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Lab 10: Naive Bayes (NB) Classification

```
Kidney diseases are disorders that affect the functions of the kidney. During the late stages, kidney d
iseases can cause kidney failure to prevent chronic kidney disease-CKD by utilising machine learning te
chniques to diagnose kidney disease at an early stage. We describe the most prominent supervised machin
e learning algorithms (SML), their characteristics, Generalisation capacity of each method, Time comple
xity, Hyper-parameter tuning, and Advantages and disadvantages of each technique comparatively.

The Kidney Disease dataset obtained from UCI was used to determine and test its highest percentage of a
ccuracy and benchmark.
```

Importing basic libraries

In [1]:
```
import pandas as pd
import numpy as np
import time
import seaborn as sns
import matplotlib.pyplot as plt
import matplotlib as mpl
```

Reading the dataset

In [2]:
```
ckd_df = pd.read_csv('kidney_disease.csv')

#Check the shape
print(ckd_df.shape)
```

```
(400, 26)
```

In [3]:
```
#check the columns
ckd_df.columns
```

Out[3]:
```
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')
```

Rename the columns to have meaningful names

```
In [4]: col_dict={"bp":"blood_pressure",
                  "sg":"specific_gravity",
                  "al":"albumin",
                  "su":"sugar",
                  "rbc":"red_blood_cells",
                  "pc":"pus_cell",
                  "pcc":"pus_cell_clumps",
                  "ba":"bacteria",
                  "bgr":"blood_glucose_random",
                  "bu":"blood_urea",
                  "sc":"serum_creatinine",
                  "sod":"sodium",
                  "pot":"potassium",
                  "hemo":"hemoglobin",
                  "pcv":"packed_cell_volume",
                  "wc":"white_blood_cell_count",
                  "rc":"red_blood_cell_count",
                  "htn":"hypertension",
                  "dm":"diabetes_mellitus",
                  "cad":"coronary_artery_disease",
                  "appet":"appetite",
                  "pe":"pedal_edema",
                  "ane":"anemia"}

        ckd_df.rename(columns=col_dict, inplace=True)

        #Check the column names again
        ckd_df.columns
```

```
Out[4]: Index(['id', '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', 'hemoglobin', 'packed_cell_volume',
               'white_blood_cell_count', 'red_blood_cell_count', 'hypertension',
               'diabetes_mellitus', 'coronary_artery_disease', 'appetite',
               'pedal_edema', 'anemia', 'classification'],
              dtype='object')
```

Observing the data

```
In [5]: ckd_df.head(11).T
```

Out[5]:

	0	1	2	3	4	5	6	7	8	9	10
id	0	1	2	3	4	5	6	7	8	9	10
age	48	7	62	48	51	60	68	24	52	53	50
blood_pressure	80	50	80	70	80	90	70	NaN	100	90	60
specific_gravity	1.02	1.02	1.01	1.005	1.01	1.015	1.01	1.015	1.015	1.02	1.01
albumin	1	4	2	4	2	3	0	2	3	2	2
sugar	0	0	3	0	0	0	0	4	0	0	4
red_blood_cells	NaN	NaN	normal	normal	normal	NaN	NaN	normal	normal	abnormal	NaN
pus_cell	normal	normal	normal	abnormal	normal	NaN	normal	abnormal	abnormal	abnormal	abnormal
pus_cell_clumps	notpresent	notpresent	notpresent	present	notpresent	notpresent	notpresent	notpresent	present	present	present
bacteria	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent
blood_glucose_random	121	NaN	423	117	106	74	100	410	138	70	490
blood_urea	36	18	53	56	26	25	54	31	60	107	55
serum_creatinine	1.2	0.8	1.8	3.8	1.4	1.1	24	1.1	1.9	7.2	4
sodium	NaN	NaN	NaN	111	NaN	142	104	NaN	NaN	114	NaN
potassium	NaN	NaN	NaN	2.5	NaN	3.2	4	NaN	NaN	3.7	NaN
hemoglobin	15.4	11.3	9.6	11.2	11.6	12.2	12.4	12.4	10.8	9.5	9.4
packed_cell_volume	44	38	31	32	35	39	36	44	33	29	28
white_blood_cell_count	7800	6000	7500	6700	7300	7800	NaN	6900	9600	12100	NaN
red_blood_cell_count	5.2	NaN	NaN	3.9	4.6	4.4	NaN	5	4.0	3.7	NaN
hypertension	yes	no	no	yes	no	yes	no	no	yes	yes	yes
diabetes_mellitus	yes	no	yes	no	no	yes	no	yes	yes	yes	yes
coronary_artery_disease	no	no	no	no	no	no	no	no	no	no	no
appetite	good	good	poor	poor	good	good	good	good	good	poor	good
pedal_edema	no	no	no	yes	no	yes	no	yes	no	no	no
anemia	no	no	yes	yes	no	no	no	no	yes	yes	yes
classification	ckd	ckd	ckd	ckd	ckd	ckd	ckd	ckd	ckd	ckd	ckd

