```
# Importing Libraries:
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt


dataset=pd.read_csv(r"/content/kidney_disease.csv")



# Top 5 records:
dataset.head()
```

	id	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	bu	sc	sod	pot	hemo	pcv	wc	rc	htn
0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	121.0	36.0	1.2	NaN	NaN	15.4	44	7800	5.2	yes
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	NaN	18.0	0.8	NaN	NaN	11.3	38	6000	NaN	no
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	423.0	53.0	1.8	NaN	NaN	9.6	31	7500	NaN	no
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	117.0	56.0	3.8	111.0	2.5	11.2	32	6700	3.9	yes
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	106.0	26.0	1.4	NaN	NaN	11.6	35	7300	4.6	no

```
# Dropping unneccsary feature :
dataset = dataset.drop('id', axis=1)


# Shape of dataset:
dataset.shape
```

```
(400, 25)
```

```
# Cheaking Missing (NaN) Values:
dataset.isnull().sum()
```

```
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               70
wc               105
rc               130
htn                2
dm                 2
cad                2
appet              1
pe                 1
ane                1
classification     0
dtype: int64
```

```
# Description:
dataset.describe()
```

	age	bp	sg	al	su	bgr	bu	sc	sod	pot	
count	391.000000	388.000000	353.000000	354.000000	351.000000	356.000000	381.000000	383.000000	313.000000	312.000000	348.0(
mean	51.483376	76.469072	1.017408	1.016949	0.450142	148.036517	57.425722	3.072454	137.528754	4.627244	12.5(
std	17.169714	13.683637	0.005717	1.352679	1.099191	79.281714	50.503006	5.741126	10.408752	3.193904	2.9(
min	2.000000	50.000000	1.005000	0.000000	0.000000	22.000000	1.500000	0.400000	4.500000	2.500000	3.1(
25%	42.000000	70.000000	1.010000	0.000000	0.000000	99.000000	27.000000	0.900000	135.000000	3.800000	10.3(

```
# Datatypes:
dataset.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
```

```
dataset.head()
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane
0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	121.0	...	44	7800	5.2	yes	yes	no	good	no	no
1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	NaN	...	38	6000	NaN	no	no	no	good	no	no
2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	423.0	...	31	7500	NaN	no	yes	no	poor	no	yes
3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	117.0	...	32	6700	3.9	yes	no	no	poor	yes	yes
4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	106.0	...	35	7300	4.6	no	no	no	good	no	no

5 rows × 25 columns

```
dataset['rbc'].value_counts()
```

```
normal      201
abnormal     47
Name: rbc, dtype: int64
```

```
dataset['rbc'] = dataset['rbc'].replace(to_replace = {'normal' : 0, 'abnormal' : 1})
```

```
dataset['pc'].value_counts()
```

```
normal      259
abnormal     76
Name: pc, dtype: int64
```

```
dataset['pc'] = dataset['pc'].replace(to_replace = {'normal' : 0, 'abnormal' : 1})
```

```
dataset['pcc'].value_counts()
```

```
notpresent    354
```

```
present        42
Name: pcc, dtype: int64
```

```
dataset['pcc'] = dataset['pcc'].replace(to_replace = {'notpresent':0,'present':1})
```

```
dataset['ba'].value_counts()
```

```
notpresent    374
present        22
Name: ba, dtype: int64
```

```
dataset['ba'] = dataset['ba'].replace(to_replace = {'notpresent':0,'present':1})
```

```
dataset['htn'].value_counts()
```

```
no     251
yes    147
Name: htn, dtype: int64
```

```
dataset['htn'] = dataset['htn'].replace(to_replace = {'yes' : 1, 'no' : 0})
```

```
dataset['dm'].value_counts()
```

```
no       258
yes      134
\tno       3
\tyes      2
 yes       1
Name: dm, dtype: int64
```

```
dataset['dm'] = dataset['dm'].replace(to_replace = {'\tyes':'yes', ' yes':'yes', '\tno':'no'})
```

```
dataset['dm'] = dataset['dm'].replace(to_replace = {'yes' : 1, 'no' : 0})
```

```
dataset['cad'].value_counts()
```

```
no      362
yes      34
\tno      2
Name: cad, dtype: int64
```

```
dataset['cad'] = dataset['cad'].replace(to_replace = {'\tno':'no'})
```

```
dataset['cad'] = dataset['cad'].replace(to_replace = {'yes' : 1, 'no' : 0})
```

```
dataset['appet'].unique()
```

```
array(['good', 'poor', nan], dtype=object)
```

```
dataset['appet'] = dataset['appet'].replace(to_replace={'good':1,'poor':0,'no':np.nan})
```

