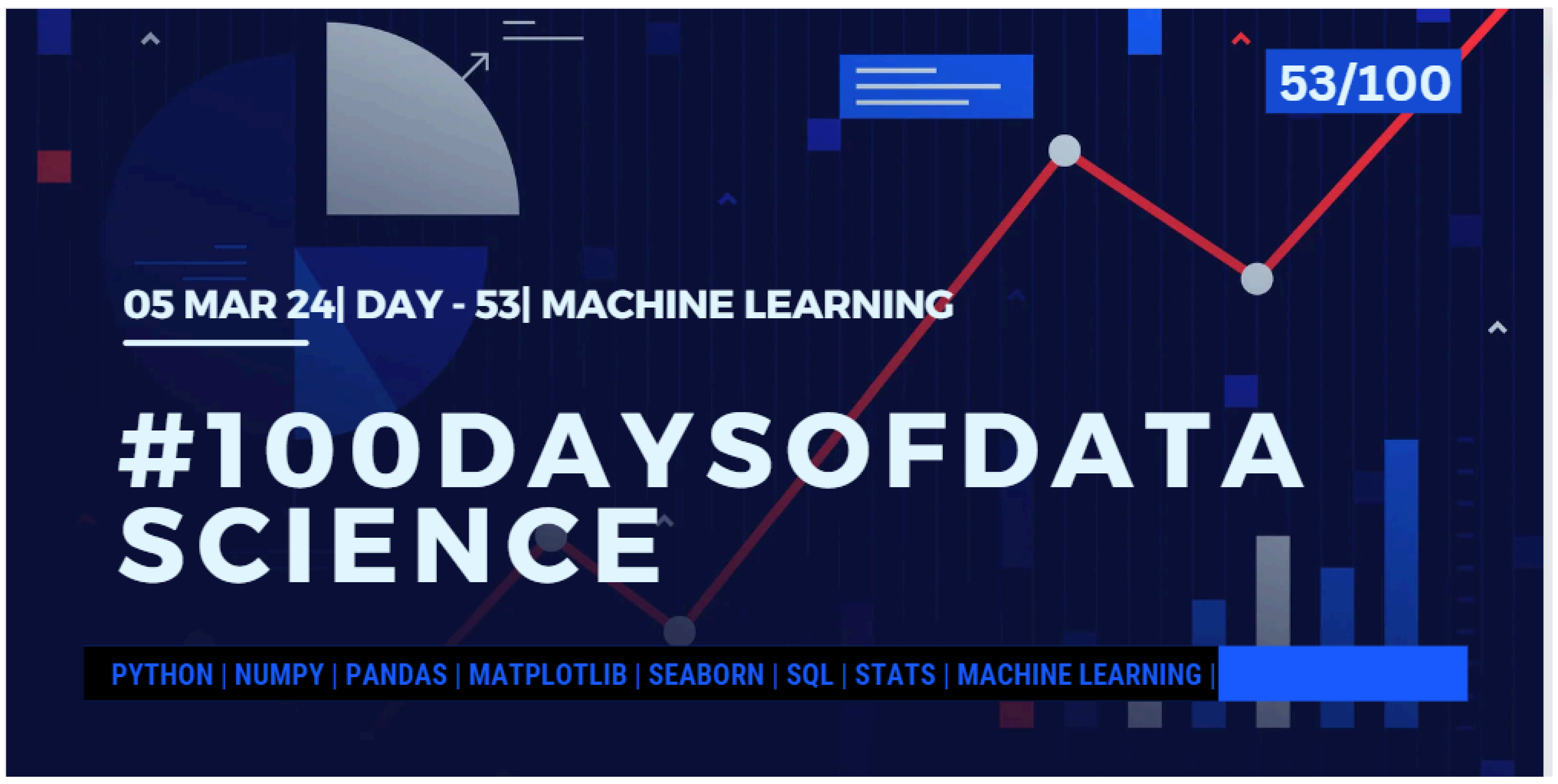

53/100
05 MAR 24| DAY - 53| MACHINE LEARNING
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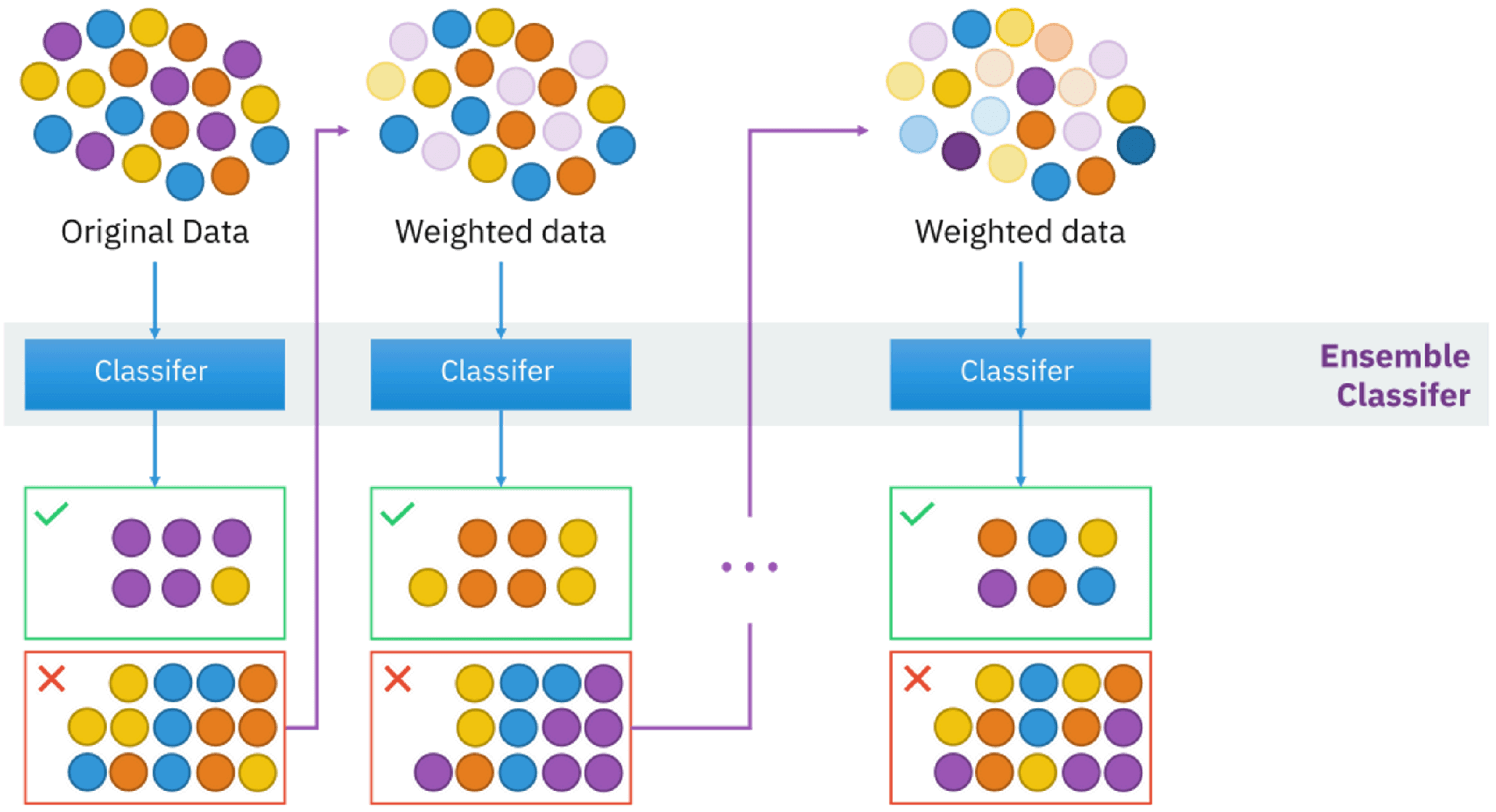
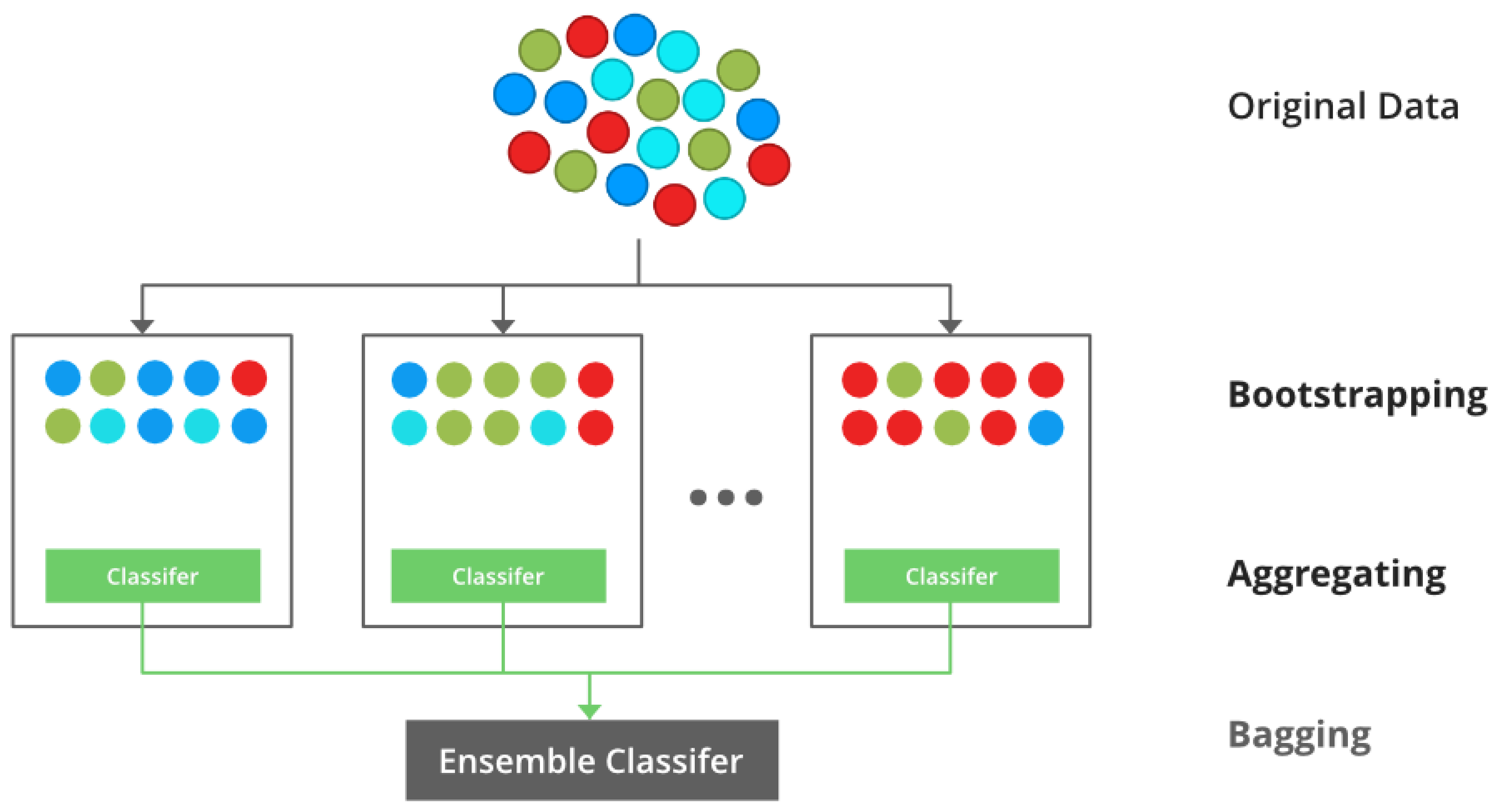
AdaBoost: The Adaptive Learner



- AdaBoost, short for Adaptive Boosting, is a pioneering algorithm in the world of boosting. It works by iteratively training a series of weak learners, typically decision trees. Here's how it tackles the learning process:
  1. Start with Equal Weights: Initially, all data points are assigned equal importance.
  2. Train a Weak Learner: AdaBoost trains a weak decision tree on the data.
  3. Analyze Performance: It then evaluates the performance of this learner, identifying data points that were misclassified.
  4. Increase Difficulty: In the next iteration, AdaBoost increases the weights of the misclassified points, essentially forcing the next learner to focus on these challenging examples.
  5. Repeat and Combine: This process of training, analyzing, and adjusting weights continues for a predetermined number of iterations. Finally, AdaBoost combines the predictions from all the weak learners to make a final, more robust prediction.
- **Strengths of AdaBoost:**
  - **Interpretability:** Since AdaBoost relies on decision trees as weak learners, it offers a certain level of interpretability. You can analyze the decision rules within each tree to gain insights into the model's reasoning.
  - **Simplicity:** The core concept of AdaBoost is relatively straightforward, making it a good starting point for understanding boosting algorithms.
  - **Effectiveness:** AdaBoost can be effective for a variety of classification tasks, especially when dealing with imbalanced datasets.
- **Considerations for AdaBoost:**
  - **Overfitting Potential:** While AdaBoost focuses on challenging examples, it can still be susceptible to overfitting if not carefully tuned.