Data DeepDive

```
In [6]: for i in ckd_df.drop("id",axis=1).columns:
            print('unique values in "{}":\n'.format(i),ckd_df[i].unique())
```

```
unique values in "age":
 [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.]
unique values in "blood_pressure":
 [ 80.  50.  70.  90.  nan 100.  60. 110. 140. 180. 120.]
unique values in "specific_gravity":
 [1.02  1.01  1.005 1.015   nan 1.025]
unique values in "albumin":
 [ 1.  4.  2.  3.  0. nan  5.]
unique values in "sugar":
 [ 0.  3.  4.  1. nan  2.  5.]
unique values in "red_blood_cells":
 [nan 'normal' 'abnormal']
unique values in "pus_cell":
 ['normal' 'abnormal' nan]
unique values in "pus_cell_clumps":
```

In [7]:
```python
#Replace incorrect values
ckd_df['diabetes_mellitus'] =ckd_df['diabetes_mellitus'].replace(to_replace={'\tno':'no','\tyes':'yes',' yes':'
ckd_df['coronary_artery_disease'] = ckd_df['coronary_artery_disease'].replace(to_replace='\tno',value='no')
ckd_df['white_blood_cell_count'] = ckd_df['white_blood_cell_count'].replace(to_replace='\t8400',value='8400')
ckd_df["classification"]=ckd_df["classification"].replace("ckd\t", "ckd")

for i in range(ckd_df.shape[0]):
    if ckd_df.iloc[i,16]=='\t?':
        ckd_df.iloc[i,16]=np.nan
    if ckd_df.iloc[i,16]=='\t43':
        ckd_df.iloc[i,16]='43'
    if ckd_df.iloc[i,17]=='\t?':
        ckd_df.iloc[i,17]=np.nan
    if ckd_df.iloc[i,17]=='\t6200':
        ckd_df.iloc[i,17]= '6200'
    if ckd_df.iloc[i,18]=='\t?':
        ckd_df.iloc[i,18]=np.nan
    if ckd_df.iloc[i,25]=='ckd':
        ckd_df.iloc[i,25]='1'
    if ckd_df.iloc[i,25]=='notckd':
        ckd_df.iloc[i,25]='0'

for i in ckd_df.drop("id",axis=1).columns:
    print('unique values in "{}":\n'.format(i),ckd_df[i].unique())
```

```
unique values in "age":
 [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.]
unique values in "blood_pressure":
 [ 80.  50.  70.  90.  nan 100.  60. 110. 140. 180. 120.]
unique values in "specific_gravity":
 [1.02  1.01  1.005 1.015   nan 1.025]
unique values in "albumin":
 [ 1.  4.  2.  3.  0. nan  5.]
unique values in "sugar":
 [ 0.  3.  4.  1. nan  2.  5.]
unique values in "red_blood_cells":
 [nan 'normal' 'abnormal']
unique values in "pus_cell":
 ['normal' 'abnormal' nan]
unique values in "pus_cell_clumps":
 ['notpresent' 'present' nan]
unique values in "bacteria":
 ['notpresent' 'present' nan]
unique values in "blood_glucose_random":
 [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.]
unique values in "blood_urea":
 [ 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. ]
unique values in "serum_creatinine":
 [ 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 ]
unique values in "sodium":
 [  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. ]
unique values in "potassium":
 [ 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]
unique values in "hemoglobin":
 [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]
unique values in "packed_cell_volume":
 ['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']
unique values in "white_blood_cell_count":
 ['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']
unique values in "red_blood_cell_count":
 ['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'
 '5.4' '6.1' '6.2' '6.3' '5.1' '5.8' '5.5' '5.3' '6.4' '5.7' '5.9' '6.5']
unique values in "hypertension":
 ['yes' 'no' nan]
unique values in "diabetes_mellitus":
 ['yes' 'no' nan]
unique values in "coronary_artery_disease":
 ['no' 'yes' nan]
unique values in "appetite":
 ['good' 'poor' nan]
unique values in "pedal_edema":
 ['no' 'yes' nan]
unique values in "anemia":
 ['no' 'yes' nan]
unique values in "classification":
 ['1' '0']
```

