

In [1]:

1

import numpy as np

2

import pandas as pd

In [2]:

1

dataset=pd.read_csv("kidney_disease.csv")

2

dataset

Out[2]:

	id	age	F	sg	al	su	rbc	pc	pcc	ba	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane	classification
0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	...	44.0	7800.0	5.2	yes	yes	no	good	no	no	ck
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	...	38.0	6000.0	NaN	no	no	no	good	no	no	ck
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	...	31.0	7500.0	NaN	no	yes	no	poor	no	yes	ck
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32.0	6700.0	3.9	yes	no	no	poor	yes	yes	ck
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	...	35.0	7300.0	4.6	no	no	no	good	no	no	ck
...
395	395	55.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	...	47.0	6700.0	4.9	no	no	no	good	no	no	notck
396	396	42.0	70.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	54.0	7800.0	6.2	no	no	no	good	no	no	notck
397	397	12.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	...	49.0	6600.0	5.4	no	no	no	good	no	no	notck
398	398	17.0	60.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	51.0	7200.0	5.9	no	no	no	good	no	no	notck
399	399	58.0	80.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	53.0	6800.0	6.1	no	no	no	good	no	no	notck

400 rows × 26 columns

In [3]:

1

dataset.info()

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 26 columns):
#   Column                Non-Null Count  Dtype
---  -
0   id                    400 non-null    int64
1   age                   391 non-null    float64
2   F                     388 non-null    float64
3   sg                    353 non-null    float64
4   al                    354 non-null    float64
5   su                    351 non-null    float64
6   rbc                   248 non-null    object
7   pc                    335 non-null    object
8   pcc                   396 non-null    object
9   ba                    396 non-null    object
10  bgr                   356 non-null    float64
11  bu                    381 non-null    float64
12  sc                    383 non-null    float64
13  sod                   313 non-null    float64
14  pot                   312 non-null    float64
15  hemo                  348 non-null    float64
16  pcv                   329 non-null    float64
17  wc                    294 non-null    float64
18  rc                    269 non-null    float64
19  htn                   398 non-null    object
20  dm                    398 non-null    object
21  cad                   398 non-null    object
22  appet                 399 non-null    object
23  pe                    399 non-null    object
24  ane                   399 non-null    object
25  classification        400 non-null    object
dtypes: float64(14), int64(1), object(11)
memory usage: 81.4+ KB
```

In [4]:

1dataset.isnull().sum().T

2#*print(a,end='')*

Out[4]:

id	0
age	9
F	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

Deleting Certain Rows with Missing Values

In [5]:

1dataset.dropna(subset=['age', 'pcc', 'ba', 'htn', 'dm', 'cad', 'appet', 'pe', 'ane'], inplace=True)

2dataset

Out[5]:

	id	age	F	sg	al	su	rbc	pc	pcc	ba	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane	classification
0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	...	44.0	7800.0	5.2	yes	yes	no	good	no	no	ck
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	...	38.0	6000.0	NaN	no	no	no	good	no	no	ck
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	...	31.0	7500.0	NaN	no	yes	no	poor	no	yes	ck
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32.0	6700.0	3.9	yes	no	no	poor	yes	yes	ck
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	...	35.0	7300.0	4.6	no	no	no	good	no	no	ck
...
395	395	55.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	...	47.0	6700.0	4.9	no	no	no	good	no	no	notck
396	396	42.0	70.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	54.0	7800.0	6.2	no	no	no	good	no	no	notck
397	397	12.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	...	49.0	6600.0	5.4	no	no	no	good	no	no	notck
398	398	17.0	60.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	51.0	7200.0	5.9	no	no	no	good	no	no	notck
399	399	58.0	80.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	53.0	6800.0	6.1	no	no	no	good	no	no	notck

384 rows × 26 columns

Filling Missing Numerical Values with Median Values

In [6]:

1

dataset.fillna(dataset.median(), inplace=True)

2

dataset

/var/folders/07/ykgp85052b11h5kz22ghn8l40000gn/T/ipykernel_3973/3113556935.py:1: FutureWarning: The default value of numeric_only in DataFrame.median 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.
dataset.fillna(dataset.median(), inplace=True)

Out[6]:

	id	age	F	sg	al	su	rbc	pc	pcc	ba	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane	classification
0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	...	44.0	7800.0	5.2	yes	yes	no	good	no	no	ckd
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	...	38.0	6000.0	4.7	no	no	no	good	no	no	ckd
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	...	31.0	7500.0	4.7	no	yes	no	poor	no	yes	ckd
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32.0	6700.0	3.9	yes	no	no	poor	yes	yes	ckd
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	...	35.0	7300.0	4.6	no	no	no	good	no	no	ckd
...
395	395	55.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	...	47.0	6700.0	4.9	no	no	no	good	no	no	notckd
396	396	42.0	70.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	54.0	7800.0	6.2	no	no	no	good	no	no	notckd
397	397	12.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	...	49.0	6600.0	5.4	no	no	no	good	no	no	notckd
398	398	17.0	60.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	51.0	7200.0	5.9	no	no	no	good	no	no	notckd
399	399	58.0	80.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	53.0	6800.0	6.1	no	no	no	good	no	no	notckd

384 rows × 26 columns

In [7]:

1

dataset.isna().sum()

Out[7]:

id	0
age	0
F	0
sg	0
al	0
su	0
rbc	146
pc	60
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

Finding Mode to Replace Missing Categorical Values

In [8]:

1

categorical_columns = ['rbc', 'pc']

2

modes = dataset[categorical_columns].mode()

3

modes

Out[8]:

	rbc	pc
0	normal	normal

Replacing the Missing Categorical Values With Calculated Mode

In [9]:

1

dataset[dataset.select_dtypes(include=['object']).columns] = dataset.select_dtypes(include=['object']).dataset

Out[9]:

	id	age	F	sg	al	su	rbc	pc	pcc	ba	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane	classification
0	0	48.0	80.0	1.020	1.0	0.0	normal	normal	notpresent	notpresent	...	44.0	7800.0	5.2	yes	yes	no	good	no	no	ckd
1	1	7.0	50.0	1.020	4.0	0.0	normal	normal	notpresent	notpresent	...	38.0	6000.0	4.7	no	no	no	good	no	no	ckd
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	...	31.0	7500.0	4.7	no	yes	no	poor	no	yes	ckd
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32.0	6700.0	3.9	yes	no	no	poor	yes	yes	ckd
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	...	35.0	7300.0	4.6	no	no	no	good	no	no	ckd
...
395	395	55.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	...	47.0	6700.0	4.9	no	no	no	good	no	no	notckd
396	396	42.0	70.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	54.0	7800.0	6.2	no	no	no	good	no	no	notckd
397	397	12.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	...	49.0	6600.0	5.4	no	no	no	good	no	no	notckd
398	398	17.0	60.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	51.0	7200.0	5.9	no	no	no	good	no	no	notckd
399	399	58.0	80.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	53.0	6800.0	6.1	no	no	no	good	no	no	notckd

384 rows × 26 columns

In [10]:

1

dataset.isnull().sum()

Out[10]:

id	0
age	0
F	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

Defining Quan & Qual for Outlier Removal

In [11]:

1

def quanQual(dataset):

2

quan=[]

3

qual=[]

4

for columnName in dataset.columns:

5

#print(columnName)

6

if(dataset[columnName].dtype=='0'):

7

#print("qual")

8

qual.append(columnName)

9

else:

10

#print("quan")

11

quan.append(columnName)

12

return quan,qual

In [12]:

