Project Name:	Project - Early Detection of Chronic Kidney	
	Disease using Machine Learning	
Team ID:	PNT2022TMID13778	

# **SPRINT 1**

## Collecting, Visualizing, and Preprocessing the Dataset

## 1.Importing the packages

import numpy as np

import pandas as pd

import matplotlib.pyplot as plt

from collections import Counter as c

import seaborn as sns

import missingno as msng

from sklearn.metrics import accuracy\_score,confusion\_matrix

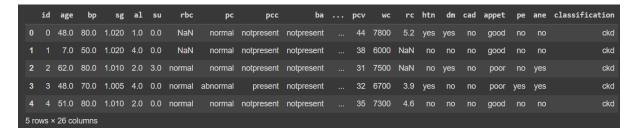
from sklearn.model\_selection import train\_test\_split

from sklearn.preprocessing import LabelEncoder

from sklearn.linear\_model import LogisticRegression

#### **#Data Collections**

data=pd.read\_csv("/content/drive/MyDrive/chronickidneydisease.csv")
data.head()



data.drop(['id'],axis=1,inplace=True)

data.columns

```
data.columns=['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']
```

#### data.columns

## data['classification'].unique()

data.info()

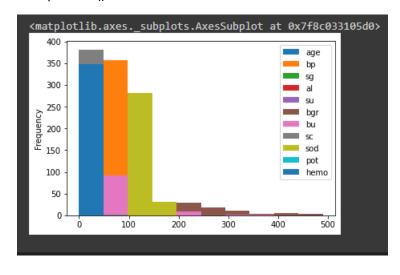
RangeIndex: 400 entries, 0 to 399				
	columns (total			B.t
#	Column	Non-	-Null Count	Dtype
		304	11	6364
0	age		non-null	float64
1	bp		non-null	float64
2	sg		non-null	float64
3	al		non-null	float64
4	su		non-null	float64
5	rbc		non-null	object
6	pc		non-null	object
7	рсс		non-null	object
8	ba	396	non-null	object
9	bgr	356	non-null	float64
10	bu	381	non-null	float64
11	sc	383	non-null	float64
12	sod	313	non-null	float64
13	pot	312	non-null	float64
14	hemo	348	non-null	float64
15	pcv	330	non-null	object
16	WC	295	non-null	object
17	rc	270	non-null	object
18	htn	398	non-null	object
19	dm	398	non-null	object
20	cad	398	non-null	object
21	appet	399	non-null	object
22	pe	399	non-null	object
23	ane	399	non-null	object
24	classification	400	non-null	object
dtypes: float64(11), object(14)				

## 2. Data visualization

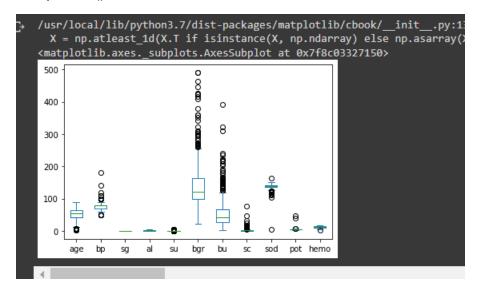
from matplotlib import pyplot

data.plot

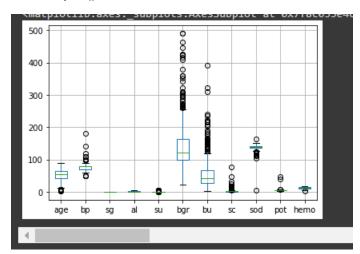
data.plot.hist()



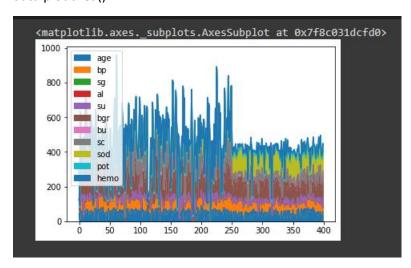
## data.plot.box()



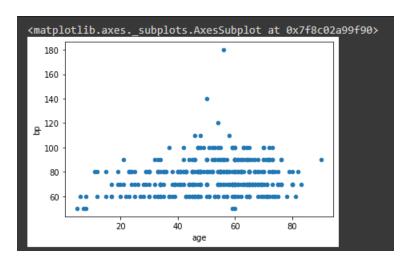
## data.boxplot()



## data.plot.area()



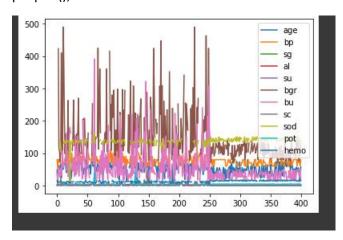
data.plot.scatter(x='age',y='bp')



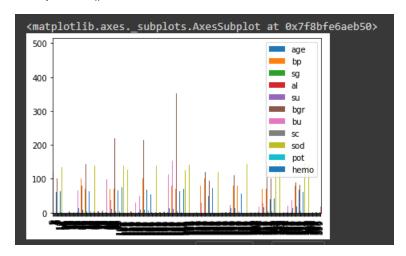
pie = data

pie

pie.plot();



data.plot.bar()



data.corr()

plt.figure(figsize=(15,8));

plt.title("Correlation",color="green")