In [8]:
```
# Observing the summarized information of data
ckd_df.info()
```

```
<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   blood_pressure           388 non-null    float64
 3   specific_gravity         353 non-null    float64
 4   albumin                  354 non-null    float64
 5   sugar                    351 non-null    float64
 6   red_blood_cells          248 non-null    object 
 7   pus_cell                 335 non-null    object 
 8   pus_cell_clumps          396 non-null    object 
 9   bacteria                 396 non-null    object 
 10  blood_glucose_random     356 non-null    float64
 11  blood_urea               381 non-null    float64
 12  serum_creatinine         383 non-null    float64
 13  sodium                   313 non-null    float64
 14  potassium                312 non-null    float64
 15  hemoglobin               348 non-null    float64
 16  packed_cell_volume       329 non-null    object 
 17  white_blood_cell_count   294 non-null    object 
 18  red_blood_cell_count     269 non-null    object 
 19  hypertension             398 non-null    object 
 20  diabetes_mellitus        398 non-null    object 
 21  coronary_artery_disease  398 non-null    object 
 22  appetite                 399 non-null    object 
 23  pedal_edema              399 non-null    object 
 24  anemia                   399 non-null    object 
 25  classification           400 non-null    object 
dtypes: float64(11), int64(1), object(14)
memory usage: 81.4+ KB
```

```
In [9]: ckd_df.iloc[:,-1]=ckd_df.iloc[:,-1].astype('int64')
        ckd_df.head(11).T
```

Out[9]:

	0	1	2	3	4	5	6	7	8	9	10
id	0	1	2	3	4	5	6	7	8	9	10
age	48	7	62	48	51	60	68	24	52	53	50
blood_pressure	80	50	80	70	80	90	70	NaN	100	90	60
specific_gravity	1.02	1.02	1.01	1.005	1.01	1.015	1.01	1.015	1.015	1.02	1.01
albumin	1	4	2	4	2	3	0	2	3	2	2
sugar	0	0	3	0	0	0	0	4	0	0	4
red_blood_cells	NaN	NaN	normal	normal	normal	NaN	NaN	normal	normal	abnormal	NaN
pus_cell	normal	normal	normal	abnormal	normal	NaN	normal	abnormal	abnormal	abnormal	abnormal
pus_cell_clumps	notpresent	notpresent	notpresent	present	notpresent	notpresent	notpresent	notpresent	present	present	present
bacteria	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent
blood_glucose_random	121	NaN	423	117	106	74	100	410	138	70	490
blood_urea	36	18	53	56	26	25	54	31	60	107	55
serum_creatinine	1.2	0.8	1.8	3.8	1.4	1.1	24	1.1	1.9	7.2	4
sodium	NaN	NaN	NaN	111	NaN	142	104	NaN	NaN	114	NaN
potassium	NaN	NaN	NaN	2.5	NaN	3.2	4	NaN	NaN	3.7	NaN
hemoglobin	15.4	11.3	9.6	11.2	11.6	12.2	12.4	12.4	10.8	9.5	9.4
packed_cell_volume	44	38	31	32	35	39	36	44	33	29	28
white_blood_cell_count	7800	6000	7500	6700	7300	7800	NaN	6900	9600	12100	NaN
red_blood_cell_count	5.2	NaN	NaN	3.9	4.6	4.4	NaN	5	4.0	3.7	NaN
hypertension	yes	no	no	yes	no	yes	no	no	yes	yes	yes
diabetes_mellitus	yes	no	yes	no	no	yes	no	yes	yes	yes	yes
coronary_artery_disease	no	no	no	no	no	no	no	no	no	no	no
appetite	good	good	poor	poor	good	good	good	good	good	poor	good
pedal_edema	no	no	no	yes	no	yes	no	yes	no	no	no
anemia	no	no	yes	yes	no	no	no	no	yes	yes	yes
classification	1	1	1	1	1	1	1	1	1	1	1

```
In [10]: print(ckd_df['packed_cell_volume'].unique())
         print(ckd_df['white_blood_cell_count'].unique())
         print(ckd_df['red_blood_cell_count'].unique())
```

```
['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']
['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']
['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'
 '5.4' '6.1' '6.2' '6.3' '5.1' '5.8' '5.5' '5.3' '6.4' '5.7' '5.9' '6.5']
```

```
In [11]: mistyped=['packed_cell_volume','white_blood_cell_count','red_blood_cell_count']
         for col in mistyped:
                 ckd_df[col]=ckd_df[col].astype('float')

         numeric=[]
         for i in ckd_df.columns:
             if ckd_df[i].dtype=='float64':
                 numeric.append(i)

         numeric
```

```
Out[11]: ['age',
          'blood_pressure',
          'specific_gravity',
          'albumin',
          'sugar',
          'blood_glucose_random',
          'blood_urea',
          'serum_creatinine',
          'sodium',
          'potassium',
          'hemoglobin',
          'packed_cell_volume',
          'white_blood_cell_count',
          'red_blood_cell_count']
```