  - **Sequential Dependence:** The performance of AdaBoost relies on the quality of each individual weak learner. A poor initial learner can negatively impact the entire ensemble.

XGBoost: The Scalable Champion



- XGBoost (eXtreme Gradient Boosting) is a powerful and widely-used boosting algorithm. It builds upon the foundation of AdaBoost by introducing several advancements:
  - Gradient Boosting: XGBoost utilizes gradient boosting, a technique that focuses on minimizing the error made by the current model to improve the next learner in the sequence. This leads to a more efficient learning process.
  - Regularization: XGBoost incorporates regularization techniques that penalize overly complex models, helping to prevent overfitting.
  - Parallelization: XGBoost is optimized for parallel and distributed computing, allowing it to handle large datasets efficiently.
- **Strengths of XGBoost:**
  - **High Performance:** XGBoost is known for its exceptional accuracy and ability to handle complex problems, often outperforming other boosting algorithms.
  - **Scalability:** Due to its parallel processing capabilities, XGBoost can effectively tackle massive datasets.
  - **Flexibility:** XGBoost can be applied to various tasks, including classification, regression, and ranking problems.
- **Considerations for XGBoost:**
  - **Complexity::** XGBoost has a wider range of hyperparameters compared to AdaBoost, requiring more careful tuning for optimal performance.
  - **Interpretability::** While XGBoost offers some level of interpretability through feature importance scores, it can be less interpretable than simpler algorithms like AdaBoost.

Choosing Between AdaBoost and XGBoost:

The choice between AdaBoost and XGBoost depends on your specific needs. If interpretability and simplicity are priorities, AdaBoost could be a good starting point. However, if you require high accuracy, scalability, and the ability to handle complex problems, XGBoost offers a powerful solution.

