



**BACHELOR OF TECHNOLOGY  
IN ARTIFICIAL INTELLIGENCE AND MACHINE LEARNING**

**TITLE:**

**“Prediction of chronic kidney disease using datamining techniques”**

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**ROLL NUMBER:2111CS020237**

## **1. Objectives**

To predict the chronic kidney disease using data mining techniques.

## **2. Dataset Description**

### **Dataset Name: Chronic Kidney Disease**

The Dataset we are using is from UCI machine learning repository. The Dataset contains 24 health related attributes like age, blood pressure, sugar, glucose, taken in 2-month period of 400 patients in which 11 numeric and 14 nominal attributes in which it consists of class label named 'Class' which classifies patients having disease and not present

[https://archive.ics.uci.edu/ml/datasets/chronic\\_kidney\\_disease](https://archive.ics.uci.edu/ml/datasets/chronic_kidney_disease)

### **Data Set Information:**

There are 24 features + class = 25 attributes

1. Age(numerical): age in years
2. Blood Pressure(numerical): bp in mm/Hg
3. Specific Gravity(nominal): sg - (1.005,1.010,1.015,1.020,1.025)
4. Albumin(nominal): al - (0,1,2,3,4,5)
5. Sugar(nominal): su - (0,1,2,3,4,5)
6. Red Blood Cells(nominal): rbc - (normal,abnormal)
7. Pus Cell (nominal): pc - (normal,abnormal)
8. Pus Cell clumps(nominal): pcc - (present,notpresent)
9. Bacteria(nominal): ba - (present,notpresent)
- 10.Blood Glucose Random(numerical): bgr in mgs/dl
- 11.Blood Urea(numerical): bu in mgs/dl
- 12.Serum Creatinine(numerical): sc in mgs/dl
- 13.Sodium(numerical): sod in mEq/L
- 14.Potassium(numerical): pot in mEq/L
- 15.Hemoglobin(numerical): hemo in gms
- 16.Packed Cell Volume(numerical)
17. White Blood Cell Count(numerical): wc in cells/cumm

- 18.Red Blood Cell Count(numerical): rc in millions/cmm
- 19.Hypertension(nominal): htn - (yes,no)
- 20.Diabetes Mellitus(nominal): dm - (yes,no)
- 21.Coronary Artery Disease(nominal): cad - (yes,no)
- 22.Appetite(nominal): appet - (good,poor)
- 23.Pedal Edema(nominal): pe - (yes,no)
- 24.Anemia(nominal): ane - (yes,no)
- 25.Class (nominal): class - (ckd, notckd)

### **3. Data Pre-Processing Steps used**

- The techniques used for filling the null values is mode.
- Used Box plot to find the outliers.
- Performed label encoding for categorical attributes.
- We used PCA to reduce the number of independent variables.
- Performed normalization of values using min-max normalization.

#### **3.1 Code**

```
import warnings
warnings.filterwarnings("ignore")
import numpy as np
import pandas as pd
from sklearn.preprocessing import MinMaxScaler
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
import seaborn as sns
df = pd.read_csv('kidney_disease.csv')
df.head()
df.shape
df.isnull().sum()
# Impuing Null values
from sklearn.impute import SimpleImputer
imp_mode = SimpleImputer(missing_values=np.nan, strategy='most_frequent')
df_imputed=pd.DataFrame(imp_mode.fit_transform(df))
```

```

df_imputed.columns=df.columns
df_imputed
df_imputed.isnull().sum()
# Finding Unique values in the columns
for i in df_imputed.columns:

print("*****",i,"*****")

print()
print(set(df_imputed[i].tolist()))
print()
print(df_imputed["rc"].mode())
print(df_imputed["wc"].mode())
print(df_imputed["pcv"].mode())
df_imputed["classification"]
df_imputed["classification"]=df_imputed["classification"].apply(lambda x:'ckd' if x=="ckd\t" else x)
df_imputed["cad"]=df_imputed["cad"].apply(lambda x:'no' if x=="\tno" else x)
df_imputed["dm"]=df_imputed["dm"].apply(lambda x:'no' if x=="\tno" else x)
df_imputed["dm"]=df_imputed["dm"].apply(lambda x:'yes' if x=="\tyes" else x)
df_imputed["dm"]=df_imputed["dm"].apply(lambda x:'yes' if x==" yes" else x)
df_imputed["rc"]=df_imputed["rc"].apply(lambda x:'5.2' if x=="\t?" else x)
df_imputed["wc"]=df_imputed["wc"].apply(lambda x:'9800' if x=="\t6200" else x)
df_imputed["wc"]=df_imputed["wc"].apply(lambda x:'9800' if x=="\t8400" else x)
df_imputed["wc"]=df_imputed["wc"].apply(lambda x:'9800' if x=="\t?" else x)
df_imputed["pcv"]=df_imputed["pcv"].apply(lambda x:'41' if x=="\t43" else x)
df_imputed["pcv"]=df_imputed["pcv"].apply(lambda x:'41' if x=="\t?" else x)
# Finding Unique values in the columns
for i in df_imputed.columns:

print("*****",i,"*****")

print()
print(set(df_imputed[i].tolist()))
print()
#Check Label Imbalance
import matplotlib.pyplot as plt
import seaborn as sns

```

```

temp=df_imputed["classification"].value_counts()
temp_df= pd.DataFrame({'classification': temp.index,'values': temp.values })
print(sns.barplot(x = 'classification', y="values", data=temp_df))
df.dtypes
# fixing data types
df_imputed.dtypes
for i in df.select_dtypes(exclude=["object"]).columns:
    df_imputed[i]=df_imputed[i].apply(lambda x: float(x))
df_imputed.dtypes
sns.pairplot(df_imputed)
# Find and remove outliers of data
def boxplots(col):
    sns.boxplot(df[col])
    plt.show()
    for i in list(df_imputed.select_dtypes(exclude=["object"]).columns)[1:]:
        boxplots(i)
# Find the distribution of data
def distplots(col):
    sns.distplot(df[col])
    plt.show()
    for i in list(df_imputed.select_dtypes(exclude=["object"]).columns)[1:]:
        distplots(i)
# Label encoding to convert categorical values to numerical
from sklearn import preprocessing
df_enco=df_imputed.apply(preprocessing.LabelEncoder().fit_transform)
df_enco
# Finding Correlations
import matplotlib.pyplot as plt
plt.figure(figsize=(20,20))
corr=df_enco.corr()
sns.heatmap(corr,annot=True)

```

### 3.2 Screenshots

```

In [2]: import warnings
warnings.filterwarnings("ignore")
import numpy as np
import pandas as pd
from sklearn.preprocessing import MinMaxScaler
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
import seaborn as sns

In [3]: df = pd.read_csv('kidney_disease.csv')
df.head()

Out[3]:
```

	id	age	bp	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	7800	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	6000	NaN	no	no	no	good	no	no	ckd
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	...	31	7500	NaN	no	yes	no	poor	no	yes	ckd
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32	6700	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	7300	4.6	no	no	no	good	no	no	ckd

```

5 rows x 26 columns

In [4]: df.shape
Out[4]: (406, 26)

In [5]: df

Out[5]:
```

	id	age	bp	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	7800	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	6000	NaN	no	no	no	good	no	no	ckd

Successful Pr... X

VIT Vellore - V X

FALLSEM202... X

VIT Vellore - V X

19MIS0393\_V... X

Successful Pr... X

Home Page - X

Home Page - X

Final Review - X

Final Review - X

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Logout

In [5]: df

Out[5]:

	id	age	bp	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	7800	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	6000	NaN	no	no	no	good	no	no	ckd
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	...	31	7500	NaN	no	yes	no	poor	no	yes	ckd
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32	6700	3.9	yes	no	poor	yes	yes	yes	ckd
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	...	35	7300	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	6700	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	7800	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	6600	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	7200	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	6800	6.1	no	no	no	good	no	no	notckd

400 rows x 26 columns

In [6]: df.isnull().sum()

Out[6]:

id	0
age	9
bp	12
sg	47
al	46
su	49
rbc	152
pc	65
pcc	4
ba	4
bgr	44
...	...