```
dataset['pe'].value_counts()
```

```
no     323
yes     76
Name: pe, dtype: int64
```

```
dataset['pe'] = dataset['pe'].replace(to_replace = {'yes' : 1, 'no' : 0})
```

```
dataset['ane'].value_counts()
```

```
no     339
yes     60
Name: ane, dtype: int64
```

```
dataset['ane'] = dataset['ane'].replace(to_replace = {'yes' : 1, 'no' : 0})

dataset['classification'].value_counts()
```

```
ckd       248
notckd    150
ckd\t       2
Name: classification, dtype: int64
```

```
dataset['classification'] = dataset['classification'].replace(to_replace={'ckd\t':'ckd'})


dataset["classification"] = [1 if i == "ckd" else 0 for i in dataset["classification"]]


dataset.head()
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane	classification
0	48.0	80.0	1.020	1.0	0.0	NaN	0.0	0.0	0.0	121.0	...	44	7800	5.2	1.0	1.0	0.0	1.0	0.0	0.0	1
1	7.0	50.0	1.020	4.0	0.0	NaN	0.0	0.0	0.0	NaN	...	38	6000	NaN	0.0	0.0	0.0	1.0	0.0	0.0	1
2	62.0	80.0	1.010	2.0	3.0	0.0	0.0	0.0	0.0	423.0	...	31	7500	NaN	0.0	1.0	0.0	0.0	0.0	1.0	1
3	48.0	70.0	1.005	4.0	0.0	0.0	1.0	1.0	0.0	117.0	...	32	6700	3.9	1.0	0.0	0.0	0.0	1.0	1.0	1
4	51.0	80.0	1.010	2.0	0.0	0.0	0.0	0.0	0.0	106.0	...	35	7300	4.6	0.0	0.0	0.0	1.0	0.0	0.0	1

5 rows × 25 columns

```
# Datatypes:
dataset.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                object
wc                 object
rc                 object
htn               float64
dm                float64
cad               float64
appet             float64
pe                float64
ane               float64
classification      int64
dtype: object
```

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

```
# Datatypes:
dataset.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
```

```
# Description:
dataset.describe()
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...

```
# Cheaking Missing (NaN) Values:
dataset.isnull().sum().sort_values(ascending=False)
```

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

```
dataset.columns
```

```
Index(['age', 'bp', 'sg', 'al', 'su', 'rbc', 'pc', 'pcc', 'ba', 'bgr', 'bu',
       'sc', 'sod', 'pot', 'hemo', 'pcv', 'wc', 'rc', 'htn', 'dm', 'cad',
       'appet', 'pe', 'ane', 'classification'],
      dtype='object')
```

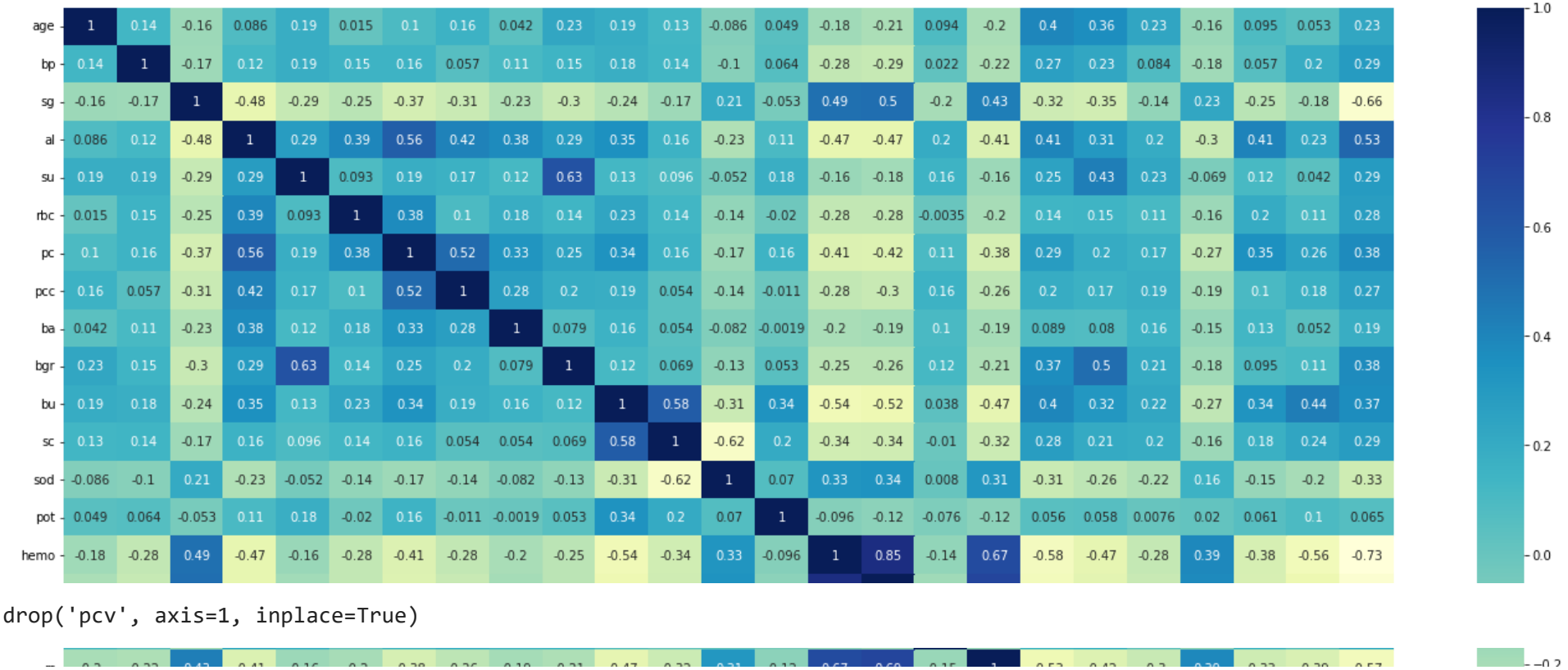
```
features = ['age', 'bp', 'sg', 'al', 'su', 'rbc', 'pc', 'pcc', 'ba', 'bgr', 'bu',
           'sc', 'sod', 'pot', 'hemo', 'pcv', 'wc', 'rc', 'htn', 'dm', 'cad',
           'appet', 'pe', 'ane']