In [1]:
```
### Importing Libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import plotly.express as px
import plotly.figure_factory as ff
from sklearn.metrics import confusion_matrix, accuracy_score, classification_report
from sklearn.metrics import mean_squared_error, r2_score
import warnings
warnings.filterwarnings('ignore')
```

In [2]:
```
### Import the Dataset
df = pd.read_csv(r'C:\Users\hp\Desktop\100DaysOfDataScience\Day 53\kidney_disease.csv',header=0)
df.head()
```

Out[2]:

	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 × 26 columns

In [3]:
```
df.shape ### Checking Shape
```

Out[3]:
```
(400, 26)
```

In [4]:
```
df.describe() ### Get information of the Dataset
```

Out[4]:

	id	age	bp	sg	al	su	bgr	bu	sc	sod	pot	hemo
count	400.000000	391.000000	388.000000	353.000000	354.000000	351.000000	356.000000	381.000000	383.000000	313.000000	312.000000	348.000000
mean	199.500000	51.483376	76.469072	1.017408	1.016949	0.450142	148.036517	57.425722	3.072454	137.528754	4.627244	12.526437
std	115.614301	17.169714	13.683637	0.005717	1.352679	1.099191	79.281714	50.503006	5.741126	10.408752	3.193904	2.912587
min	0.000000	2.000000	50.000000	1.005000	0.000000	0.000000	22.000000	1.500000	0.400000	4.500000	2.500000	3.100000
25%	99.750000	42.000000	70.000000	1.010000	0.000000	0.000000	99.000000	27.000000	0.900000	135.000000	3.800000	10.300000
50%	199.500000	55.000000	80.000000	1.020000	0.000000	0.000000	121.000000	42.000000	1.300000	138.000000	4.400000	12.650000
75%	299.250000	64.500000	80.000000	1.020000	2.000000	0.000000	163.000000	66.000000	2.800000	142.000000	4.900000	15.000000
max	399.000000	90.000000	180.000000	1.025000	5.000000	5.000000	490.000000	391.000000	76.000000	163.000000	47.000000	17.800000

In [5]:
```
df.columns ### Checking Columns
```

Out[5]:
```
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')
```

In [6]:
```
df.info() ### Checking Information About a DataFrame
```
```
<class 'pandas.core.frame.DataFrame'>
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
```

In [7]:
```
df.isnull().sum() ### Checking Null Values in the Data
```
Out[7]:
```
id                  0
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
```

In [8]:
```
df1 = pd.DataFrame.copy(df)
df1.shape
```
Out[8]:
```
(400, 26)
```

In [9]:
```
### Dropping id column
df1.drop('id', axis = 1, inplace = True)
```

In [10]:
```
### Renaming columns
df1.columns = ['age', 'blood_pressure', 'specific_gravity', 'albumin', 'sugar', 'red_blood_cells', 'pus_cell',
              'pus_cell_clumps', 'bacteria', 'blood_glucose_random', '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']
df1.head()
```
Out[10]:

	age	blood_pressure	specific_gravity	albumin	sugar	red_blood_cells	pus_cell	pus_cell_clumps	bacteria	blood_glucose_random	...	packed_cell_volume	white_blood_cell_count	red_blood_cell_count	hypertension
0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	121.0	...	44	7800	5.2	yes
1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	NaN	...	38	6000	NaN	no
2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	423.0	...	31	7500	NaN	no
3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	117.0	...	32	6700	3.9	yes
4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	106.0	...	35	7300	4.6	no

5 rows × 25 columns

In [11]:
```
### Dropping diabetes_mellitus column
df1.drop('diabetes_mellitus', axis = 1, inplace = True)
```