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```
In [7]: # Imputing Null values
from sklearn.impute import SimpleImputer
imp_mode = SimpleImputer(missing_values=np.nan, strategy='most_frequent')
df_imputed=pd.DataFrame(imp_mode.fit_transform(df))
df_imputed.columns=df.columns
df_imputed
```

Out[7]:

	id	age	bp	sg	al	su	rbc	pc	pcc	ba	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane	classification
0	0	48.0	80.0	1.02	1.0	0.0	normal	normal	notpresent	notpresent	...	44	7800	5.2	yes	yes	no	good	no	no	ckd
1	1	7.0	50.0	1.02	4.0	0.0	normal	normal	notpresent	notpresent	...	38	6000	5.2	no	no	no	good	no	no	ckd
2	2	62.0	80.0	1.01	2.0	3.0	normal	normal	notpresent	notpresent	...	31	7500	5.2	no	yes	no	poor	no	yes	ckd
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32	6700	3.9	yes	no	no	poor	yes	yes	ckd
4	4	51.0	80.0	1.01	2.0	0.0	normal	normal	notpresent	notpresent	...	35	7300	4.6	no	no	no	good	no	no	ckd
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
395	395	55.0	80.0	1.02	0.0	0.0	normal	normal	notpresent	notpresent	...	47	6700	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	7800	6.2	no	no	no	good	no	no	notckd
397	397	12.0	80.0	1.02	0.0	0.0	normal	normal	notpresent	notpresent	...	49	6600	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	7200	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	6800	6.1	no	no	no	good	no	no	notckd

400 rows x 26 columns

```
In [8]: df_imputed.isnull().sum()
```

Out[8]:

id	0
age	0
bp	0
sg	0

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400 rows x 26 columns

```
In [8]: df_imputed.isnull().sum()
```

Out[8]:

id	0
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

```
In [9]: # Finding unique values in the columns
for i in df_imputed.columns:
    print("*****",i,"*****")
    print()
```

```
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In [9]: # Finding Unique values in the columns
for i in df_imputed.columns:
    print("*****", i, "*****")
    print()
    print(set(df_imputed[i].tolist()))
    print()

***** id *****
{0, 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, 26, 27, 28, 29, 30, 31, 32, 3
3, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 6
4, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 9
5, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 1
21, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 1
46, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 1
71, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 1
96, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 2
21, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 2
46, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 2
71, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 2
96, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 3
21, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 3
46, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 3
71, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 3
96, 397, 398, 399}

In [10]: print(df_imputed["rc"].mode())
print(df_imputed["wc"].mode())
print(df_imputed["pcv"].mode())

0    5.2
Name: rc, dtype: object
0    9800
Name: wc, dtype: object
```

```
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In [10]: print(df_imputed["rc"].mode())
print(df_imputed["wc"].mode())
print(df_imputed["pcv"].mode())

0    5.2
Name: rc, dtype: object
0    9800
Name: wc, dtype: object
0    41
Name: pcv, dtype: object

In [11]: df_imputed["classification"]
Out[11]:
0      ckd
1      ckd
2      ckd
3      ckd
4      ckd
...
395  notckd
396  notckd
397  notckd
398  notckd
399  notckd
Name: classification, Length: 400, dtype: object

In [12]: df_imputed["classification"] = df_imputed["classification"].apply(lambda x: 'ckd' if x == 'ckd\t' else x)
df_imputed["cad"] = df_imputed["cad"].apply(lambda x: 'no' if x == "\tno" else x)
df_imputed["dm"] = df_imputed["dm"].apply(lambda x: 'no' if x == "\tno" else x)
df_imputed["dm"] = df_imputed["dm"].apply(lambda x: 'yes' if x == "\tyes" else x)
df_imputed["dm"] = df_imputed["dm"].apply(lambda x: 'yes' if x == 'yes' else x)
df_imputed["rc"] = df_imputed["rc"].apply(lambda x: '5.2' if x == '\t?' else x)
```



Successful Pr... VIT Vellore - V... FALLSEM2022... VIT Vellore - V... 19MIS0393\_V... Successful Pr... Home Page - x Home Page - x Final Review - x

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In [13]: # Finding Unique values in the columns

```
for i in df_imputed.columns:
    print("*****", i, "*****")
    print()
    print(set(df_imputed[i].tolist()))
    print()
```

```
{0.0, 1.0, 2.0, 3.0, 4.0, 5.0}
***** su *****

{0.0, 1.0, 2.0, 3.0, 4.0, 5.0}
***** rbc *****

{'normal', 'abnormal'}
***** pc *****

{'normal', 'abnormal'}
***** pcc *****

{'notpresent', 'present'}
***** hgs *****
```

In [14]: #check Label Imbalance

```
import matplotlib.pyplot as plt
import seaborn as sns

temp=df_imputed["classification"].value_counts()
temp_df= pd.DataFrame({'classification': temp.index,'values': temp.values})
print(sns.barplot(x = 'classification', y="values", data=temp_df))
```

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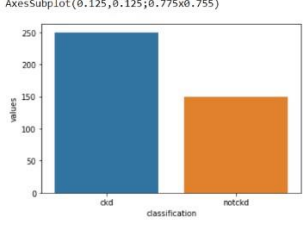
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In [14]: #check Label Imbalance

```
import matplotlib.pyplot as plt
import seaborn as sns

temp=df_imputed["classification"].value_counts()
temp_df= pd.DataFrame({'classification': temp.index,'values': temp.values})
print(sns.barplot(x = 'classification', y="values", data=temp_df))
```

AxesSubplot(0.125,0.125;0.775x0.755)



Out[15]: df.dtypes

```
id          int64
age        float64
bp         float64
sg         float64
al         float64
su         float64
rbc        object
pc         object
```

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```
In [15]: df.dtypes
Out[15]: id          int64
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
dtype: object

In [16]: # fixing data types
df_imputed.dtypes
Out[16]: id          object
age         object
```

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Successful Ph... x VIT Vellore - V x FALLSEM2022 x VIT Vellore - V x 19MIS0393\_V x Successful Ph... x Home Page - x Home Page - x Final Review - x +