#### sns.heatmap(data.corr(),linewidth=1,annot=True);



sns.set\_theme(style="white")

fig, ((ax1, ax2,ax3,ax4,ax5), (ax6, ax7,ax8,ax9,ax10))= plt.subplots(nrows=2, ncols=5, figsize=(18,14))

sns.boxplot(data=data,x="age",ax=ax1)

sns.boxplot(data=data,x="bp",ax=ax2)

sns.boxplot(data=data,x="sg",ax=ax3)

sns.boxplot(data=data,x="al",ax=ax4)

sns.boxplot(data=data,x="bgr",ax=ax5)

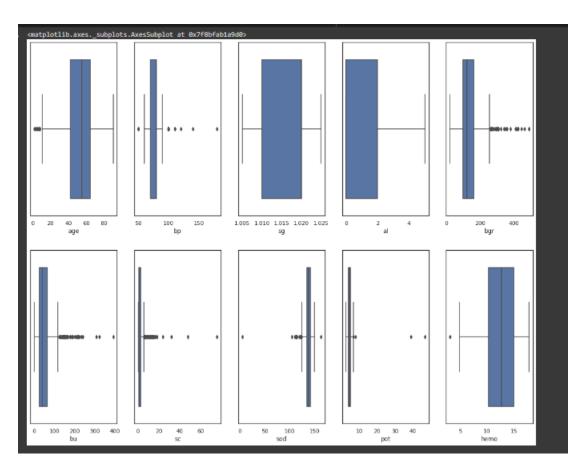
sns.boxplot(data=data,x="bu",ax=ax6)

sns.boxplot(data=data,x="sc",ax=ax7)

sns.boxplot(data=data,x="sod",ax=ax8)

sns.boxplot(data=data,x="pot",ax=ax9)

sns.boxplot(data=data,x="hemo",ax=ax10)



## 3. Data Preprocessing

```
data['classification']=data['classification'].replace("ckd\t",'ckd')
catcols=set(data.dtypes[data.dtypes=='O'].index.values)
print(catcols)
for i in catcols:
    print("columns:",i)
    print(c(data[i]))
    print('*'*120+'\n')
catcols.remove('rbc')
catcols.remove('pcv')
catcols.remove('wc')
```

```
appeť',
      classification',
contcols=set(data.dtypes[data.dtypes!='O'].index.values)
contcols
for i in catcols:
  print("continuous columns :",i)
  print(c(data[i]))
  print('*'*120+'\n')
contcols.remove('sg')
contcols.remove('al')
contcols.remove('su')
print(contcols)
contcols.add('rbc')
contcols.add('pc')
contcols.add('wc')
print(contcols)
catcols.add('sg')
catcols.add('al')
catcols.add('su')
print(catcols)
data['cad']=data.cad.replace('\tno','no')
c(data['cad'])
data['dm']=data.dm.replace(to_replace={'\tno':'no','\tyes':'yes',' yes':'yes'})
c(data['dm'])
```

data.isna().any()

age bp sg al su rbc pc pcc ba bgr bu sc sod pot hemo pcv wc rc htn dm	True True True True True True True True
sod pot hemo pcv wc rc htn	True True True True True True True
classification dtype: bool	False

data.isna().sum()

```
9
age
                      12
bр
                      47
sg
                      46
al
                      49
su
                     152
rbc
                      65
рс
pcc
ba
                      44
bgr
                      19
bu
                      17
                      87
sod
                      88
pot
hemo
pcv
                      70
                     105
WC
                     130
rc
htn
dm
                       2
cad
                       1
appet
                       1
pe
                       1
classification
                       0
dtype: int64
```

data.pcv=pd.to\_numeric(data.pcv,errors='coerce')
data.wc=pd.to\_numeric(data.wc,errors='coerce')
data.rc=pd.to\_numeric(data.rc,errors='coerce')
data['bgr'].fillna(data['bgr'].mean(),inplace=True)
data['bp'].fillna(data['bp'].mean(),inplace=True)
data['bu'].fillna(data['bu'].mean(),inplace=True)
data['hemo'].fillna(data['hemo'].mean(),inplace=True)
data['pcv'].fillna(data['pcv'].mean(),inplace=True)
data['pot'].fillna(data['pot'].mean(),inplace=True)
data['rc'].fillna(data['rc'].mean(),inplace=True)
data['sc'].fillna(data['sc'].mean(),inplace=True)
data['sod'].fillna(data['sod'].mean(),inplace=True)
data['wc'].fillna(data['wc'].mean(),inplace=True)
data['htn'].fillna(data['htn'].mode()[0],inplace=True)
data['htn'].fillna(data['htn'].mode()[0],inplace=True)

data['pcc'].fillna(data['pcc'].mode()[0],inplace=True)
data['appet'].fillna(data['appet'].mode()[0],inplace=True)
data['al'].fillna(data['al'].mode()[0],inplace=True)
data['pc'].fillna(data['pc'].mode()[0],inplace=True)
data['rbc'].fillna(data['rbc'].mode()[0],inplace=True)
data['cad'].fillna(data['cad'].mode()[0],inplace=True)
data['ba'].fillna(data['ba'].mode()[0],inplace=True)
data['ane'].fillna(data['ane'].mode()[0],inplace=True)
data['su'].fillna(data['su'].mode()[0],inplace=True)
data['dm'].fillna(data['dm'].mode()[0],inplace=True)
data['pe'].fillna(data['pe'].mode()[0],inplace=True)
data['sg'].fillna(data['sg'].mode()[0],inplace=True)