In [12]:
```python
for i in df1.columns:
    print({i:df1[i].unique()}) ### Checking Unique values in each columns
```

```
{'age': array([48.,  7., 62., 51., 60., 68., 24., 52., 53., 50., 63., 40., 47.,
       61., 21., 42., 75., 69., nan, 73., 70., 65., 76., 72., 82., 46.,
       45., 35., 54., 11., 59., 67., 15., 55., 44., 26., 64., 56.,  5.,
       74., 38., 58., 71., 34., 17., 12., 43., 41., 57.,  8., 39., 66.,
       81., 14., 27., 83., 30.,  4.,  3.,  6., 32., 80., 49., 90., 78.,
       19.,  2., 33., 36., 37., 23., 25., 20., 29., 28., 22., 79.])}
{'blood_pressure': array([ 80.,  50.,  70.,  90.,  nan, 100.,  60., 110., 140., 180., 120.])}
{'specific_gravity': array([1.02 , 1.01 , 1.005, 1.015,   nan, 1.025])}
{'albumin': array([ 1.,  4.,  2.,  3.,  0., nan,  5.])}
{'sugar': array([ 0.,  3.,  4.,  1., nan,  2.,  5.])}
{'red_blood_cells': array([nan, 'normal', 'abnormal'], dtype=object)}
{'pus_cell': array(['normal', 'abnormal', nan], dtype=object)}
{'pus_cell_clumps': array(['notpresent', 'present', nan], dtype=object)}
{'bacteria': array(['notpresent', 'present', nan], dtype=object)}
{'blood_glucose_random': array([121.,  nan, 423., 117., 106.,  74., 100., 410., 138.,  70., 490.,
       380., 208.,  98., 157.,  76.,  99., 114., 263., 173.,  95., 108.,
       156., 264., 123.,  93., 107., 159., 140., 171., 270.,  92., 137.,
       204.,  79., 207., 124., 144.,  91., 162., 246., 253., 141., 182.,
        86., 150., 146., 425., 112., 250., 360., 163., 129., 133., 102.,
       158., 165., 132., 104., 127., 415., 169., 251., 109., 280., 210.,
       219., 295.,  94., 172., 101., 298., 153.,  88., 226., 143., 115.,
        89., 297., 233., 294., 323., 125.,  90., 308., 118., 224., 128.,
       122., 214., 213., 268., 256.,  84., 105., 288., 139.,  78., 273.,
       242., 424., 303., 148., 160., 192., 307., 220., 447., 309.,  22.,
       111., 261., 215., 234., 131., 352.,  80., 239., 110., 130., 184.,
       252., 113., 230., 341., 255., 103., 238., 248., 120., 241., 269.,
       201., 203., 463., 176.,  82., 119.,  97.,  96.,  81., 116., 134.,
        85.,  83.,  87.,  75.])}
{'blood_urea': array([ 36. ,  18. ,  53. ,  56. ,  26. ,  25. ,  54. ,  31. ,  60. ,
       107. ,  55. ,  72. ,  86. ,  90. , 162. ,  46. ,  87. ,  27. ,
       148. , 180. , 163. ,   nan,  50. ,  75. ,  45. ,  28. , 155. ,
        33. ,  39. , 153. ,  29. ,  65. , 103. ,  70. ,  80. ,  20. ,
       202. ,  77. ,  89. ,  24. ,  17. ,  32. , 114. ,  66. ,  38. ,
       164. , 142. ,  96. , 391. ,  15. , 111. ,  73. ,  19. ,  92. ,
        35. ,  16. , 139. ,  48. ,  85. ,  98. , 186. ,  37. ,  47. ,
        52. ,  82. ,  51. , 106. ,  22. , 217. ,  88. , 118. ,  50.1,
        71. ,  34. ,  40. ,  21. , 219. ,  30. , 125. , 166. ,  49. ,
       208. , 176. ,  68. , 145. , 165. , 322. ,  23. , 235. , 132. ,
        76. ,  42. ,  44. ,  41. , 113. ,   1.5, 146. ,  58. , 133. ,
       137. ,  67. , 115. , 223. ,  98.6, 158. ,  94. ,  74. , 150. ,
        61. ,  57. ,  95. , 191. ,  93. , 241. ,  64. ,  79. , 215. ,
       309. ,  10. ])}
{'serum_creatinine': array([ 1.2 ,  0.8 ,  1.8 ,  3.8 ,  1.4 ,  1.1 , 24.  ,  1.9 ,  7.2 ,
        4.  ,  2.7 ,  2.1 ,  4.6 ,  4.1 ,  9.6 ,  2.2 ,  5.2 ,  1.3 ,
        1.6 ,  3.9 , 76.  ,  7.7 ,   nan,  2.4 ,  7.3 ,  1.5 ,  2.5 ,
        2.  ,  3.4 ,  0.7 ,  1.  , 10.8 ,  6.3 ,  5.9 ,  0.9 ,  3.  ,
        3.25,  9.7 ,  6.4 ,  3.2 , 32.  ,  0.6 ,  6.1 ,  3.3 ,  6.7 ,
        8.5 ,  2.8 , 15.  ,  2.9 ,  1.7 ,  3.6 ,  5.6 ,  6.5 ,  4.4 ,
       10.2 , 11.5 ,  0.5 , 12.2 ,  5.3 ,  9.2 , 13.8 , 16.9 ,  6.  ,
        7.1 , 18.  ,  2.3 , 13.  , 48.1 , 14.2 , 16.4 ,  2.6 ,  7.5 ,
        4.3 , 18.1 , 11.8 ,  9.3 ,  6.8 , 13.5 , 12.8 , 11.9 , 12.  ,
       13.4 , 15.2 , 13.3 ,  0.4 ])}
{'sodium': array([  nan, 111. , 142. , 104. , 114. , 131. , 138. , 135. , 130. ,
       141. , 139. ,   4.5, 136. , 129. , 140. , 132. , 133. , 134. ,
       125. , 163. , 137. , 128. , 143. , 127. , 146. , 126. , 122. ,
       147. , 124. , 115. , 145. , 113. , 120. , 150. , 144. ])}
{'potassium': array([ nan,  2.5,  3.2,  4. ,  3.7,  4.2,  5.8,  3.4,  6.4,  4.9,  4.1,
        4.3,  5.2,  3.8,  4.6,  3.9,  4.7,  5.9,  4.8,  4.4,  6.6, 39. ,
        5.5,  5. ,  3.5,  3.6,  7.6,  2.9,  4.5,  5.7,  5.4,  5.3, 47. ,
        6.3,  5.1,  5.6,  3. ,  2.8,  2.7,  6.5,  3.3])}
{'haemoglobin': array([15.4, 11.3,  9.6, 11.2, 11.6, 12.2, 12.4, 10.8,  9.5,  9.4,  9.7,
        9.8,  5.6,  7.6, 12.6, 12.1, 12.7, 10.3,  7.7, 10.9,  nan, 11.1,
        9.9, 12.5, 12.9, 10.1, 12. , 13. ,  7.9,  9.3, 15. , 10. ,  8.6,
       13.6, 10.2, 10.5,  6.6, 11. ,  7.5, 15.6, 15.2,  4.8,  9.1,  8.1,
       11.9, 13.5,  8.3,  7.1, 16.1, 10.4,  9.2,  6.2, 13.9, 14.1,  6. ,
       11.8, 11.7, 11.4, 14. ,  8.2, 13.2,  6.1,  8. , 12.3,  8.4, 14.3,
        9. ,  8.7, 10.6, 13.1, 10.7,  5.5,  5.8,  6.8,  8.8,  8.5, 13.8,
       11.5,  7.3, 13.7, 12.8, 13.4,  6.3,  3.1, 17. , 15.9, 14.5, 15.5,
       16.2, 14.4, 14.2, 16.3, 14.8, 16.5, 15.7, 13.3, 14.6, 16.4, 16.9,
       16. , 14.7, 16.6, 14.9, 16.7, 16.8, 15.8, 15.1, 17.1, 17.2, 15.3,
       17.3, 17.4, 17.7, 17.8, 17.5, 17.6])}
{'packed_cell_volume': array(['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'], dtype=object)}
{'white_blood_cell_count': array(['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'],
      dtype=object)}
{'red_blood_cell_count': array(['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'], dtype=object)}
{'hypertension': array(['yes', 'no', nan], dtype=object)}
{'coronary_artery_disease': array(['no', 'yes', '\tno', nan], dtype=object)}
{'appetite': array(['good', 'poor', nan], dtype=object)}
{'peda_edema': array(['no', 'yes', nan], dtype=object)}
{'aanemia': array(['no', 'yes', nan], dtype=object)}
{'class': array(['ckd', 'ckd\t', 'notckd'], dtype=object)}
```

In [13]:
```python
### Finding numerical variables
colname_num = [var for var in df1.columns if df1[var].dtype!='O']
print('There are {} numerical variables\n'.format(len(colname_num)))
print('The numerical variables are :', colname_num)
```

```
There are 11 numerical variables

The numerical variables are : ['age', 'blood_pressure', 'specific_gravity', 'albumin', 'sugar', 'blood_glucose_random', 'blood_urea', 'serum_creatinine', 'sodium', 'potassium',
'haemoglobin']
```