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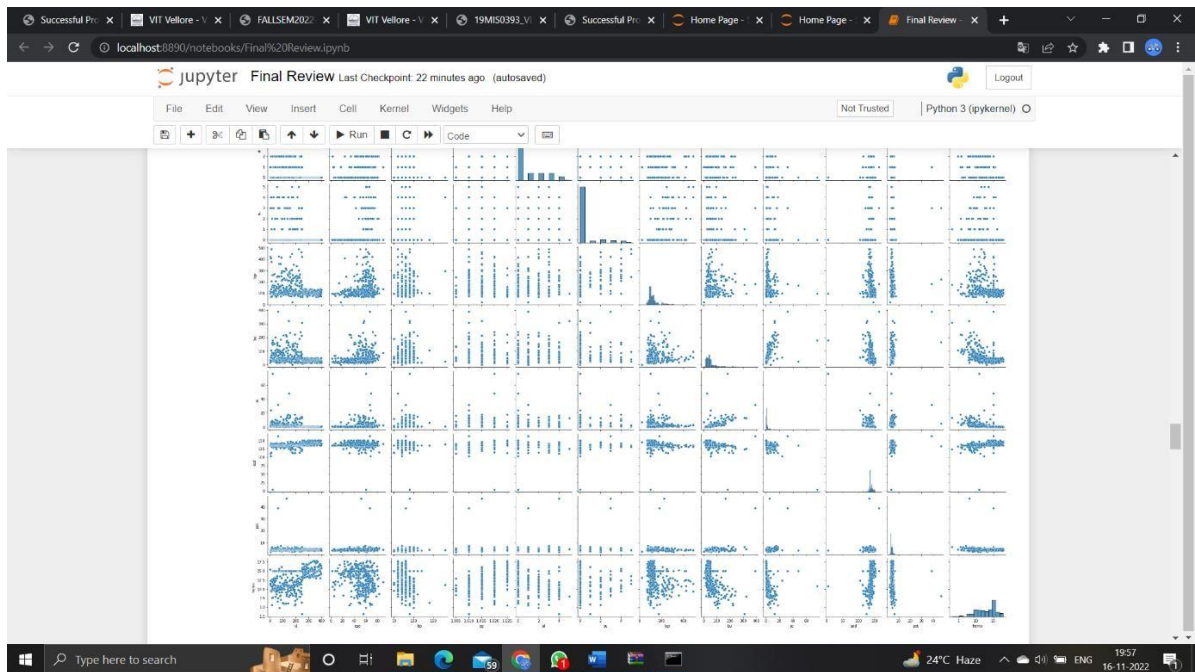
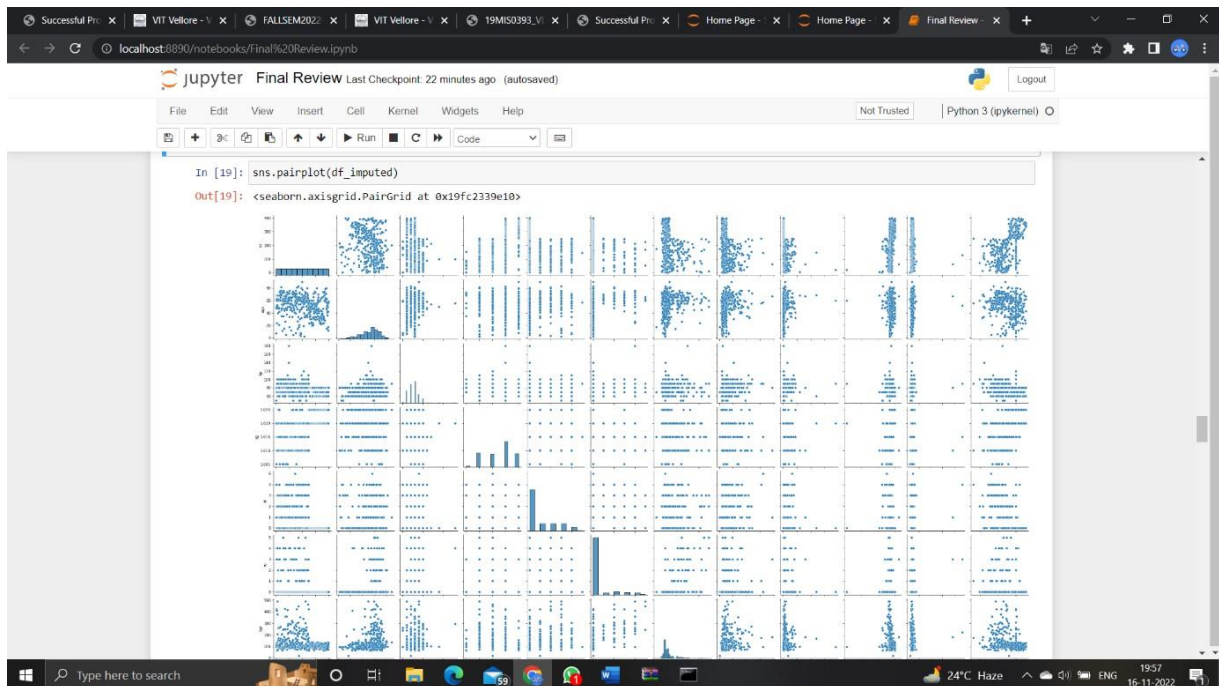
File Edit View Insert Cell Kernel Widgets Help Not Trusted Python 3 (pykernel)

```
In [17]: for i in df.select_dtypes(exclude=["object"]).columns:
df_imputed[i]=df_imputed[i].apply(lambda x: float(x))

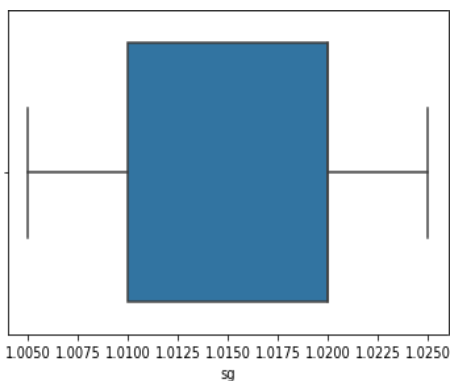
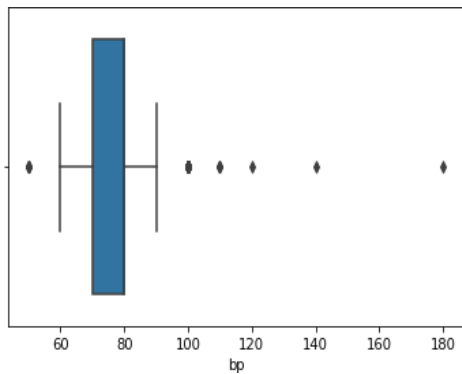
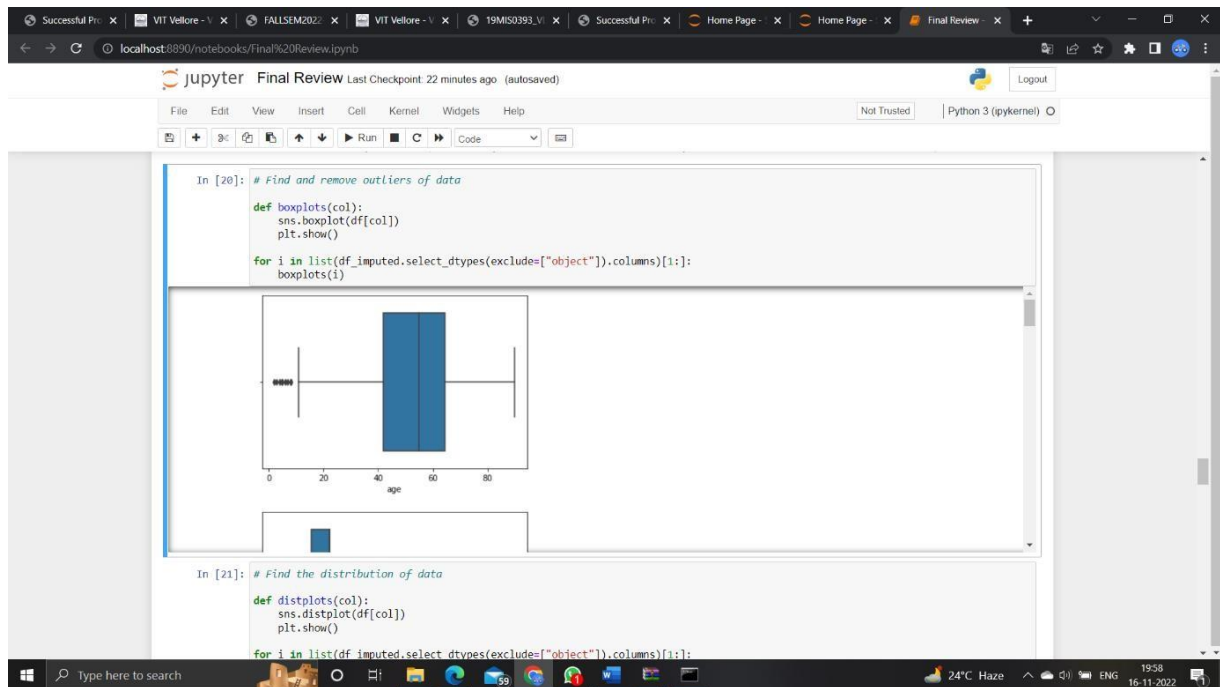
In [18]: df_imputed.dtypes
Out[18]: id          float64
age         float64
bp          float64
sg          float64
al          float64
su          float64
rbc         object
pc          object
pcc         object
ba          object
bgr         float64
bu          float64
sc          float64
sod         float64
pot         float64
hemo        float64
pcv         object
wc          object
rc          object
htn         object
dm          object
cad         object
appet       object
pe          object
ane         object
classification
dtype: object

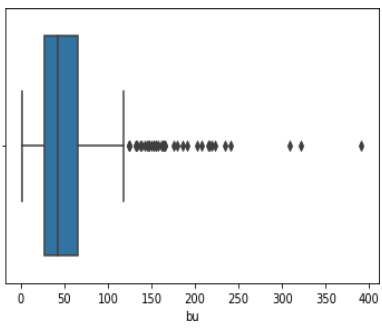
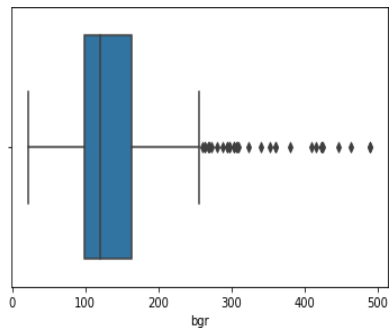
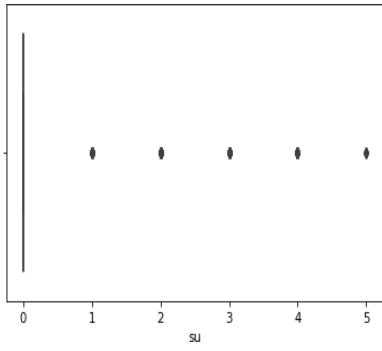
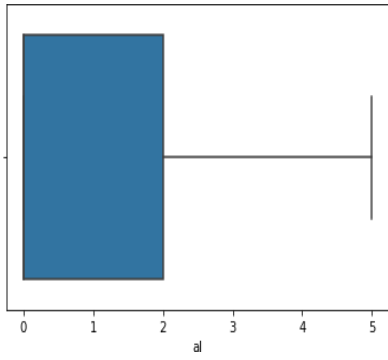
In [19]: sns.pairplot(df_imputed)
Out[19]: <seaborn.axisgrid.PairGrid at 0x19fc2339e10>
```

