

Date	09 November 2022
Team ID	PNT2022TMID05452
Project Name	Early Detection Of Chronic Kidney Disease Using Machine Learning
Dataset	Sample data/Dataset

#### Import Packages

```
In [6]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import tensorflow as tf
import tensorflow
from tensorflow import keras
from keras.layers import Dense
```

#### Read dataset

```
In [43]: data = pd.read_csv("/content/sample_data/Dataset_CKD.csv")
print(data)
```

0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	
...	...	...	...	...	...	...	...	...	...	...
395	395	55.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	
396	396	42.0	70.0	1.025	0.0	0.0	normal	normal	notpresent	
397	397	12.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	
398	398	17.0	60.0	1.025	0.0	0.0	normal	normal	notpresent	
399	399	58.0	80.0	1.025	0.0	0.0	normal	normal	notpresent	

  

0	ba	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane	\
1	notpresent	...	44	7800	5.2	yes	yes	no	good	no	no	
2	notpresent	...	38	6000	NaN	no	no	no	good	no	no	
3	notpresent	...	31	7500	NaN	no	yes	no	poor	no	yes	
4	notpresent	...	32	6700	3.9	yes	no	no	poor	yes	yes	
...	...	...	35	7300	4.6	no	no	no	good	no	no	
...	...	...	...	...	...	...	...	...	...	...	...	
395	notpresent	...	47	6700	4.9	no	no	no	good	no	no	
396	notpresent	...	54	7800	6.2	no	no	no	good	no	no	
397	notpresent	...	49	6600	5.4	no	no	no	good	no	no	
398	notpresent	...	51	7200	5.9	no	no	no	good	no	no	
399	notpresent	...	53	6800	6.1	no	no	no	good	no	no	

  

0	classification	ckd
1	classification	ckd
2	classification	ckd
3	classification	ckd
4	classification	ckd
...	...	...
395	classification	notckd
396	classification	notckd
397	classification	notckd
398	classification	notckd
399	classification	notckd

[400 rows x 26 columns]

#### Understanding Data Type and Features

```
In [44]: print(data.info())
```

```

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   bp                     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                    330 non-null   object  
17  wc                     295 non-null   object  
18  rc                     270 non-null   object  
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(11), int64(1), object(14)
memory usage: 81.4+ KB
None

```

## Handling Missing Values

### Remove null values

In [37]:

```

data=data.dropna(how="any")
print(data)

   id  age  bp  sg  al  su  rbc  pc  pcc  \
3   3  48.0  70.0  1.005  4.0  0.0  normal  abnormal  present
9   9  53.0  90.0  1.020  2.0  0.0  abnormal  abnormal  present
11  11  63.0  70.0  1.010  3.0  0.0  abnormal  abnormal  present
14  14  68.0  80.0  1.010  3.0  2.0  normal  abnormal  present
20  20  61.0  80.0  1.015  2.0  0.0  abnormal  abnormal  notpresent
..  ...  ...  ...  ...  ...  ...  ...  ...  ...
395 395  55.0  80.0  1.020  0.0  0.0  normal  normal  notpresent
396 396  42.0  70.0  1.025  0.0  0.0  normal  normal  notpresent
397 397  12.0  80.0  1.020  0.0  0.0  normal  normal  notpresent
398 398  17.0  60.0  1.025  0.0  0.0  normal  normal  notpresent
399 399  58.0  80.0  1.025  0.0  0.0  normal  normal  notpresent

   ba  ...  pcv  wc  rc  htn  dm  cad  appet  pe  ane  \
3  notpresent  ...  32  6700  3.9  yes  no  no  poor  yes  yes
9  notpresent  ...  29  12100  3.7  yes  yes  no  poor  no  yes
11 notpresent  ...  32  4500  3.8  yes  yes  no  poor  yes  no
14  present  ...  16  11000  2.6  yes  yes  yes  poor  yes  no
20 notpresent  ...  24  9200  3.2  yes  yes  yes  poor  yes  yes
..  ...  ...  ...  ...  ...  ...  ...  ...  ...  ...
395 notpresent  ...  47  6700  4.9  no  no  no  good  no  no
396 notpresent  ...  54  7800  6.2  no  no  no  good  no  no
397 notpresent  ...  49  6600  5.4  no  no  no  good  no  no
398 notpresent  ...  51  7200  5.9  no  no  no  good  no  no
399 notpresent  ...  53  6800  6.1  no  no  no  good  no  no

   ckd
9      ckd
11     ckd
14     ckd
20     ckd
..     ...
395  notckd
396  notckd
397  notckd
398  notckd
399  notckd