In [14]:
```python
# Looking at unique values in numerical columns
for col in colname_num:
    print(f"{col} has {df1[col].unique()} values\n")
```

```
age has [48.  7. 62. 51. 60. 68. 24. 52. 53. 50. 63. 40. 47. 61. 21. 42. 75. 69.
 nan 73. 70. 65. 76. 72. 82. 46. 45. 35. 54. 11. 59. 67. 15. 55. 44. 26.
 64. 56.  5. 74. 38. 58. 71. 34. 17. 12. 43. 41. 57.  8. 39. 66. 81. 14.
 27. 83. 30.  4.  3.  6. 32. 80. 49. 90. 78. 19.  2. 33. 36. 37. 23. 25.
 20. 29. 28. 22. 79.] values

blood_pressure has [ 80.  50.  70.  90.  nan 100.  60. 110. 140. 180. 120.] values

specific_gravity has [1.02  1.01  1.005 1.015   nan 1.025] values

albumin has [ 1.  4.  2.  3.  0. nan  5.] values

sugar has [ 0.  3.  4.  1. nan  2.  5.] values

blood_glucose_random has [121.  nan 423. 117. 106.  74. 100. 410. 138.  70. 490. 380. 208.  98.
 157.  76.  99. 114. 263. 173.  95. 108. 156. 264. 123.  93. 107. 159.
 140. 171. 270.  92. 137. 204.  79. 207. 124. 144.  91. 162. 246. 253.
 141. 182.  86. 150. 146. 425. 112. 250. 360. 163. 129. 133. 102. 158.
 165. 132. 104. 127. 415. 169. 251. 109. 280. 210. 219. 295.  94. 172.
 101. 298. 153.  88. 226. 143. 115.  89. 297. 233. 294. 323. 125.  90.
 308. 118. 224. 128. 122. 214. 213. 268. 256.  84. 105. 288. 139.  78.
 273. 242. 424. 303. 148. 160. 192. 307. 220. 447. 309.  22. 111. 261.
 215. 234. 131. 352.  80. 239. 110. 130. 184. 252. 113. 230. 341. 255.
 103. 238. 248. 120. 241. 269. 201. 203. 463. 176.  82. 119.  97.  96.
  81. 116. 134.  85.  83.  87.  75.] values

blood_urea has [ 36.   18.   53.   56.   26.   25.   54.   31.   60.  107.   55.   72.
  86.   90.  162.   46.   87.   27.  148.  180.  163.    nan  50.   75.
  45.   28.  155.   33.   39.  153.   29.   65.  103.   70.   80.   20.
 202.   77.   89.   24.   17.   32.  114.   66.   38.  164.  142.   96.
 391.   15.  111.   73.   19.   92.   35.   16.  139.   48.   85.   98.
 186.   37.   47.   52.   82.   51.  106.   22.  217.   88.  118.   50.1
  71.   34.   40.   21.  219.   30.  125.  166.   49.  208.  176.   68.
 145.  165.  322.   23.  235.  132.   76.   42.   44.   41.  113.    1.5
 146.   58.  133.  137.   67.  115.  223.   98.6 158.   94.   74.  150.
  61.   57.   95.  191.   93.  241.   64.   79.  215.  309.   10. ] values

serum_creatinine has [ 1.2   0.8   1.8   3.8   1.4   1.1  24.    1.9   7.2   4.    2.7   2.1
  4.6   4.1   9.6   2.2   5.2   1.3   1.6   3.9  76.    7.7    nan  2.4
  7.3   1.5   2.5   2.    3.4   0.7   1.   10.8   6.3   5.9   0.9   3.
  3.25  9.7   6.4   3.2  32.    0.6   6.1   3.3   6.7   8.5   2.8  15.
  2.9   1.7   3.6   5.6   6.5   4.4  10.2  11.5   0.5  12.2   5.3   9.2
 13.8  16.9   6.    7.1  18.    2.3  13.   48.1  14.2  16.4   2.6   7.5
  4.3  18.1  11.8   9.3   6.8  13.5  12.8  11.9  12.   13.4  15.2  13.3
  0.4 ] values

sodium has [  nan 111.  142.  104.  114.  131.  138.  135.  130.  141.  139.    4.5
 136.  129.  140.  132.  133.  134.  125.  163.  137.  128.  143.  127.
 146.  126.  122.  147.  124.  115.  145.  113.  120.  150.  144. ] values

potassium has [ nan  2.5  3.2  4.   3.7  4.2  5.8  3.4  6.4  4.9  4.1  4.3  5.2  3.8
  4.6  3.9  4.7  5.9  4.8  4.4  6.6 39.   5.5  5.   3.5  3.6  7.6  2.9
  4.5  5.7  5.4  5.3 47.   6.3  5.1  5.6  3.   2.8  2.7  6.5  3.3] values

haemoglobin has [15.4 11.3  9.6 11.2 11.6 12.2 12.4 10.8  9.5  9.4  9.7  9.8  5.6  7.6
 12.6 12.1 12.7 10.3  7.7 10.9  nan 11.1  9.9 12.5 12.9 10.1 12.  13.
  7.9  9.3 15.  10.   8.6 13.6 10.2 10.5  6.6 11.   7.5 15.6 15.2  4.8
  9.1  8.1 11.9 13.5  8.3  7.1 16.1 10.4  9.2  6.2 13.9 14.1  6.  11.8
 11.7 11.4 14.   8.2 13.2  6.1  8.  12.3  8.4 14.3  9.   8.7 10.6 13.1
 10.7  5.5  5.8  6.8  8.8  8.5 13.8 11.5  7.3 13.7 12.8 13.4  6.3  3.1
 17.  15.9 14.5 15.5 16.2 14.4 14.2 16.3 14.8 16.5 15.7 13.3 14.6 16.4
 16.9 16.  14.7 16.6 14.9 16.7 16.8 15.8 15.1 17.1 17.2 15.3 17.3 17.4
 17.7 17.8 17.5 17.6] values
```

In [15]:
```python
### Finding categorical variables
colname_cat = [var for var in df1.columns if df1[var].dtype=='O']
print('There are {} categorical variables\n'.format(len(colname_cat)))
print('The categorical variables are :', colname_cat)
```

```
There are 13 categorical variables

The categorical variables are : ['red_blood_cells', 'pus_cell', 'pus_cell_clumps', 'bacteria', 'packed_cell_volume', 'white_blood_cell_count', 'red_blood_cell_count', 'hypertensi
on', 'coronary_artery_disease', 'appetite', 'peda_edema', 'aanemia', 'class']
```

In [16]:
```python
### Converting necessary columns to numerical type
df1['packed_cell_volume'] = pd.to_numeric(df1['packed_cell_volume'], errors='coerce')
df1['white_blood_cell_count'] = pd.to_numeric(df1['white_blood_cell_count'], errors='coerce')
df1['red_blood_cell_count'] = pd.to_numeric(df1['red_blood_cell_count'], errors='coerce')
df1.dtypes
```

Out[16]:
```
age                        float64
blood_pressure             float64
specific_gravity           float64
albumin                    float64
sugar                      float64
red_blood_cells             object
pus_cell                    object
pus_cell_clumps             object
bacteria                    object
blood_glucose_random       float64
blood_urea                 float64
serum_creatinine           float64
sodium                     float64
potassium                  float64
haemoglobin                float64
packed_cell_volume         float64
white_blood_cell_count     float64
red_blood_cell_count       float64
hypertension                object
coronary_artery_disease     object
appetite                    object
peda_edema                  object
aanemia                     object
class                       object
dtype: object
```

In [17]:
```python
# looking at unique values in categorical columns
for col in colname_cat:
    print(f"{col} has {df1[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. 52. 14. 22. 18. 42. 17. 46. 23. 19. 25. 41. 26. 15. 21. 43. 20.
 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.  7100. 11800.  9400.  5500.  5800. 13200.
 12500.  5600.  7000. 11900. 10400. 10700. 12700.  6800.  6500. 13600.
 10200.  9000. 14900.  8200. 15200.  5000. 16300. 12400. 10500.  4200.
  4700. 10900.  8100.  9500.  2200. 12800. 11200. 19100. 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.  3.7 3.8 3.4 2.6 2.8 4.3 3.2 3.6 4.1 4.9 2.5
 4.2 4.5 3.1 4.7 3.5 6.  2.1 5.6 2.3 2.9 2.7 8.  3.3 3.  2.4 4.8 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

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
```

In [18]:
```python
### Cleaning categorical columns

df1['coronary_artery_disease'] = df1['coronary_artery_disease'].replace(to_replace = '\tno', value='no')
df1['class'] = df1['class'].replace(to_replace = {'ckd\t': 'ckd', 'notckd': 'not ckd'})
```

In [19]:
```python
colname_num = [var for var in df1.columns if df1[var].dtype!='O']
colname_cat = [var for var in df1.columns if df1[var].dtype=='O']
print(colname_cat)
print(colname_num)
```

```
['red_blood_cells', 'pus_cell', 'pus_cell_clumps', 'bacteria', 'hypertension', 'coronary_artery_disease', 'appetite', 'peda_edema', 'aanemia', 'class']
['age', 'blood_pressure', 'specific_gravity', 'albumin', 'sugar', 'blood_glucose_random', 'blood_urea', 'serum_creatinine', 'sodium', 'potassium', 'haemoglobin', 'packed_cell_vol
ume', 'white_blood_cell_count', 'red_blood_cell_count']
```