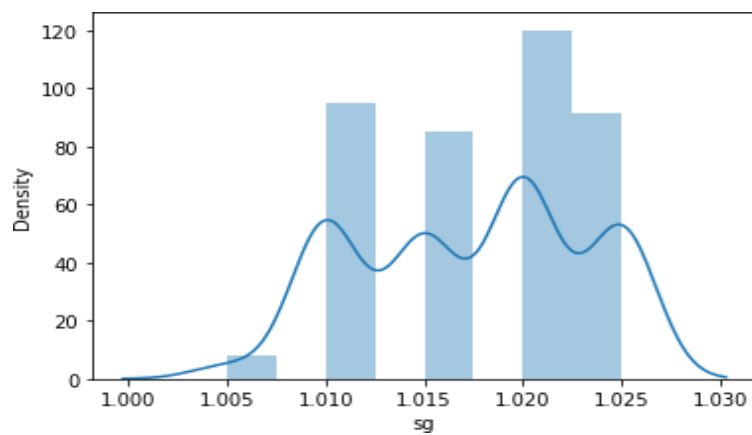
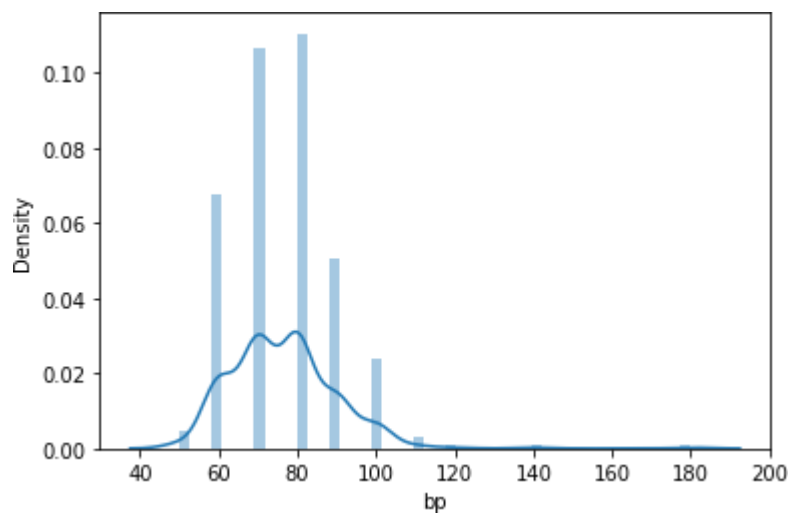
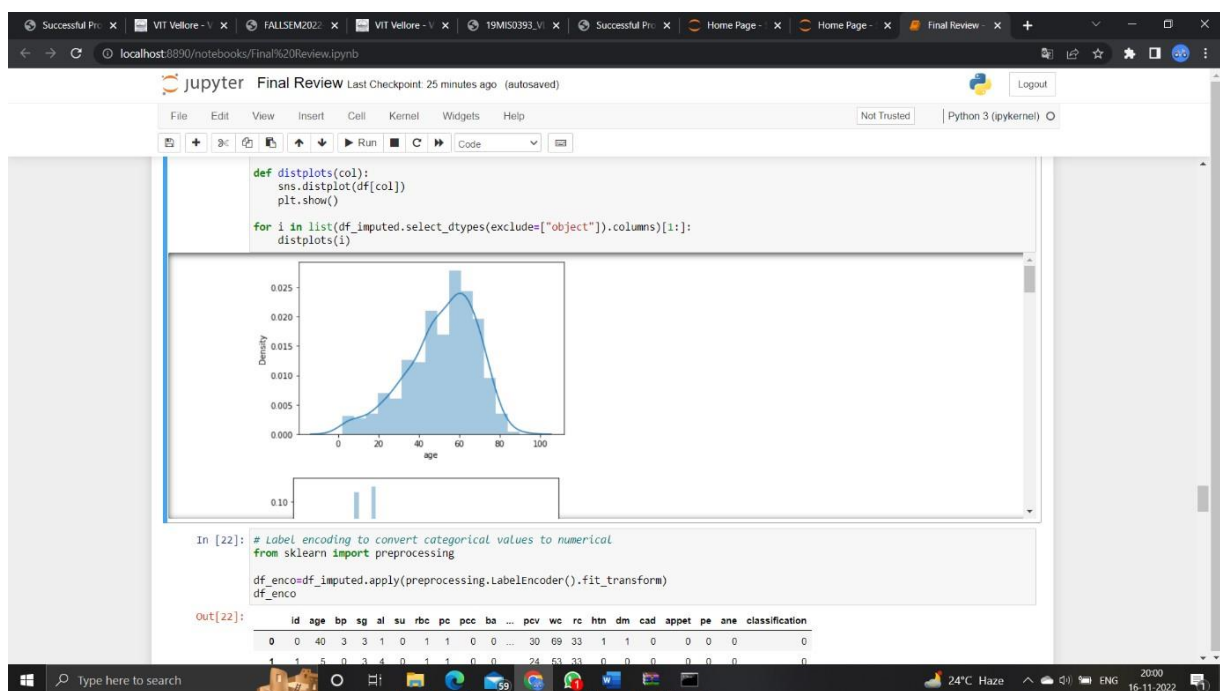
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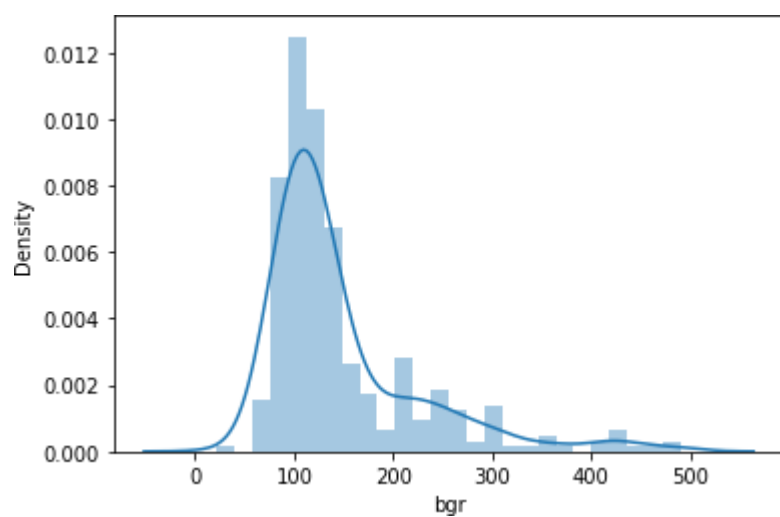
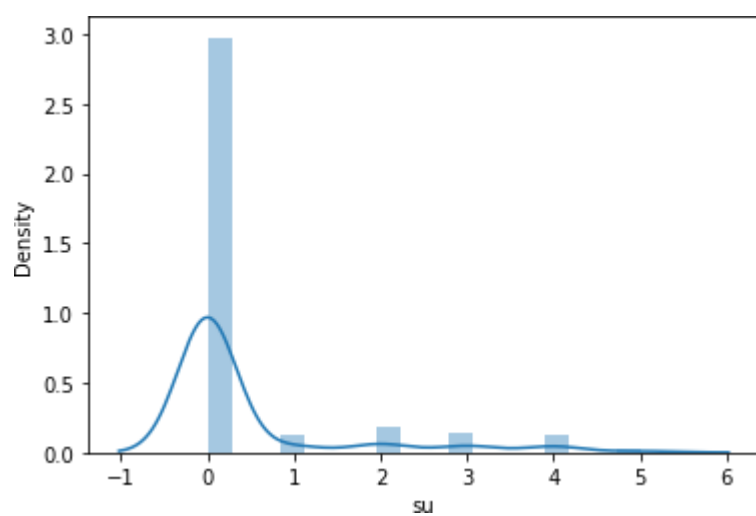
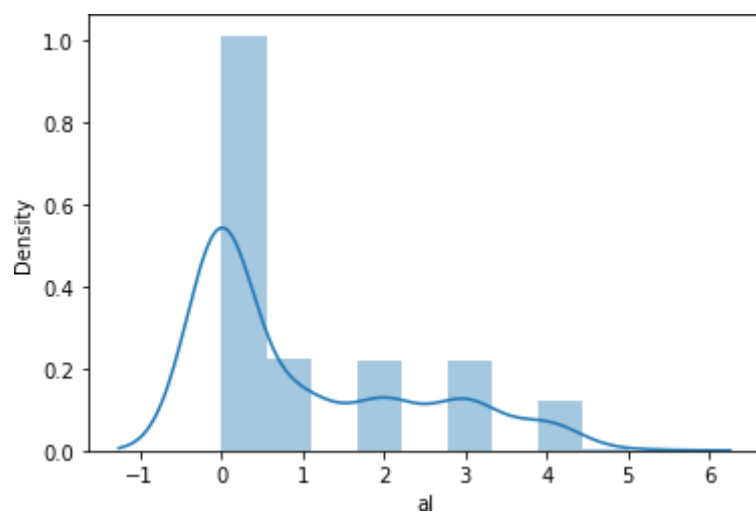