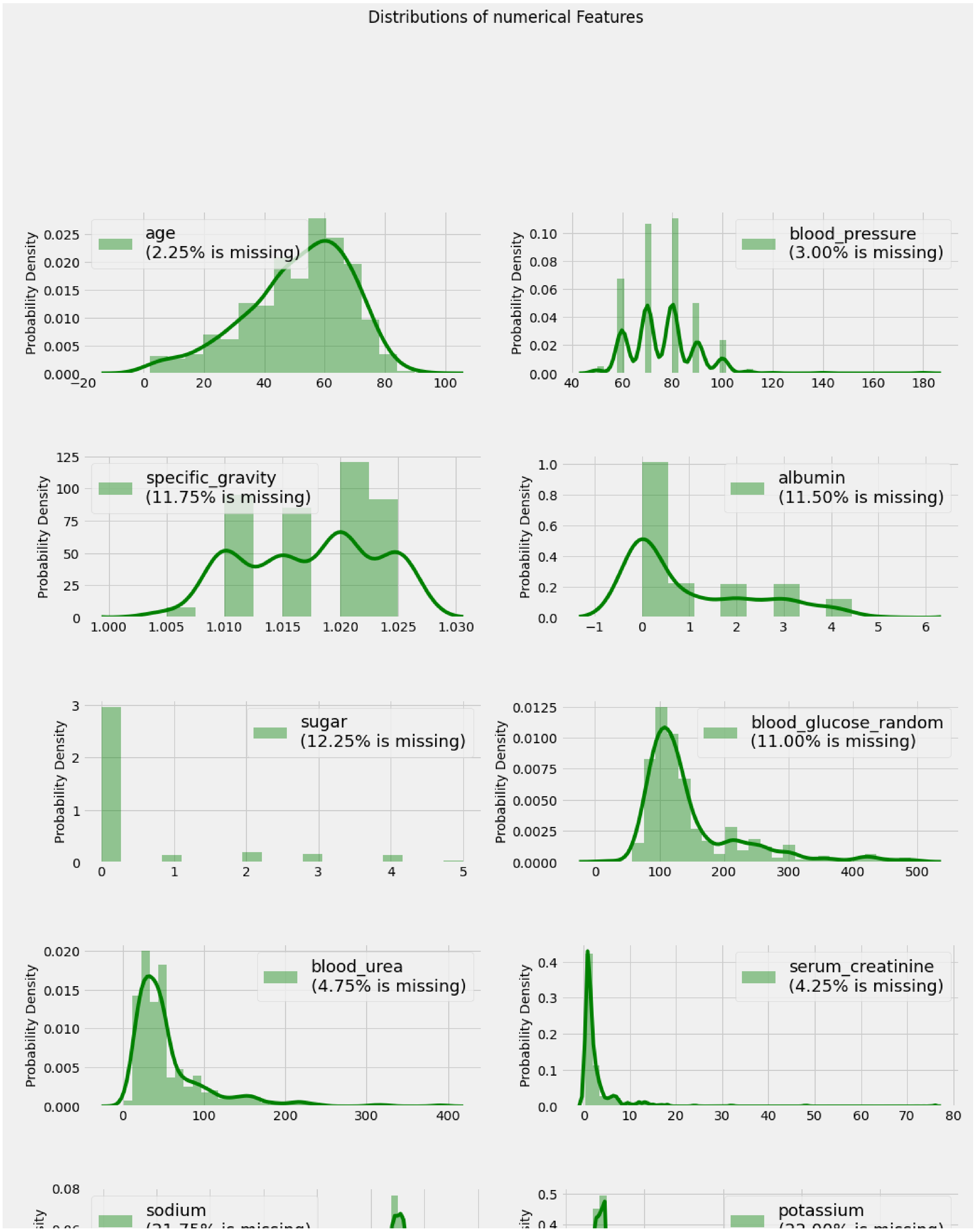
```
In [12]: ckd_df.drop('id',axis=1,inplace=True)

         categoricals=[]

         for col in ckd_df.columns:
             if not col in numeric:
                 categoricals.append(col)
         categoricals.remove('classification')

         categoricals
```