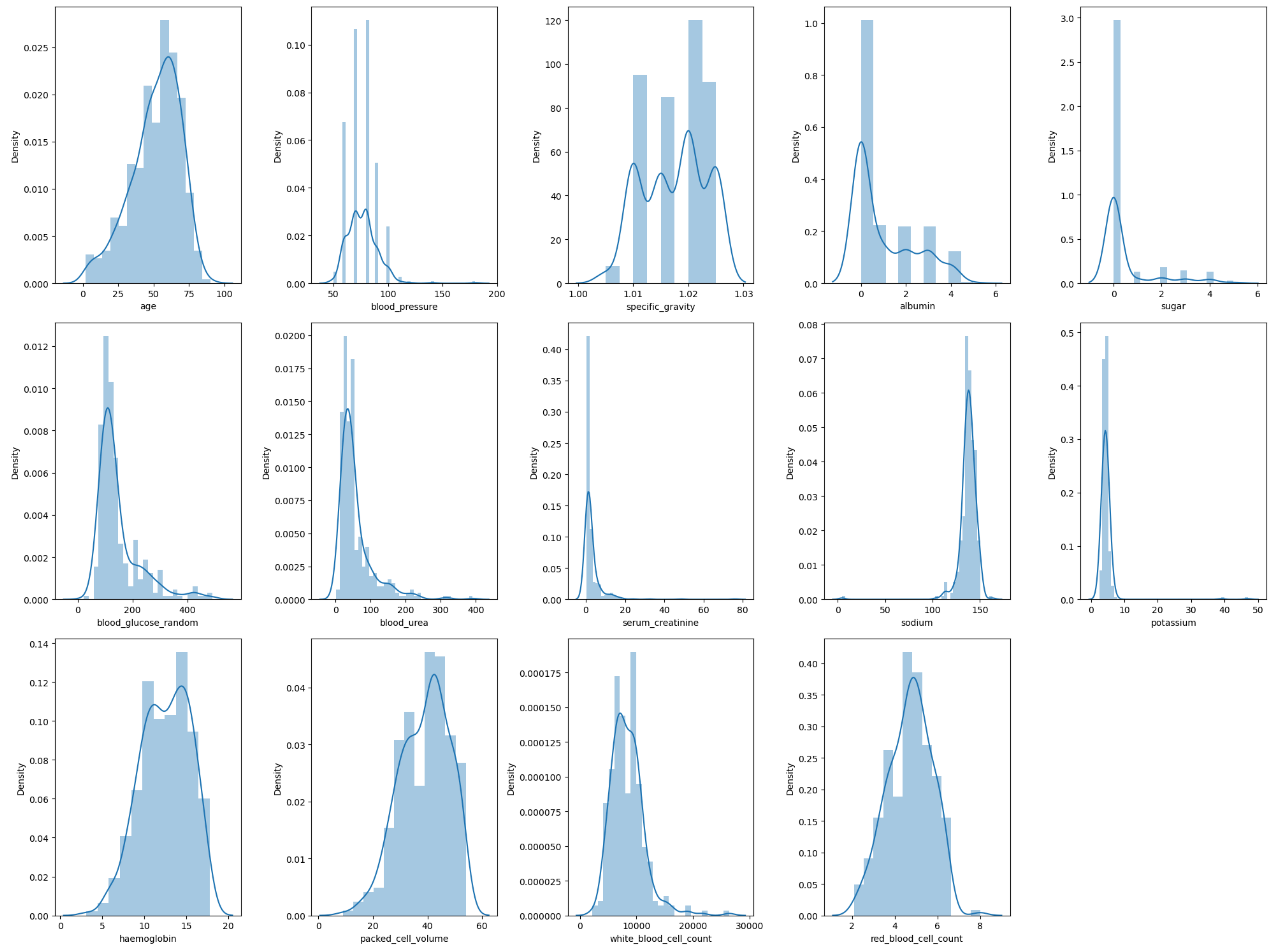
In [20]:
```
### Checking numerical features distribution

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

for column in colname_num:
    if plotnumber <= 14:
        ax = plt.subplot(3, 5, plotnumber)
        sns.distplot(df1[column])
        plt.xlabel(column)

    plotnumber += 1

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



In [21]:
```
df2 = df1.copy()
df2.shape
```

Out[21]:
```
(400, 24)
```

In [22]:
```
df2.isna().sum()
```

Out[22]:
```
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_random        44
blood_urea                  19
serum_creatinine            17
sodium                      87
potassium                   88
haemoglobin                 52
packed_cell_volume          71
white_blood_cell_count     106
red_blood_cell_count       131
hypertension                 2
coronary_artery_disease      2
appetite                     1
peda_edema                   1
aanemia                      1
class                        0
dtype: int64
```

In [23]:
```python
for i in colname_num:
    print("Column Names: ", i)
    print("Null Values: ", df2[i].isna().sum())
    print("Mean Values: ",df2[i].mean())
    print("Median Values: ",df2[i].median())
    print("Mode Values: ",df2[i].mode())
    print('-' * 50)
```

```
Column Names:  age
Null Values:  9
Mean Values:  51.48337595907928
Median Values:  55.0
Mode Values:  0    60.0
Name: age, dtype: float64
--------------------------------------------------
Column Names:  blood_pressure
Null Values:  12
Mean Values:  76.46907216494846
Median Values:  80.0
Mode Values:  0    80.0
Name: blood_pressure, dtype: float64
--------------------------------------------------
Column Names:  specific_gravity
Null Values:  47
Mean Values:  1.0174079320113314
Median Values:  1.02
Mode Values:  0    1.02
Name: specific_gravity, dtype: float64
--------------------------------------------------
Column Names:  albumin
Null Values:  46
Mean Values:  1.0169491525423728
Median Values:  0.0
Mode Values:  0    0.0
Name: albumin, dtype: float64
--------------------------------------------------
Column Names:  sugar
Null Values:  49
Mean Values:  0.45014245014245013
Median Values:  0.0
Mode Values:  0    0.0
Name: sugar, dtype: float64
--------------------------------------------------
Column Names:  blood_glucose_random
Null Values:  44
Mean Values:  148.0365168539326
Median Values:  121.0
Mode Values:  0    99.0
Name: blood_glucose_random, dtype: float64
--------------------------------------------------
Column Names:  blood_urea
Null Values:  19
Mean Values:  57.425721784776904
Median Values:  42.0
Mode Values:  0    46.0
Name: blood_urea, dtype: float64
--------------------------------------------------
Column Names:  serum_creatinine
Null Values:  17
Mean Values:  3.072454308093995
Median Values:  1.3
Mode Values:  0    1.2
Name: serum_creatinine, dtype: float64
--------------------------------------------------
Column Names:  sodium
Null Values:  87
Mean Values:  137.52875399361022
Median Values:  138.0
Mode Values:  0    135.0
Name: sodium, dtype: float64
--------------------------------------------------
Column Names:  potassium
Null Values:  88
Mean Values:  4.62724358974359
Median Values:  4.4
Mode Values:  0    3.5
1    5.0
Name: potassium, dtype: float64
--------------------------------------------------
Column Names:  haemoglobin
Null Values:  52
Mean Values:  12.526436781609195
Median Values:  12.649999999999999
Mode Values:  0    15.0
Name: haemoglobin, dtype: float64
--------------------------------------------------
Column Names:  packed_cell_volume
Null Values:  71
Mean Values:  38.88449848024316
Median Values:  40.0
Mode Values:  0    41.0
1    52.0
Name: packed_cell_volume, dtype: float64
--------------------------------------------------
Column Names:  white_blood_cell_count
Null Values:  106
Mean Values:  8406.122448979591
Median Values:  8000.0
Mode Values:  0    9800.0
Name: white_blood_cell_count, dtype: float64
--------------------------------------------------
Column Names:  red_blood_cell_count
Null Values:  131
Mean Values:  4.707434944237917
Median Values:  4.8
Mode Values:  0    5.2
Name: red_blood_cell_count, dtype: float64
--------------------------------------------------
```

In [24]:
```
df2['age'] = df2['age'].fillna(df2['age'].median())
df2['blood_pressure'] = df2['blood_pressure'].fillna(df2['blood_pressure'].median())
df2['specific_gravity'] = df2['specific_gravity'].fillna(df2['specific_gravity'].median())
df2['albumin'] = df2['albumin'].fillna(df2['albumin'].mean())
df2['sugar'] = df2['sugar'].fillna(df2['sugar'].mean())
df2['blood_glucose_random'] = df2['blood_glucose_random'].fillna(df2['blood_glucose_random'].median())
df2['blood_urea'] = df2['blood_urea'].fillna(df2['blood_urea'].mean())
df2['serum_creatinine'] = df2['serum_creatinine'].fillna(df2['serum_creatinine'].mean())
df2['sodium'] = df2['sodium'].fillna(df2['sodium'].mean())
df2['potassium'] = df2['potassium'].fillna(df2['potassium'].mean())
df2['haemoglobin'] = df2['haemoglobin'].fillna(df2['haemoglobin'].mean())
df2['packed_cell_volume'] = df2['packed_cell_volume'].fillna(df2['packed_cell_volume'].mean())
df2['white_blood_cell_count'] = df2['white_blood_cell_count'].fillna(df2['white_blood_cell_count'].median())
df2['red_blood_cell_count'] = df2['red_blood_cell_count'].fillna(df2['red_blood_cell_count'].median())
df2.isna().sum()
```

Out[24]:
```
age                          0
blood_pressure               0
specific_gravity             0
albumin                      0
sugar                        0
red_blood_cells            152
pus_cell                    65
pus_cell_clumps              4
bacteria                     4
blood_glucose_random         0
blood_urea                   0
serum_creatinine             0
sodium                       0
potassium                    0
haemoglobin                  0
packed_cell_volume           0
white_blood_cell_count       0
red_blood_cell_count         0
hypertension                 2
coronary_artery_disease      2
appetite                     1
peda_edema                   1
aanemia                      1
class                        0
dtype: int64
```

In [25]:
```
for i in colname_cat:
    print("Column Names: ", i)
    print("Unique : ", df2[i].unique())
    print("Null Values: ", df2[i].isna().sum())
    print("Mode Values: ",df2[i].mode())
    print('-' * 50)
```