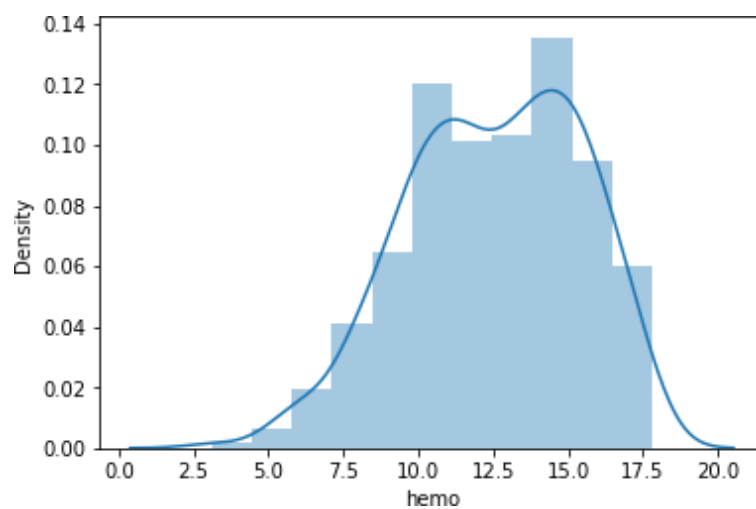
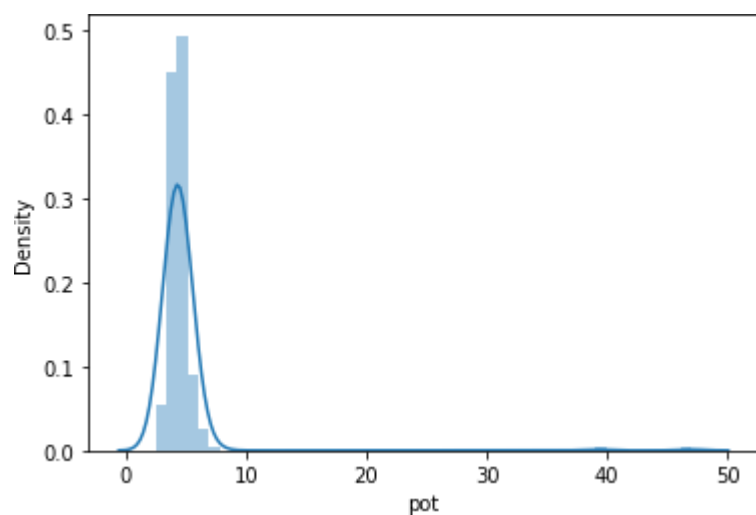
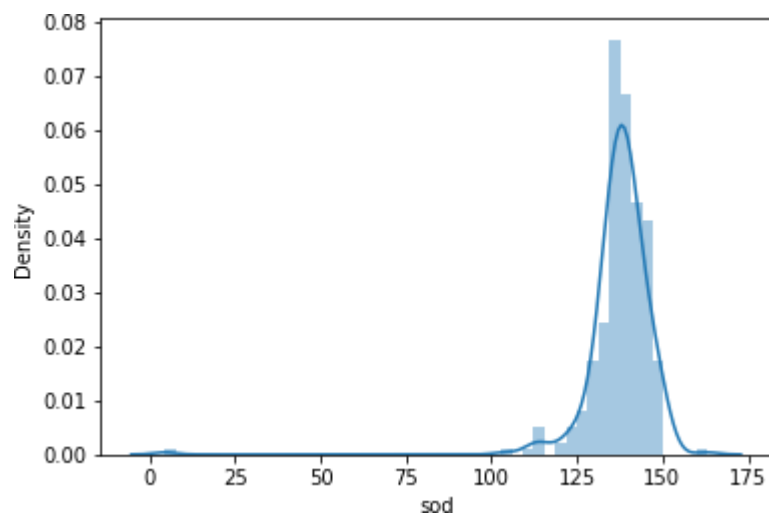
## BOXPLOT:













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In [22]: # label encoding to convert categorical values to numerical  
from sklearn import preprocessing  
df\_enco=df\_imputed.apply(preprocessing.LabelEncoder().fit\_transform)  
df\_enco

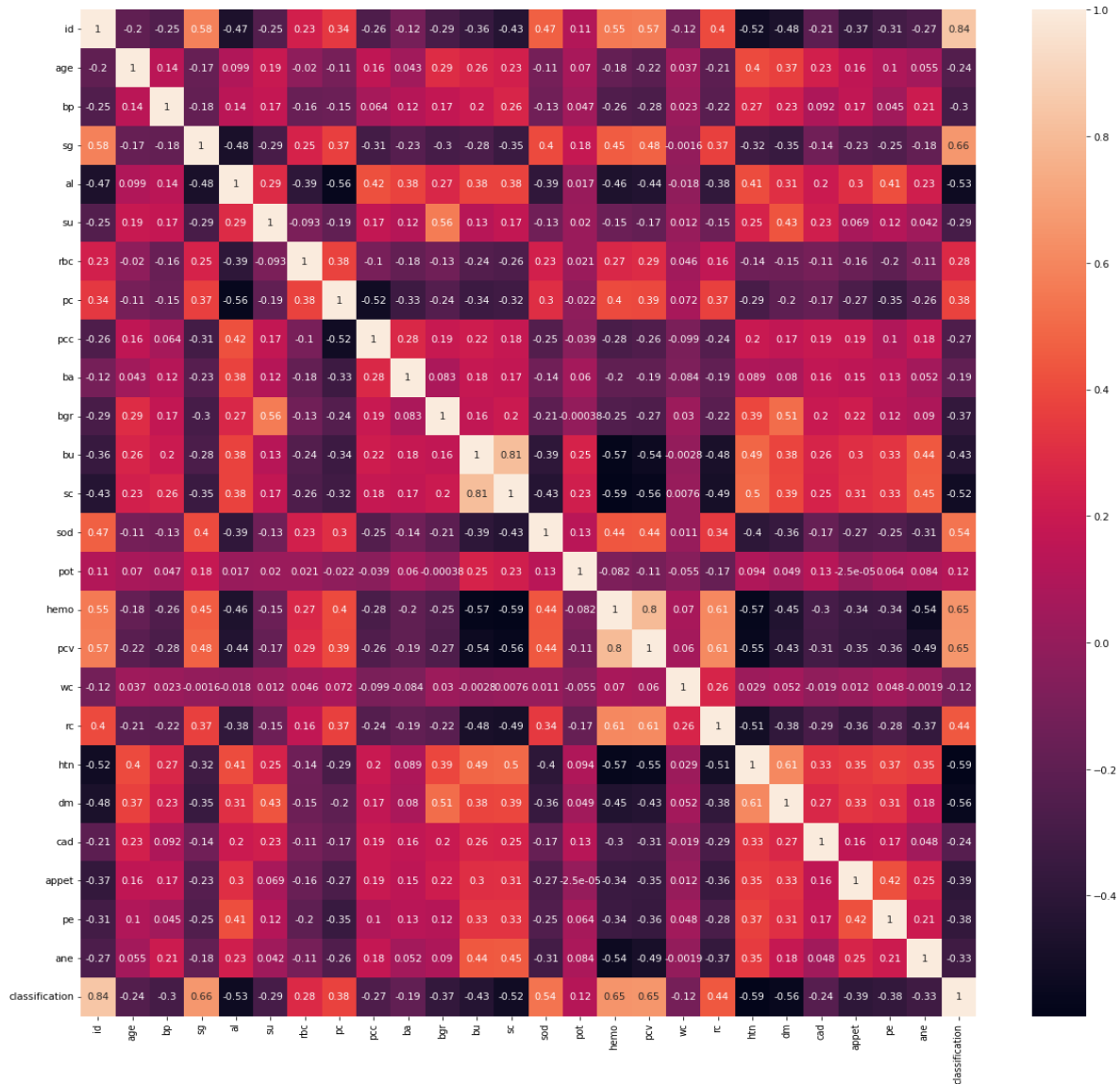
Out[22]:

	id	age	bp	sg	al	su	rbc	pc	pcc	ba	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane	classification
0	0	40	3	3	1	0	1	1	0	0	...	30	69	33	1	1	0	0	0	0	0
1	1	5	0	3	4	0	1	1	0	0	...	24	53	33	0	0	0	0	0	0	0
2	2	54	3	1	2	3	1	1	0	0	...	17	67	33	0	1	0	1	0	1	0
3	3	40	2	0	4	0	1	0	1	0	...	18	69	18	1	0	0	1	1	1	0
4	4	43	3	1	2	0	1	1	0	0	...	21	65	26	0	0	0	0	0	0	0
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
395	395	47	3	3	0	0	1	1	0	0	...	33	59	29	0	0	0	0	0	0	1
396	396	34	2	4	0	0	1	1	0	0	...	40	69	43	0	0	0	0	0	0	1
397	397	8	3	3	0	0	1	1	0	0	...	35	58	35	0	0	0	0	0	0	1
398	398	11	1	4	0	0	1	1	0	0	...	37	64	40	0	0	0	0	0	0	1
399	399	50	3	4	0	0	1	1	0	0	...	39	60	42	0	0	0	0	0	0	1

400 rows x 26 columns

In [23]: df\_enco.to\_csv("Kidney\_Disease\_Pre-Processed.csv")

In [24]: # Finding Correlations  
import matplotlib.pyplot as plt  
plt.figure(figsize=(20,20))  
corr=df\_enco.corr()  
sns.heatmap(corr,annot=True)



#### **4. Data Mining Techniques Applied:**

**Type of Classification:** Binary Classification

**Algorithms Used:**

- Decision Tree
- Naïve Bayes
- K-NN Classifier
- Random Forest

##### **4.1 Description about the Technique**

#### **Classification**

Classification is the processing of finding a set of models (or functions) that describe and distinguish data classes or concepts, for the purpose of being able to use the model to predict the class of objects whose class label is unknown. The determined model depends on the investigation of a set of training data information (i.e. data objects whose class label is known). The derived model may be represented in various forms, such as classification (if – then) rules, decision trees, and neural networks.

Data Mining has a different type of classifier:

- Decision Tree
- Naïve Bayes
- K-NN Classifier
- Random Forest

#### **Decision Tree:**

Decision Tree is a Supervised learning technique that can be used for both classification and Regression problems, but mostly it is preferred for solving Classification problems. It is a tree-structured classifier, where internal nodes represent the features of a dataset, branches represent the decision rules and each leaf node represents the outcome. In a Decision tree, there are two nodes, which are the Decision Node and Leaf Node. Decision nodes are used to make any

decision and have multiple branches, whereas Leaf nodes are the output of those decisions and do not contain any further branches. The decisions or the test are performed based on features of the given dataset. It is a graphical representation for getting all the possible solutions to a problem/decision based on given conditions. It is called a decision tree because, similar to a tree, it starts with the root node, which expands on further branches and constructs a tree-like structure. A decision tree simply asks a question, and based on the answer (Yes/No), it further split the tree into subtrees.

