```
import pandas as pd #used for data manipulation
```

```
import numpy as np #used for numerical analysis
```

```
from collections import Counter as c # return counts of number of classess
```

```
import matplotlib.pyplot as plt #used for data visualization
```

```
import seaborn as sns #data visualization librory
```

```
import missingno as msno #finding missing values
```

```
from sklearn.metrics import accuracy_score,confusion_matrix#model performance
```

```
from sklearn.model_selection import train_test_split #splics data in randam train and test array
```

```
from sklearn.preprocessing import LabelEncoder #encoding the levels of categotical fetures
```

```
from sklearn.linear_model import LogisticRegression #classification ML algorithm
```

```
import pickle #python object hierarchy is converted into a byte stream,
```

```
data = pd.read_csv(r"/content/kidney_disease.csv")# loading the csv data
```

```
data.head() #return you the first 5 rows values
```

	id	age	bp	sg	al	su	rbc	pc	pcc	ba	...	pcv	
0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	...	44	7
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	...	38	6
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	...	31	7
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32	6
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	...	35	7

5 rows × 26 columns

```
data.columns #return all the column names
```

```
    Index(['id', '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')
```

```
data.shape
data.drop('id',axis = 1,inplace = True)
```

```
data.columns = ['age', 'blood_pressure', 'specific_gravity', 'albumin',
                'sugar', 'red_blood_cells', 'pus_cell','pus_cell_clumps', 'bacteria',
                'blood_glucose_randon', 'blood_urea','serum_creatinine','sodium','potassium',
                'haemoglobin','packed_cell_volume','white_blood_cell_count','red_blood_cell_count',
                'hypertension','diabetes_mellitus','coronary_artery_disease',
                'appetite','peda_edema','aanemia','class']#manyally giving the name off the columns
```

```
data.columns
```

```
Index(['age', 'blood_pressure', 'specific_gravity', 'albumin', 'sugar',
       'red_blood_cells', 'pus_cell', 'pus_cell_clumps', 'bacteria',
       'blood_glucose_randon', 'blood_urea', 'serum_creatinine', 'sodium',
       'potassium', 'haemoglobin', 'packed_cell_volume',
       'white_blood_cell_count', 'red_blood_cell_count', 'hypertension',
       'diabetes_mellitus', 'coronary_artery_disease', 'appetite',
       'peda_edema', 'aanemia', 'class'],
      dtype='object')
```

```
data.info()#info will give you a summary of dataset
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 25 columns):
 #   Column                   Non-Null Count  Dtype
---  ------                   --------------  -----
 0   age                      391 non-null    float64
 1   blood_pressure           388 non-null    float64
 2   specific_gravity         353 non-null    float64
 3   albumin                  354 non-null    float64
 4   sugar                    351 non-null    float64
 5   red_blood_cells          248 non-null    object
 6   pus_cell                 335 non-null    object
 7   pus_cell_clumps          396 non-null    object
 8   bacteria                 396 non-null    object
 9   blood_glucose_randon     356 non-null    float64
 10  blood_urea               381 non-null    float64
 11  serum_creatinine         383 non-null    float64
 12  sodium                   313 non-null    float64
 13  potassium                312 non-null    float64
 14  haemoglobin              348 non-null    float64
 15  packed_cell_volume       330 non-null    object
 16  white_blood_cell_count   295 non-null    object
 17  red_blood_cell_count     270 non-null    object
 18  hypertension             398 non-null    object
 19  diabetes_mellitus        398 non-null    object
 20  coronary_artery_disease  398 non-null    object
 21  appetite                 399 non-null    object
 22  peda_edema               399 non-null    object
 23  aanemia                  399 non-null    object
 24  class                    400 non-null    object
dtypes: float64(11), object(14)
memory usage: 78.2+ KB
```

```
data.isnull().any() #it will return ture if any columns is having null values
```

```
age                         True