```
Column Names:  red_blood_cells
Unique :  [nan 'normal' 'abnormal']
Null Values:  152
Mode Values:  0    normal
Name: red_blood_cells, dtype: object
--------------------------------------------------
Column Names:  pus_cell
Unique :  ['normal' 'abnormal' nan]
Null Values:  65
Mode Values:  0    normal
Name: pus_cell, dtype: object
--------------------------------------------------
Column Names:  pus_cell_clumps
Unique :  ['notpresent' 'present' nan]
Null Values:  4
Mode Values:  0    notpresent
Name: pus_cell_clumps, dtype: object
--------------------------------------------------
Column Names:  bacteria
Unique :  ['notpresent' 'present' nan]
Null Values:  4
Mode Values:  0    notpresent
Name: bacteria, dtype: object
--------------------------------------------------
Column Names:  hypertension
Unique :  ['yes' 'no' nan]
Null Values:  2
Mode Values:  0    no
Name: hypertension, dtype: object
--------------------------------------------------
Column Names:  coronary_artery_disease
Unique :  ['no' 'yes' nan]
Null Values:  2
Mode Values:  0    no
Name: coronary_artery_disease, dtype: object
--------------------------------------------------
Column Names:  appetite
Unique :  ['good' 'poor' nan]
Null Values:  1
Mode Values:  0    good
Name: appetite, dtype: object
--------------------------------------------------
Column Names:  peda_edema
Unique :  ['no' 'yes' nan]
Null Values:  1
Mode Values:  0    no
Name: peda_edema, dtype: object
--------------------------------------------------
Column Names:  aanemia
Unique :  ['no' 'yes' nan]
Null Values:  1
Mode Values:  0    no
Name: aanemia, dtype: object
--------------------------------------------------
Column Names:  class
Unique :  ['ckd' 'not ckd']
Null Values:  0
Mode Values:  0    ckd
Name: class, dtype: object
--------------------------------------------------
```

In [26]:
```
df2['red_blood_cells'] = df2['red_blood_cells'].fillna(df2['red_blood_cells'].mode()[0])
df2['pus_cell'] = df2['pus_cell'].fillna(df2['pus_cell'].mode()[0])
df2['pus_cell_clumps'] = df2['pus_cell_clumps'].fillna(df2['pus_cell_clumps'].mode()[0])
df2['bacteria'] = df2['bacteria'].fillna(df2['bacteria'].mode()[0])
df2['hypertension'] = df2['hypertension'].fillna(df2['hypertension'].mode()[0])
df2['coronary_artery_disease'] = df2['coronary_artery_disease'].fillna(df2['coronary_artery_disease'].mode()[0])
df2['appetite'] = df2['appetite'].fillna(df2['appetite'].mode()[0])
df2['peda_edema'] = df2['peda_edema'].fillna(df2['peda_edema'].mode()[0])
df2['aanemia'] = df2['aanemia'].fillna(df2['aanemia'].mode()[0])
df2.isna().sum()
```

Out[26]:
```
age                        0
blood_pressure             0
specific_gravity           0
albumin                    0
sugar                      0
red_blood_cells            0
pus_cell                   0
pus_cell_clumps            0
bacteria                   0
blood_glucose_random       0
blood_urea                 0
serum_creatinine           0
sodium                     0
potassium                  0
haemoglobin                0
packed_cell_volume         0
white_blood_cell_count     0
red_blood_cell_count       0
hypertension               0
coronary_artery_disease    0
appetite                   0
peda_edema                 0
aanemia                    0
class                      0
dtype: int64
```

In [27]:
```
### Converting all categorical data into numerical data
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()

for x in colname_cat:
    df2[x]=le.fit_transform(df2[x])
    le_name_mapping = dict(zip(le.classes_, le.transform(le.classes_)))
    print("Feature",x)
    print("Mapping", le_name_mapping)
```

```
Feature red_blood_cells
Mapping {'abnormal': 0, 'normal': 1}
Feature pus_cell
Mapping {'abnormal': 0, 'normal': 1}
Feature pus_cell_clumps
Mapping {'notpresent': 0, 'present': 1}
Feature bacteria
Mapping {'notpresent': 0, 'present': 1}
Feature hypertension
Mapping {'no': 0, 'yes': 1}
Feature coronary_artery_disease
Mapping {'no': 0, 'yes': 1}
Feature appetite
Mapping {'good': 0, 'poor': 1}
Feature peda_edema
Mapping {'no': 0, 'yes': 1}
Feature aanemia
Mapping {'no': 0, 'yes': 1}
Feature class
Mapping {'ckd': 0, 'not ckd': 1}
```

In [28]:
```
df2.head(15)
```

Out[28]:

	age	blood_pressure	specific_gravity	albumin	sugar	red_blood_cells	pus_cell	pus_cell_clumps	bacteria	blood_glucose_random	...	haemoglobin	packed_cell_volume	white_blood_cell_count	red_blood_cell_coun
0	48.0	80.0	1.020	1.000000	0.000000	1	1	0	0	121.0	...	15.4	44.000000	7800.0	5.
1	7.0	50.0	1.020	4.000000	0.000000	1	1	0	0	121.0	...	11.3	38.000000	6000.0	4.
2	62.0	80.0	1.010	2.000000	3.000000	1	1	0	0	423.0	...	9.6	31.000000	7500.0	4.
3	48.0	70.0	1.005	4.000000	0.000000	1	0	1	0	117.0	...	11.2	32.000000	6700.0	3.
4	51.0	80.0	1.010	2.000000	0.000000	1	1	0	0	106.0	...	11.6	35.000000	7300.0	4.
5	60.0	90.0	1.015	3.000000	0.000000	1	1	0	0	74.0	...	12.2	39.000000	7800.0	4.
6	68.0	70.0	1.010	0.000000	0.000000	1	1	0	0	100.0	...	12.4	36.000000	8000.0	4.
7	24.0	80.0	1.015	2.000000	4.000000	1	0	0	0	410.0	...	12.4	44.000000	6900.0	5.
8	52.0	100.0	1.015	3.000000	0.000000	1	0	1	0	138.0	...	10.8	33.000000	9600.0	4.
9	53.0	90.0	1.020	2.000000	0.000000	0	0	1	0	70.0	...	9.5	29.000000	12100.0	3.
10	50.0	60.0	1.010	2.000000	4.000000	1	0	1	0	490.0	...	9.4	28.000000	8000.0	4.
11	63.0	70.0	1.010	3.000000	0.000000	0	0	1	0	380.0	...	10.8	32.000000	4500.0	3.
12	68.0	70.0	1.015	3.000000	1.000000	1	1	1	0	208.0	...	9.7	28.000000	12200.0	3.
13	68.0	70.0	1.020	1.016949	0.450142	1	1	0	0	98.0	...	9.8	38.884498	8000.0	4.
14	68.0	80.0	1.010	3.000000	2.000000	1	0	1	1	157.0	...	5.6	16.000000	11000.0	2.

15 rows × 24 columns

In [42]:
```
for col in df2.columns:
    print(f"{col} has {df2[col].nunique()} categories\n")
```