### **Naïve Bayes:**

Bayesian classifier is a statistical classifier. They can predict class membership probabilities, for instance, the probability that a given sample belongs to a particular class. Bayesian classification is created on the Bayes theorem. Studies comparing the classification algorithms have found a simple Bayesian classifier known as the naive Bayesian classifier to be comparable in performance with decision tree and neural network classifiers. Bayesian classifiers have also displayed high accuracy and speed when applied to large databases. Naive Bayesian classifiers adopt that the exact attribute value on a given class is independent of the values of the other attributes. This assumption is termed class conditional independence. It is made to simplify the calculations involved, and is considered “naive”. Bayesian belief networks are graphical replicas, which unlike naive Bayesian classifiers allow the depiction of dependencies among subsets of attributes. Bayesian belief can also be utilized for classification.

### **K-Nearest Neighbour (K-NN) classifier:**

The k-nearest neighbour (K-NN) classifier is considered as an example-based classifier, which means that the training documents are used for comparison instead of an exact class illustration, like the class profiles utilized by other classifiers. As such, there's no real training section. once a new document must

be classified, the k most similar documents (neighbours) are found and if a large enough proportion of them are allotted to a precise class, the new document is also appointed to the present class, otherwise not. Additionally, finding the closest neighbours is quickened using traditional classification strategies.

### **Random Forest:**

Random Forest is a popular machine learning algorithm that belongs to the supervised learning technique. It can be used for both Classification and Regression problems in ML. It is based on the concept of ensemble learning, which is a process of combining multiple classifiers to solve a complex problem and to improve the performance of the model. As the name suggests, "Random Forest is a classifier that contains a number of decision trees on various subsets of the given dataset and takes the average to improve the predictive accuracy of that dataset." Instead of relying on one decision tree, the random forest takes the prediction from each tree and based on the majority votes of predictions, and it predicts the final output.

## **4.2 Code**

```
# Seperate independent and dependent variables and drop the ID column
x=df_enco.drop(["id","classification"],axis=1)
y=df_enco["classification"]
scaler=MinMaxScaler((-1,1))
x=scaler.fit_transform(X_ros)
y=y_ros
from sklearn.decomposition import PCA
pca = PCA(.95)
X_PCA=pca.fit_transform(x)
print(x.shape)
print(X_PCA.shape)
X_train, X_test, y_train, y_test = train_test_split(X_ros,y_ros, test_size=0.30,
                                                    random_state=101)
from sklearn.metrics import accuracy_score
```

```

# Decision Tree model
from sklearn.tree import DecisionTreeClassifier
# instantiate the model
tree = DecisionTreeClassifier()
# fit the model
tree.fit(X_train, y_train)
#predicting the target value from the model for the samples
y_test_tree = tree.predict(X_test)
y_train_tree = tree.predict(X_train)
acc_train_tree = accuracy_score(y_train,y_train_tree)
acc_test_tree = accuracy_score(y_test,y_test_tree)
print("Decision Tree: Accuracy on training Data: {:.5f}".format(acc_train_tree))
print("Decision Tree: Accuracy on test Data: {:.5f}".format(acc_test_tree))
from sklearn.naive_bayes import GaussianNB
naive = GaussianNB()
naive.fit(X_train, y_train)
y_test_nb = naive.predict(X_test)
y_train_nb = naive.predict(X_train)
acc_train_nb = accuracy_score(y_train,y_train_nb)
acc_test_nb = accuracy_score(y_test,y_test_nb)
print("Naive Bayes: Accuracy on training Data: {:.5f}".format(acc_train_nb))
print("Naive Bayes: Accuracy on test Data: {:.5f}".format(acc_test_nb))
from sklearn.neighbors import KNeighborsClassifier
knn = KNeighborsClassifier(n_neighbors = 3)
knn.fit(X_train, y_train)
y_test_knn = knn.predict(X_test)
y_train_knn = knn.predict(X_train)
acc_train_knn = accuracy_score(y_train,y_train_knn)
acc_test_knn = accuracy_score(y_test,y_test_knn)
print("KNN: Accuracy on training Data: {:.5f}".format(acc_train_knn))
print("KNN: Accuracy on test Data: {:.5f}".format(acc_test_knn))
from sklearn.ensemble import RandomForestClassifier
rnd = RandomForestClassifier(n_estimators=5)
rnd.fit(X_train, y_train)
y_test_rnd = rnd.predict(X_test)
y_train_rnd = rnd.predict(X_train)
acc_train_rnd = accuracy_score(y_train,y_train_rnd)
acc_test_rnd = accuracy_score(y_test,y_test_rnd)
print("RandomForest: Accuracy on training Data: {:.5f}".format(acc_train_rnd))
print("RandomForest: Accuracy on test Data: {:.5f}".format(acc_test_rnd))

```

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```
In [41]: # Lets make some final changes to the data
# Separate independent and dependent variables and drop the ID column
x=df_enco.drop(["id","classification"],axis=1)
y=df_enco["classification"]

In [42]: scaler=MinMaxScaler((-1,1))
x=scaler.fit_transform(X_ros)
y=y_ros

In [43]: x
Out[43]: array([[ 0.06666667, -0.33333333,  0.5, ..., -1.,
                -1., -1., ...,  0.5, ..., -1.,
                [-0.86666667, -1., ...,  0.5, ..., -1.,
                -1., -1., ...,  0.5, ..., 1.,
                [ 0.44, ..., -0.33333333, -0.5, ..., 1.,
                -1., ..., 1., ...],
                ...,
                [ 0.25333333, -0.33333333,  1., ..., -1.,
                -1., -1., ...,  0.5, ..., -1.,
                [-0.12, ..., -0.33333333,  0.5, ..., -1.,
                -1., -1., ...,  1., ..., -1.,
                [-0.25333333, -0.33333333,  1., ..., -1.,
                -1., -1., ...]])

In [44]: from sklearn.decomposition import PCA
pca = PCA(.95)
X_PCA=pca.fit_transform(x)

print(x.shape)
print(X_PCA.shape)

(500, 24)
(500, 18)
```

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```
In [58]: X_train, X_test, y_train, y_test = train_test_split(X_PCA,y, test_size=0.3,
                random_state=191)

In [65]: from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.metrics import confusion_matrix
from sklearn.metrics import classification_report

In [69]: # Decision Tree model
from sklearn.tree import DecisionTreeClassifier
# instantiate the model
tree = DecisionTreeClassifier()
# fit the model
tree.fit(X_train, y_train)
#predicting the target value from the model for the samples
y_test_tree = tree.predict(X_test)
y_train_tree = tree.predict(X_train)
acc_train_tree = accuracy_score(y_train,y_train_tree)
acc_test_tree = accuracy_score(y_test,y_test_tree)
print("Decision Tree: Accuracy on test Data: {:.5f}".format(acc_test_tree))
print("Confusion matrix:")
print(confusion_matrix(y_test,y_test_tree))
print("Classification report:")
print(classification_report(y_test,y_test_tree))

Decision Tree: Accuracy on test Data: 0.99167
Confusion matrix:
[[81  0]
 [ 1 38]]
Classification report:
              precision    recall  f1-score   support

     0       0.99       1.00       0.99         81
     1       1.00       0.97       0.99         39

   accuracy       0.99       0.99       0.99        120
  macro avg       0.99       0.99       0.99        120
 weighted avg       0.99       0.99       0.99        120
```

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0 0.99 1.00 0.99 81  
1 1.00 0.97 0.99 39

accuracy 1.00 1.00 1.00 120  
macro avg 0.99 0.99 0.99 120  
weighted avg 0.99 0.99 0.99 120

```
In [70]: from sklearn.naive_bayes import GaussianNB
naive = GaussianNB()
naive.fit(X_train, y_train)
y_test_nb = naive.predict(X_test)
y_train_nb = naive.predict(X_train)
acc_train_nb = accuracy_score(y_train, y_train_nb)
acc_test_nb = accuracy_score(y_test, y_test_nb)
print("Naive Bayes: Accuracy on test Data: {:.5f}".format(acc_test_nb))
print("Confusion matrix:")
print(confusion_matrix(y_test, y_test_nb))
print("Classification report:")
print(classification_report(y_test, y_test_nb))
```