for feature in features:
    dataset[feature] = dataset[feature].fillna(dataset[feature].median())


dataset.isnull().any().sum()
```

```
0
```

```
plt.figure(figsize=(24,14))
sns.heatmap(dataset.corr(), annot=True, cmap='YlGnBu')
plt.show()
```




```
dataset.drop('pcv', axis=1, inplace=True)
```

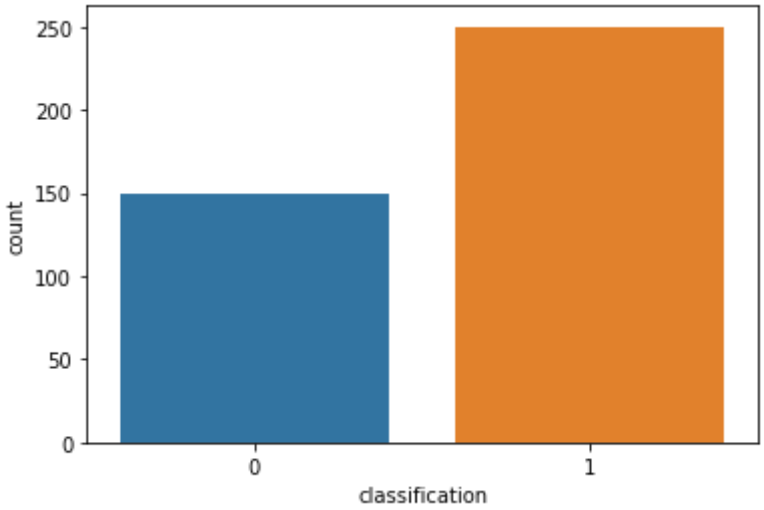
```
dataset.head()
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	hemo	wc	rc	htn	dm	cad	appet	pe	ane	classification
0	48.0	80.0	1.020	1.0	0.0	0.0	0.0	0.0	0.0	121.0	...	15.4	7800.0	5.2	1.0	1.0	0.0	1.0	0.0	0.0	1
1	7.0	50.0	1.020	4.0	0.0	0.0	0.0	0.0	0.0	121.0	...	11.3	6000.0	4.8	0.0	0.0	0.0	1.0	0.0	0.0	1
2	62.0	80.0	1.010	2.0	3.0	0.0	0.0	0.0	0.0	423.0	...	9.6	7500.0	4.8	0.0	1.0	0.0	0.0	0.0	1.0	1
3	48.0	70.0	1.005	4.0	0.0	0.0	1.0	1.0	0.0	117.0	...	11.2	6700.0	3.9	1.0	0.0	0.0	0.0	1.0	1.0	1
4	51.0	80.0	1.010	2.0	0.0	0.0	0.0	0.0	0.0	106.0	...	11.6	7300.0	4.6	0.0	0.0	0.0	1.0	0.0	0.0	1

5 rows × 24 columns

```
# Target feature:
sns.countplot(dataset['classification'])
```

```
/usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pass the following variable as a keyword arg:
  FutureWarning
<matplotlib.axes._subplots.AxesSubplot at 0x7f82460d0790>
```



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