphasizes the need for managing blood pressure strictly in patients at risk for or diagnosed with CKD to prevent further renal deterioration.

These interpretations help in understanding which variables are most predictive of CKD and should be closely monitored in clinical settings to manage and potentially prevent the progression of kidney disease. The significance of these predictors also assists in educating patients about risk factors and the importance of regular screening for early detection of kidney problems.

Question 15

Group members:

Zien Xiong (400366281) (Question 1-5)
Wen Yang(400312905) (Question 6-9)
Jiaying Xie(400307943) (Question 10-13)

Each group member contributed equally to the assignment.

Question 16

link: https://github.com/Echosu0/stats_3da_ass6.git

Rubini, Soundarapandian, L., and P. Eswaran. 2015. "Chronic Kidney Disease." UCI Machine Learning Repository.