```
age has 76 categories

blood_pressure has 10 categories

specific_gravity has 5 categories

albumin has 7 categories

sugar has 7 categories

red_blood_cells has 2 categories

pus_cell has 2 categories

pus_cell_clumps has 2 categories

bacteria has 2 categories

blood_glucose_random has 146 categories

blood_urea has 119 categories

serum_creatinine has 85 categories

sodium has 35 categories

potassium has 41 categories

haemoglobin has 116 categories

packed_cell_volume has 43 categories

white_blood_cell_count has 89 categories

red_blood_cell_count has 45 categories

hypertension has 2 categories

coronary_artery_disease has 2 categories

appetite has 2 categories

peda_edema has 2 categories

aanemia has 2 categories

class has 2 categories
```

In [43]:
```
df3 = df2.copy()
df3.columns
```

Out[43]:
```
Index(['age', 'blood_pressure', 'specific_gravity', 'albumin', 'sugar',
       'red_blood_cells', 'pus_cell', 'pus_cell_clumps', 'bacteria',
       'blood_glucose_random', 'blood_urea', 'serum_creatinine', 'sodium',
       'potassium', 'haemoglobin', 'packed_cell_volume',
       'white_blood_cell_count', 'red_blood_cell_count', 'hypertension',
       'coronary_artery_disease', 'appetite', 'peda_edema', 'aanemia',
       'class'],
      dtype='object')
```

In [44]:
```
### Spliting Data into X and y
X = df3.values[:,:-1]
y = df3.values[:,-1]
print('X:',X.shape)
print('*' * 13)
print('y:',y.shape)
```

```
X: (400, 23)
*************
y: (400,)
```

In [45]:
```
### Feature Scaling
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
scaler.fit(X)
X = scaler.transform(X)
#x = scaler.fit_transform(x)
print(X)
```

```
[[-0.21003135  0.25421378  0.4214856  ... -0.50780078 -0.4843221
  -0.42008403]
 [-2.62723421 -1.97247624  0.4214856  ... -0.50780078 -0.4843221
  -0.42008403]
 [ 0.615355    0.25421378 -1.4210744  ...  1.96927621 -0.4843221
   2.38047614]
 ...
 [-2.33245337  0.25421378  0.4214856  ... -0.50780078 -0.4843221
  -0.42008403]
 [-2.03767254 -1.23024623  1.3427656  ... -0.50780078 -0.4843221
  -0.42008403]
 [ 0.37953033  0.25421378  1.3427656  ... -0.50780078 -0.4843221
  -0.42008403]]
```

In [46]:
```
y = y.astype(int) ### convert y in to integer always perform this operation
```

In [47]:
```
### Spliting into Training and Testing Data
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X,y,test_size=0.2,random_state=10)

print("X_train: ",X_train.shape)
print("X_test: ",X_test.shape)
print("y_train: ",y_train.shape)
print("y_test: ",y_test.shape)
```

```
X_train:  (320, 23)
X_test:  (80, 23)
y_train:  (320,)
y_test:  (80,)
```

In [48]:
```python
#importing model
from xgboost import XGBClassifier
#create a model object
model_xgb = XGBClassifier(objective = 'binary:logistic', learning_rate = 0.5, max_depth = 5, n_estimators = 150)
#train the model object
model_xgb.fit(X_train,y_train)
#predict using the model
y_pred = model_xgb.predict(X_test)
print(y_pred)
```

```
[1 0 1 0 0 1 0 0 0 0 0 0 1 1 0 1 0 0 0 1 0 0 1 1 1 0 0 1 1 1 0 0 0 0 1 0 1
 0 0 0 0 1 0 0 1 0 1 0 1 0 0 0 1 0 1 1 1 0 1 0 0 0 0 0 0 1 0 0 0 0 0 1 0 0
 0 1 0 0 0 0]
```

In [49]:
```python
# Checking confusion matrix for the model
cfm = confusion_matrix(y_test,y_pred)
dff = pd.DataFrame(cfm)
dff.style.set_properties(**{"background-color": "#F3FFFF","color":"black","border": "2px  solid black"})
```

Out[49]:

	0	1
0	52	0
1	1	27

In [50]:
```python
# Checking classification report score for the model
cr = classification_report(y_test,y_pred)
print("Classification report: ")
print(cr)

# Checking accuracy score for the model
acc = accuracy_score(y_test,y_pred)
print("Accuracy of the model: ",acc)
```

```
Classification report: 
              precision    recall  f1-score   support

           0       0.98      1.00      0.99        52
           1       1.00      0.96      0.98        28

    accuracy                           0.99        80
   macro avg       0.99      0.98      0.99        80
weighted avg       0.99      0.99      0.99        80

Accuracy of the model:  0.9875
```

In [51]:
```python
#importing model
from sklearn.ensemble import AdaBoostClassifier
#create a model object
model_ada = AdaBoostClassifier(n_estimators=100, learning_rate=2.0)
#train the model object
model_ada.fit(X_train,y_train)
#predict using the model
y_pred = model_ada.predict(X_test)
print(y_pred)
```

```
[1 0 1 0 0 1 0 0 0 0 0 0 1 1 0 1 0 0 0 1 0 0 1 1 1 0 0 1 1 1 0 0 0 0 1 0 1
 0 0 0 0 1 0 0 1 0 1 0 1 0 0 0 1 0 1 1 1 0 1 0 0 0 1 0 0 1 0 0 0 0 0 1 0 0
 0 0 0 0 0 0]
```

In [52]:
```python
# Checking confusion matrix for the model
cfm = confusion_matrix(y_test,y_pred)
dff = pd.DataFrame(cfm)
dff.style.set_properties(**{"background-color": "#F3FFFF","color":"black","border": "2px  solid black"})
```

Out[52]:

	0	1
0	52	0
1	1	27

In [53]:
```python
# Checking classification report score for the model
cr = classification_report(y_test,y_pred)
print("Classification report: ")
print(cr)

# Checking accuracy score for the model
acc = accuracy_score(y_test,y_pred)
print("Accuracy of the model: ",acc)
```

```
Classification report: 
              precision    recall  f1-score   support

           0       0.98      1.00      0.99        52
           1       1.00      0.96      0.98        28

    accuracy                           0.99        80
   macro avg       0.99      0.98      0.99        80
weighted avg       0.99      0.99      0.99        80

Accuracy of the model:  0.9875
```

Made with ❤ by Zahid Salim Shaikh

In [ ]:
```python

```