```
1 quan,qual=quanQual(dataset)
2 quan
```

Out[12]:

```
['id',
'age',
'F',
'sg',
'al',
'su',
'bgr',
'bu',
'sc',
'sod',
'pot',
'hemo',
'pcv',
'wc',
'rc']
```

In [13]:

```
1 dataset[qual]
```

Out[13]:

	rbc	pc	pcc	ba	htn	dm	cad	appet	pe	ane	classification
0	normal	normal	notpresent	notpresent	yes	yes	no	good	no	no	ckd
1	normal	normal	notpresent	notpresent	no	no	no	good	no	no	ckd
2	normal	normal	notpresent	notpresent	no	yes	no	poor	no	yes	ckd
3	normal	abnormal	present	notpresent	yes	no	no	poor	yes	yes	ckd
4	normal	normal	notpresent	notpresent	no	no	no	good	no	no	ckd
...
395	normal	normal	notpresent	notpresent	no	no	no	good	no	no	notckd
396	normal	normal	notpresent	notpresent	no	no	no	good	no	no	notckd
397	normal	normal	notpresent	notpresent	no	no	no	good	no	no	notckd
398	normal	normal	notpresent	notpresent	no	no	no	good	no	no	notckd
399	normal	normal	notpresent	notpresent	no	no	no	good	no	no	notckd

384 rows × 11 columns

Outlier Removal

In [14]:

```
1 descriptive=pd.DataFrame(index=["Mean","Median","Mode","Q1:25%","Q2:50%",
2                               "Q3:75%","99%","Q4:100%","IQR","1.5rule","Lesser","Greater","Min","Max"],
3
4 for columnName in quan:
5     descriptive[columnName]["Mean"]=dataset[columnName].mean()
6     descriptive[columnName]["Median"]=dataset[columnName].median()
7     descriptive[columnName]["Mode"]=dataset[columnName].mode()[0]
8     descriptive[columnName]["Q1:25%"]=dataset.describe()[columnName]["25%"]
9     descriptive[columnName]["Q2:50%"]=dataset.describe()[columnName]["50%"]
10    descriptive[columnName]["Q3:75%"]=dataset.describe()[columnName]["75%"]
11    descriptive[columnName]["99%"]=np.percentile(dataset[columnName],99)
12    descriptive[columnName]["Q4:100%"]=dataset.describe()[columnName]["max"]
13    descriptive[columnName]["IQR"]=descriptive[columnName]["Q3:75%"]-descriptive[columnName]["Q1:25%"]
14    descriptive[columnName]["1.5rule"]=1.5*descriptive[columnName]["IQR"]
15    descriptive[columnName]["Lesser"]=descriptive[columnName]["Q1:25%"]-descriptive[columnName]["1.5rule"]
16    descriptive[columnName]["Greater"]=descriptive[columnName]["Q3:75%"]+descriptive[columnName]["1.5rule"]
17    descriptive[columnName]["Min"]=dataset[columnName].min()
18    descriptive[columnName]["Max"]=dataset[columnName].max()
```

In [15]:

```
1 lesser=[]
2 greater=[]
3
4 for columnName in quan:
5     if(descriptive[columnName]["Lesser"]>descriptive[columnName]["Min"]):
6         lesser.append(columnName)
7     if(descriptive[columnName]["Greater"]<descriptive[columnName]["Q4:100%"]):
8         greater.append(columnName)
9
```

In [16]:

```
1 lesser
```

Out[16]:

```
['age', 'F', 'sg', 'bgr', 'sod', 'pot', 'hemo', 'pcv', 'wc', 'rc']
```

In [17]:

```
1 greater
```

Out[17]:

```
['F', 'su', 'bgr', 'bu', 'sc', 'sod', 'pot', 'wc', 'rc']
```

In [18]:

```
1 for column in lesser:
2     dataset[column][dataset[column]<descriptive[column]["Lesser"]]=descriptive[column]["Lesser"]
3 for column in greater:
4     dataset[column][dataset[column]>descriptive[column]["Greater"]]=descriptive[column]["Greater"]
5
```

/var/folders/07/ykgp85052b11h5kz22ghn8l40000gn/T/ipykernel_3973/3400726572.py:2: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy (https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy)

```
dataset[column][dataset[column]<descriptive[column]["Lesser"]]=descriptive[column]["Lesser"]
```

/var/folders/07/ykgp85052b11h5kz22ghn8l40000gn/T/ipykernel_3973/3400726572.py:2: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy (https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy)

```
dataset[column][dataset[column]<descriptive[column]["Lesser"]]=descriptive[column]["Lesser"]
```

/var/folders/07/ykgp85052b11h5kz22ghn8l40000gn/T/ipykernel_3973/3400726572.py:2: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy (https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy)

In [19]:

```
1 descriptive=pd.DataFrame(index=["Mean","Median","Mode","Q1:25%","Q2:50%",
2                               "Q3:75%","99%","Q4:100%","IQR","1.5rule","Lesser","Greater","Min","Max"])
3 for columnName in quan:
4     descriptive[columnName]["Mean"]=dataset[columnName].mean()
5     descriptive[columnName]["Median"]=dataset[columnName].median()
6     descriptive[columnName]["Mode"]=dataset[columnName].mode()[0]
7     descriptive[columnName]["Q1:25%"]=dataset.describe()[columnName]["25%"]
8     descriptive[columnName]["Q2:50%"]=dataset.describe()[columnName]["50%"]
9     descriptive[columnName]["Q3:75%"]=dataset.describe()[columnName]["75%"]
10    descriptive[columnName]["99%"]=np.percentile(dataset[columnName],99)
11    descriptive[columnName]["Q4:100%"]=dataset.describe()[columnName]["max"]
12    descriptive[columnName]["IQR"]=descriptive[columnName]["Q3:75%"]-descriptive[columnName]["Q1:25%"]
13    descriptive[columnName]["1.5rule"]=1.5*descriptive[columnName]["IQR"]
14    descriptive[columnName]["Lesser"]=descriptive[columnName]["Q1:25%"]-descriptive[columnName]["1.5rule"]
15    descriptive[columnName]["Greater"]=descriptive[columnName]["Q3:75%"]+descriptive[columnName]["1.5rule"]
16    descriptive[columnName]["Min"]=dataset[columnName].min()
17    descriptive[columnName]["Max"]=dataset[columnName].max()
```

In [20]:

```
1 descriptive
```

Out[20]:

	id	age	F	sg	al	su	bgr	bu	sc	sod	pot	hemo	pcv
Mean	198.979167	51.574219	76.002604	1.017728	0.90625	0.0	134.552083	49.758984	2.061328	138.205729	4.378385	12.544434	39.114583
Median	198.5	55.0	80.0	1.02	0.0	0.0	122.0	42.0	1.3	138.0	4.4	12.6	40.0
Mode	0	60.0	80.0	1.02	0.0	0.0	224.25	110.125	5.4	138.0	4.4	12.6	40.0
Q1:25%	97.75	42.0	70.0	1.015	0.0	0.0	101.75	27.0	0.9	135.0	4.0	10.9	34.0
Q2:50%	198.5	55.0	80.0	1.02	0.0	0.0	122.0	42.0	1.3	138.0	4.4	12.6	40.0
Q3:75%	301.25	65.0	80.0	1.02	2.0	0.0	150.75	60.25	2.7	141.0	4.8	14.525	44.0
99%	395.17	80.17	95.0	1.025	4.0	0.0	224.25	110.125	5.4	150.0	6.0	17.617	53.17
Q4:100%	399.0	90.0	95.0	1.025	5.0	0.0	224.25	110.125	5.4	150.0	6.0	17.8	54.0
IQR	203.5	23.0	10.0	0.005	2.0	0.0	49.0	33.25	1.8	6.0	0.8	3.625	10.0
1.5rule	305.25	34.5	15.0	0.0075	3.0	0.0	73.5	49.875	2.7	9.0	1.2	5.4375	15.0
Lesser	-207.5	7.5	55.0	1.0075	-3.0	0.0	28.25	-22.875	-1.8	126.0	2.8	5.4625	19.0
Greater	606.5	99.5	95.0	1.0275	5.0	0.0	224.25	110.125	5.4	150.0	6.0	19.9625	59.0
Min	0	7.5	55.0	1.0075	0.0	0.0	28.25	1.5	0.4	126.0	2.8	5.4625	19.0
Max	399	90.0	95.0	1.025	5.0	0.0	224.25	110.125	5.4	150.0	6.0	17.8	54.0

In [21]:

```
1 lesser=[]
2 greater=[]
3
4 for columnName in quan:
5     if(descriptive[columnName]["Lesser"]>descriptive[columnName]["Min"]):
6         lesser.append(columnName)
7     if(descriptive[columnName]["Greater"]<descriptive[columnName]["Q4:100%"]):
8         greater.append(columnName)
```

In [22]:

```
1 lesser
```

Out[22]: []

In [23]:

1

greater

Out[23]:

[]

In [24]:

1

dataset

Out[24]:

	id	age	F	sg	al	su	rbc	pc	pcc	ba	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane	classification
0	0	48.0	80.0	1.0200	1.0	0.0	normal	normal	notpresent	notpresent	...	44.0	7800.0	5.2000	yes	yes	no	good	no	no	
1	1	7.5	55.0	1.0200	4.0	0.0	normal	normal	notpresent	notpresent	...	38.0	6000.0	4.7000	no	no	no	good	no	no	
2	2	62.0	80.0	1.0100	2.0	0.0	normal	normal	notpresent	notpresent	...	31.0	7500.0	4.7000	no	yes	no	poor	no	yes	
3	3	48.0	70.0	1.0075	4.0	0.0	normal	abnormal	present	notpresent	...	32.0	6700.0	3.9000	yes	no	no	poor	yes	yes	
4	4	51.0	80.0	1.0100	2.0	0.0	normal	normal	notpresent	notpresent	...	35.0	7300.0	4.6000	no	no	no	good	no	no	
...	
395	395	55.0	80.0	1.0200	0.0	0.0	normal	normal	notpresent	notpresent	...	47.0	6700.0	4.9000	no	no	no	good	no	no	no
396	396	42.0	70.0	1.0250	0.0	0.0	normal	normal	notpresent	notpresent	...	54.0	7800.0	5.8125	no	no	no	good	no	no	no
397	397	12.0	80.0	1.0200	0.0	0.0	normal	normal	notpresent	notpresent	...	49.0	6600.0	5.4000	no	no	no	good	no	no	no
398	398	17.0	60.0	1.0250	0.0	0.0	normal	normal	notpresent	notpresent	...	51.0	7200.0	5.8125	no	no	no	good	no	no	no
399	399	58.0	80.0	1.0250	0.0	0.0	normal	normal	notpresent	notpresent	...	53.0	6800.0	5.8125	no	no	no	good	no	no	no

384 rows × 26 columns

Saving the Preprocessed dataset as a New File

In [25]:

1

dataset.to_csv("PreProcessed_kidney_disease.csv", index=False)