Naive Bayes: Accuracy on test Data: 1.00000

Confusion matrix:  
[[81 0]  
[ 0 39]]

Classification report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	81
1	1.00	1.00	1.00	39
accuracy			1.00	120
macro avg	1.00	1.00	1.00	120
weighted avg	1.00	1.00	1.00	120

```
In [71]: from sklearn.neighbors import KNeighborsClassifier
knn = KNeighborsClassifier(n_neighbors = 3)
knn.fit(X_train, y_train)
y_test_knn = knn.predict(X_test)
y_train_knn = knn.predict(X_train)
```

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1 1.00 1.00 1.00 39

accuracy 1.00 1.00 1.00 120  
macro avg 1.00 1.00 1.00 120  
weighted avg 1.00 1.00 1.00 120

```
In [71]: from sklearn.neighbors import KNeighborsClassifier
knn = KNeighborsClassifier(n_neighbors = 3)
knn.fit(X_train, y_train)
y_test_knn = knn.predict(X_test)
y_train_knn = knn.predict(X_train)
acc_train_knn = accuracy_score(y_train, y_train_knn)
acc_test_knn = accuracy_score(y_test, y_test_knn)
print("KNN: Accuracy on test Data: {:.5f}".format(acc_test_knn))
print("Confusion matrix:")
print(confusion_matrix(y_test, y_test_knn))
print("Classification report:")
print(classification_report(y_test, y_test_knn))
```

KNN: Accuracy on test Data: 0.97500

Confusion matrix:  
[[78 3]  
[ 0 39]]

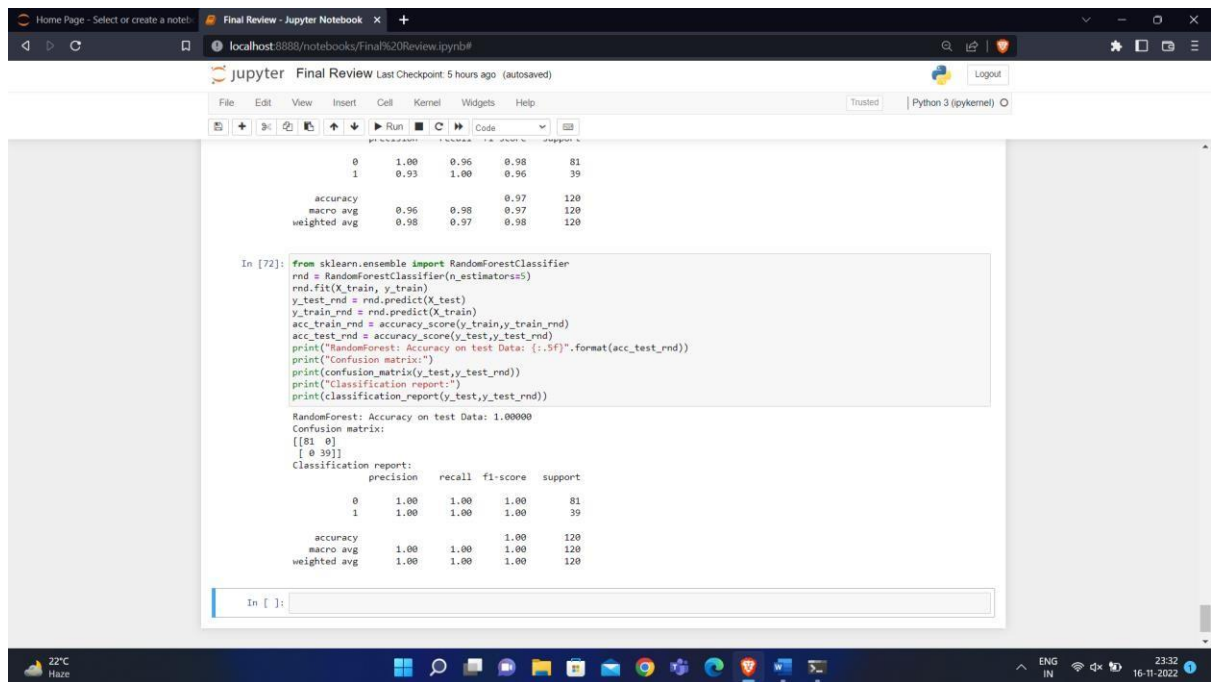
Classification report:

	precision	recall	f1-score	support
0	1.00	0.96	0.98	81
1	0.93	1.00	0.96	39
accuracy			0.97	120
macro avg	0.96	0.98	0.97	120
weighted avg	0.98	0.97	0.98	120

```
In [72]: from sklearn.ensemble import RandomForestClassifier
rnd = RandomForestClassifier(n_estimators=5)
rnd.fit(X_train, y_train)
y_test_rnd = rnd.predict(X_test)
y_train_rnd = rnd.predict(X_train)
acc_train_rnd = accuracy_score(y_train, y_train_rnd)
```

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## 5. Results

### 5.1 Evaluation of Error Measures

#### Decision Tree:

Decision Tree: Accuracy on test Data: 0.99167

Confusion matrix:

```
[[81  0]
```

```
[ 1 38]]
```

Classification report:

	precision	recall	f1-score	support
0	0.99	1.00	0.99	81
1	1.00	0.97	0.99	39
accuracy			0.99	120
macro avg	0.99	0.99	0.99	120
weighted avg	0.99	0.99	0.99	120



## Naïve Bayes:

Naive Bayes: Accuracy on test Data: 1.00000

Confusion matrix:

```
[[81  0]
```

```
[ 0 39]]
```

Classification report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	81
1	1.00	1.00	1.00	39
accuracy			1.00	120
macro avg	1.00	1.00	1.00	120
weighted avg	1.00	1.00	1.00	120

## KNN:

KNN: Accuracy on test Data: 0.97500

Confusion matrix:

```
[[78  3]
```

```
[ 0 39]]
```

Classification report:

	precision	recall	f1-score	support
0	1.00	0.96	0.98	81
1	0.93	1.00	0.96	39
accuracy			0.97	120
macro avg	0.96	0.98	0.97	120
weighted avg	0.98	0.97	0.98	120

## Random Forest:

RandomForest: Accuracy on test Data: 1.00000

Confusion matrix:

```
[[81  0]
```

```
[ 0 39]]
```

Classification report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	81
1	1.00	1.00	1.00	39
accuracy			1.00	120
macro avg	1.00	1.00	1.00	120
weighted avg	1.00	1.00	1.00	120

## **5.2 Discussion on Results**

In this project, we have used different classification models for classification of chronic kidney disease in patients. The four machine learning techniques that were used they are Decision Tree, KNN, Naïve Bayes and Random Forest. The accuracy of different algorithms on the dataset was evaluated. The dataset contains 400 rows. It contains data of 250 not chronic kidney data and 150 chronic kidney disease data. The dataset spitted into training and testing data. Accuracy was evaluated based on TP, TN, FP, FN. The accuracy achieved by naïve bayes and random forest is 100%. This project could be useful in the current medical field with advancement in sciences and new emerging technologies it would be of good help.

## **6. Conclusion**

From this we conclude that for the given dataset Random Forest and Naïve Bayes classifier that gives us the best accuracy results. But the same may not be true if a different testing set is used the accuracy will vary. In the real world, if the size of dataset increases by a large amount in the future. Then the overfitting problem of the models will be resolved.

## **References**

[https://archive.ics.uci.edu/ml/datasets/chronic\\_kidney\\_disease](https://archive.ics.uci.edu/ml/datasets/chronic_kidney_disease)