blood_pressure              True
specific_gravity            True
albumin                     True
sugar                       True
red_blood_cells             True
pus_cell                    True
pus_cell_clumps             True
bacteria                    True
blood_glucose_randon        True
blood_urea                  True
serum_creatinine            True
sodium                      True
potassium                   True
haemoglobin                 True
packed_cell_volume          True
white_blood_cell_count      True
red_blood_cell_count        True
hypertension                True
diabetes_mellitus           True
coronary_artery_disease     True
appetite                    True
peda_edema                  True
aanemia                     True
class                      False
dtype: bool
```

```
#extracting numatic and categorical data
```

```
num_cols = [col for col in data.columns if data[col].dtype != 'object']
cat_cols = [col for col in data.columns if data[col].dtype == 'object']
```

```
num_cols
```

```
['age',
 'blood_pressure',
 'specific_gravity',
 'albumin',
 'sugar',
 'blood_glucose_randon',
 'blood_urea',
 'serum_creatinine',
 'sodium',
 'potassium',
 'haemoglobin']
```

```
#####check unique values in the categorical data
```

```
for col in cat_cols:
    print(f"{col} has {data[col].unique()} values\n")
```

```
red_blood_cells has [nan 'normal' 'abnormal'] values

pus_cell has ['normal' 'abnormal' nan] values

pus_cell_clumps has ['notpresent' 'present' nan] values

bacteria has ['notpresent' 'present' nan] values

packed_cell_volume has ['44' '38' '31' '32' '35' '39' '36' '33' '29' '28' nan '16' '24' '37' '30'
 '34' '40' '45' '27' '48' '\t?' '52' '14' '22' '18' '42' '17' '46' '23'
 '19' '25' '41' '26' '15' '21' '43' '20' '\t43' '47' '9' '49' '50' '53'
 '51' '54'] values

white_blood_cell_count has ['7800' '6000' '7500' '6700' '7300' nan '6900' '9600' '12100' '4500'
 '12200' '11000' '3800' '11400' '5300' '9200' '6200' '8300' '8400' '10300'
 '9800' '9100' '7900' '6400' '8600' '18900' '21600' '4300' '8500' '11300'
 '7200' '7700' '14600' '6300' '\t6200' '7100' '11800' '9400' '5500' '5800'
 '13200' '12500' '5600' '7000' '11900' '10400' '10700' '12700' '6800'
 '6500' '13600' '10200' '9000' '14900' '8200' '15200' '5000' '16300'
 '12400' '\t8400' '10500' '4200' '4700' '10900' '8100' '9500' '2200'
 '12800' '11200' '19100' '\t?' '12300' '16700' '2600' '26400' '8800'
 '7400' '4900' '8000' '12000' '15700' '4100' '5700' '11500' '5400' '10800'
 '9900' '5200' '5900' '9300' '9700' '5100' '6600'] values

red_blood_cell_count has ['5.2' nan '3.9' '4.6' '4.4' '5' '4.0' '3.7' '3.8' '3.4' '2.6' '2.8' '4.3'
 '3.2' '3.6' '4' '4.1' '4.9' '2.5' '4.2' '4.5' '3.1' '4.7' '3.5' '6.0'
 '5.0' '2.1' '5.6' '2.3' '2.9' '2.7' '8.0' '3.3' '3.0' '3' '2.4' '4.8'
 '\t?' '5.4' '6.1' '6.2' '6.3' '5.1' '5.8' '5.5' '5.3' '6.4' '5.7' '5.9'
 '6.5'] values

hypertension has ['yes' 'no' nan] values

diabetes_mellitus has ['yes' 'no' ' yes' '\tno' '\tyes' nan] values

coronary_artery_disease has ['no' 'yes' '\tno' nan] values

appetite has ['good' 'poor' nan] values

peda_edema has ['no' 'yes' nan] values

aanemia has ['no' 'yes' nan] values

class has ['ckd' 'ckd\t' 'notckd'] values
```

```
#####to handel the skewness in the data
def handel_outlier(col):
    data[col] =np.log1p(data[col])
```

```
handel_outlier('blood_urea')
handel_outlier('sodium')
handel_outlier('potassium')
handel_outlier('serum_creatinine')
handel_outlier('sugar')


##that explins why soe data still skeness although we to process on it, beacaus it stil has null data
data.isna().sum()
```

```
age                         9
blood_pressure             12
specific_gravity           47
albumin                    46
sugar                      49
red_blood_cells           152
pus_cell                   65
pus_cell_clumps             4
bacteria                    4
blood_glucose_randon       44
blood_urea                 19
serum_creatinine           17
sodium                     87
potassium                  88
haemoglobin                52
packed_cell_volume         70
white_blood_cell_count    105
red_blood_cell_count      130
hypertension                2
diabetes_mellitus           2
coronary_artery_disease     2
appetite                    1
peda_edema                  1
aanemia                     1
class                       0
dtype: int64
```