```

[158 rows x 26 columns]

### Label Encoding (String values to Numeric values)

In [38]:

```

data['rbc'] = data['rbc'].map({"abnormal":1,"normal":0})
data['pc'] = data['pc'].map({"abnormal":1,"normal":0})
data['pcc'] = data['pcc'].map({"present":1,"notpresent":0})
data['ba'] = data['ba'].map({"present":1,"notpresent":0})
data['htn'] = data['htn'].map({"yes":1,"no":0})
data['dm'] = data['dm'].map({"yes":1,"no":0})
data['cad'] = data['cad'].map({"yes":1,"no":0})
data['pe'] = data['pe'].map({"yes":1,"no":0})
data['ane'] = data['ane'].map({"yes":1,"no":0})
data['appet'] = data['appet'].map({"poor":1,"good":0})
data['classification'] = data['classification'].map({"ckd":1,"notckd":0})
data['pcv'] = data['pcv'].astype('int')
data['wc'] = data['wc'].astype('int')
data['rc'] = data['rc'].astype('float')
print(data)

   id  age  bp  sg  al  su  rbc  pc  pcc  ba  ...  pcv  wc  rc  \
3   3  48.0  70.0  1.005  4.0  0.0  0  1  1  0  ...  32  6700  3.9
9   9  53.0  90.0  1.020  2.0  0.0  1  1  1  0  ...  29  12100  3.7
11  11  63.0  70.0  1.010  3.0  0.0  1  1  1  0  ...  32  4500  3.8
14  14  68.0  80.0  1.010  3.0  2.0  0  1  1  1  ...  16  11000  2.6
20  20  61.0  80.0  1.015  2.0  0.0  1  1  0  0  ...  24  9200  3.2
..  ...  ...  ...  ...  ...  ...  ...  ...  ...  ...  ...  ...
395 395  55.0  80.0  1.020  0.0  0.0  0  0  0  0  ...  47  6700  4.9
396 396  42.0  70.0  1.025  0.0  0.0  0  0  0  0  ...  54  7800  6.2
397 397  12.0  80.0  1.020  0.0  0.0  0  0  0  0  ...  49  6600  5.4
398 398  17.0  60.0  1.025  0.0  0.0  0  0  0  0  ...  51  7200  5.9
399 399  58.0  80.0  1.025  0.0  0.0  0  0  0  0  ...  53  6800  6.1

```

	htn	dm	cad	appet	pe	ane	classification
3	1	0	0	1	1	1	1
9	1	1	0	1	0	1	1
11	1	1	0	1	1	0	1
14	1	1	1	1	1	0	1
20	1	1	1	1	1	1	1
...	...	...	...	...	...	...	...
395	0	0	0	0	0	0	0
396	0	0	0	0	0	0	0
397	0	0	0	0	0	0	0
398	0	0	0	0	0	0	0
399	0	0	0	0	0	0	0

[158 rows x 26 columns]

### Splitting Dependent and Independent Variable

```
In [39]: X = data.iloc[:,1:25].values
y = data.iloc[:, 25].values
```

### Split Train and Test set

```
In [41]: from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.30,
random_state = 121)#101
print("X train value")
print(X_train)
print("Y train value")
print(y_train)
```

```
X train value
[[75.  70.   1.02 ...  0.   0.   0. ]
 [57.  60.   1.02 ...  0.   0.   0. ]
 [66.  70.   1.025 ...  0.   0.   0. ]
 ...
 [58.  80.   1.02 ...  0.   0.   0. ]
 [73.  80.   1.02 ...  0.   0.   0. ]
 [46.  60.   1.025 ...  0.   0.   0. ]]

Y train value
[0 0 0 0 0 1 0 0 0 1 0 0 1 1 0 0 1 1 0 1 0 0 1 1 1 0 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 1 0 0 0 0 1 0 0 0 0 1 0 1 0 0 1 1 0 1 0 0 0 0 1 0 1 0 1 0 1 0 0 0 0
 0 1 1 0 1 0 0 0 1 0 0 0 1 0 0 0 0 0 1 0 1 1 0 0 0 1 0 0 1 0 0 0 0 0 0 1 0]
```