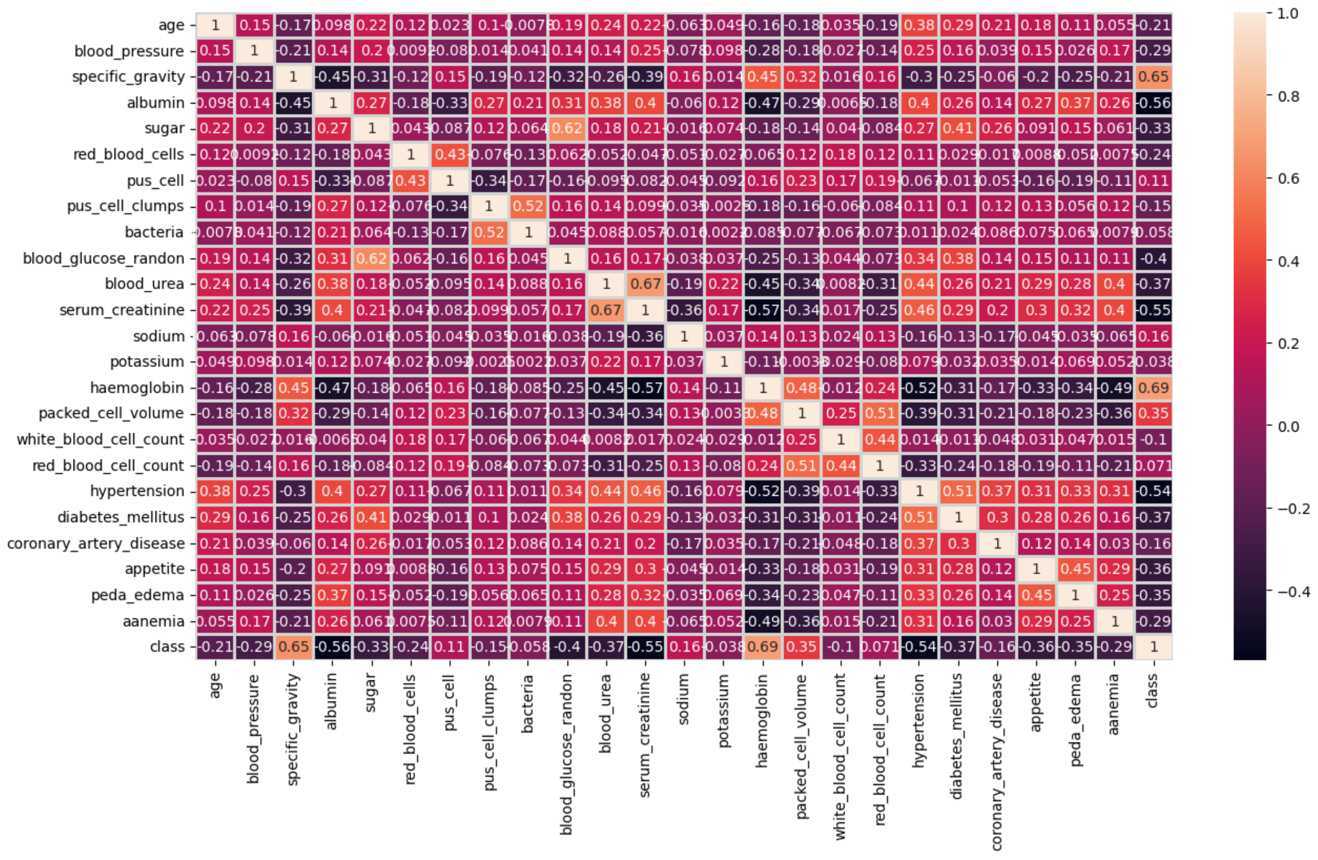
```
#filling null values,we will use two methods, rndom sampling for higher null values and
# mean/mide sampling for lower null values



def random_value_imputation(feature):
    random_sample = data[feature].dropna().sample(data[feature].isna().sum())
    random_sample.index = data[data[feature].isnull()].index
    data.loc[data[feature].isnull(),feature] =random_sample


def impute_mode(feature):
    mode = data[feature].mode()[0]
    data[feature] =data[feature].fillna(mode)


###filling num columns null values uysing rando sampling method




for col in num_cols:
     random_value_imputation(col)


data[num_cols].isnull().sum()
```

```
age                    0
blood_pressure         0
specific_gravity       0
albumin                0
sugar                  0
blood_glucose_randon   0
blood_urea             0
serum_creatinine       0
sodium                 0
potassium              0
haemoglobin            0
dtype: int64
```

```
###label encoding for categorical data
from sklearn.preprocessing import LabelEncoder


encode = LabelEncoder()


for col in cat_cols:
    data[col]=encode.fit_transform(data[col])


data.head()
```

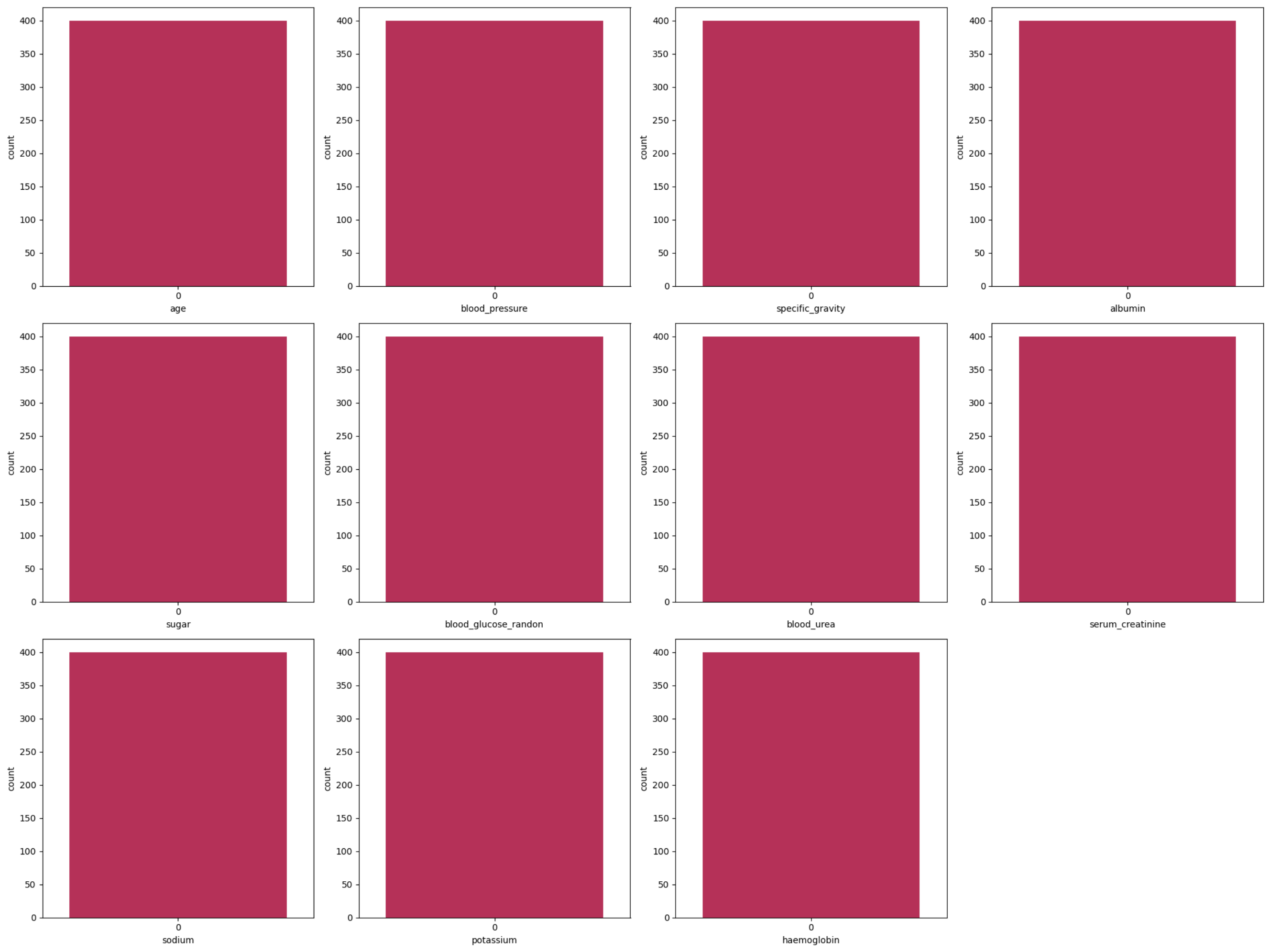
```
   age  blood_pressure  specific_gravity  albumin     sugar  red_blood_cells  pus_cell  pus_cell_clumps  bacteria
0  48.0           80.0             1.020      1.0  0.000000                2         1                0         0
1   7.0           50.0             1.020      4.0  0.000000                2         1                0         0
2  62.0           80.0             1.010      2.0  1.386294                1         1                0         0
3  48.0           70.0             1.005      4.0  0.000000                1         0                1         0
4  51.0           80.0             1.010      2.0  0.000000                1         1                0         0

5 rows × 25 columns
```

```
#heatmap of data


plt.figure(figsize = (15,8))
sns.heatmap(data.corr(),annot = True, linewidths =2, linecolor = 'lightgrey')
plt.show()
```



```
#looking at categorical columns
plt.figure(figsize =(20,15))
plotnumber = 1
```

```
for column in num_cols:
    if plotnumber<=11:
        ax = plt.subplot(3, 4, plotnumber)
        sns.countplot(data[column],palette = 'rocket')
        plt.xlabel(column)

    plotnumber +=1

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



```
data[cat_cols].isnull().sum()
```

```
red_blood_cells           0
pus_cell                  0
pus_cell_clumps           0
bacteria                  0
packed_cell_volume        0
white_blood_cell_count    0
red_blood_cell_count      0
hypertension              0
diabetes_mellitus         0
coronary_artery_disease   0
appetite                  0
peda_edema                0
aanemia                   0
class                     0
dtype: int64
```

```
#checking for null values
```

```
data.isna().sum().sort_values(ascending = False)
```

```
    age                        0
    potassium                  0
    aanemia                    0
    peda_edema                 0
    appetite                   0
    coronary_artery_disease    0
    diabetes_mellitus          0
    hypertension               0
    red_blood_cell_count       0
    white_blood_cell_count     0
    packed_cell_volume         0
    haemoglobin                0
    sodium                     0
    blood_pressure             0
    serum_creatinine           0
    blood_urea                 0
    blood_glucose_randon       0
    bacteria                   0
    pus_cell_clumps            0
    pus_cell                   0
    red_blood_cells            0
    sugar                      0
    albumin                    0
    specific_gravity           0
    class                      0
    dtype: int64
```

```
#checking numerical features distribution
```

```
plt.figure(figsize = (20, 15))
plotnumber = 1

for column in num_cols:
    if plotnumber <=14:
        ax = plt.subplot(3, 5, plotnumber)
        sns.distplot(data[column])
        plt.xlabel(column)

    plotnumber += 1

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

```
<ipython-input-53-89eda4e8a1a5>:7: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with
similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see
https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

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```

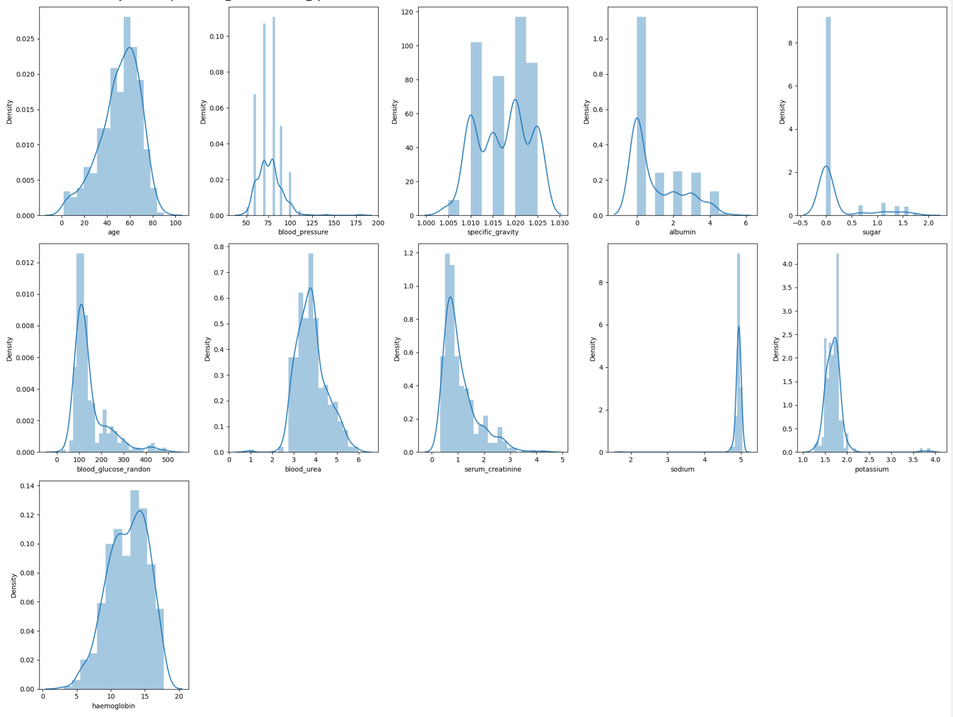
Density
age
blood_pressure
specific_gravity
albumin
sugar
blood_glucose_randon
blood_urea
serum_creatinine
sodium
potassium
haemoglobin