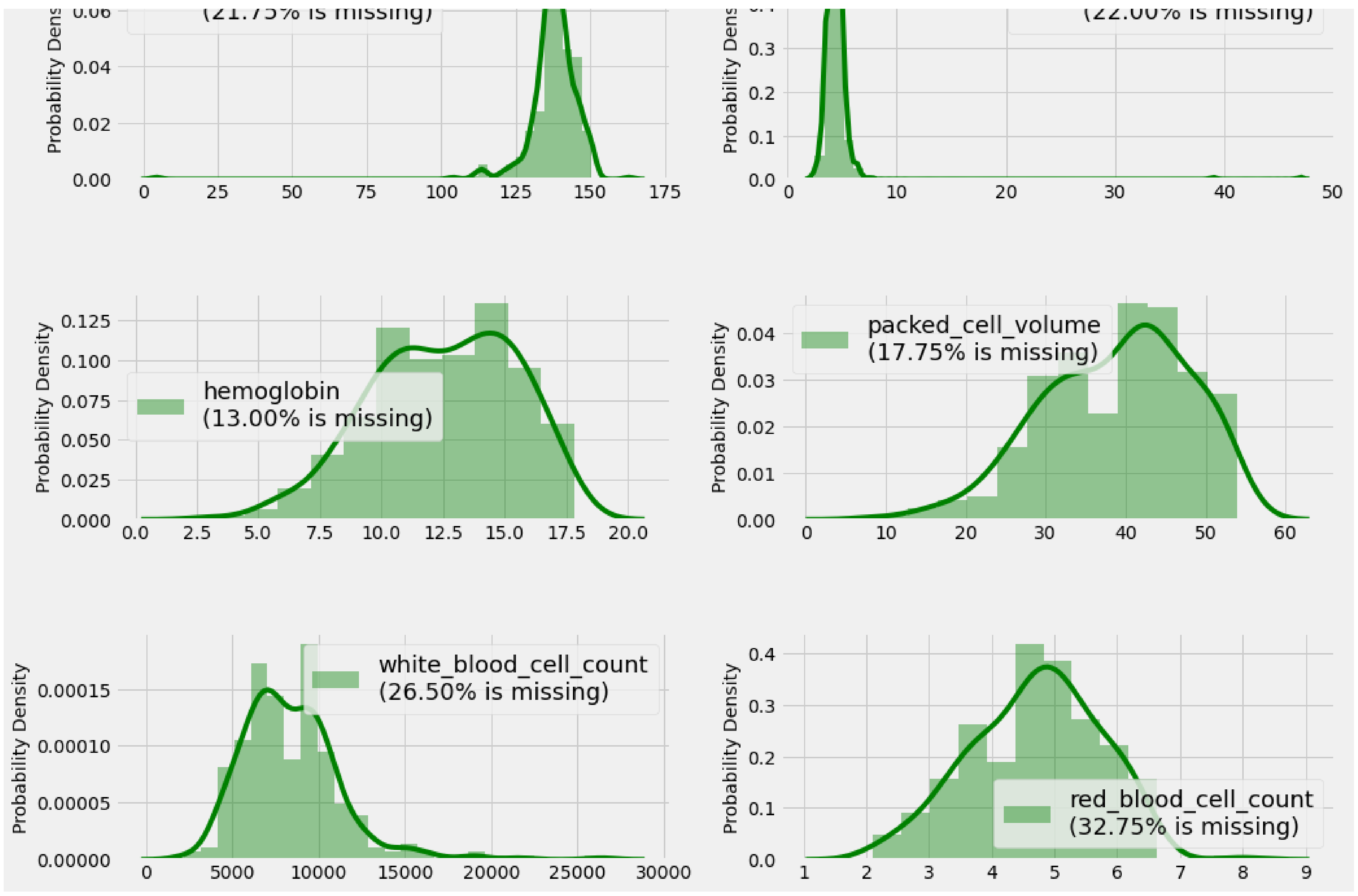
```
Out[12]: ['red_blood_cells',
          'pus_cell',
          'pus_cell_clumps',
          'bacteria',
          'hypertension',
          'diabetes_mellitus',
          'coronary_artery_disease',
          'appetite',
          'pedal_edema',
          'anemia']
```

```
In [13]: import warnings
         warnings.simplefilter('ignore')

         import matplotlib.style as style
         style.use('fivethirtyeight')
```

Checking distribution of the numerical features

In [14]:
```python
fig, axes = plt.subplots(nrows=7, ncols=2, figsize=(15,30))
fig.subplots_adjust(hspace=0.5)
fig.suptitle('Distributions of numerical Features')

n_rows, n_cols = (7,2)

for index, column in enumerate(numeric):

    i,j = (index // n_cols), (index % n_cols)
    miss_perc="%.2f"%(100*(1-(ckd_df[column].dropna().shape[0])/ckd_df.shape[0]))
    collabel=column+"\n({}% is missing)".format(miss_perc)
    fig=sns.distplot(ckd_df[column], color="green", label=collabel,
                     norm_hist=True, ax=axes[i,j], kde_kws={"lw":4})
    fig=fig.legend(loc='best', fontsize=18)

    axes[i,j].set_ylabel("Probability Density",fontsize='medium')
    axes[i,j].set_xlabel(None)

plt.show()
```



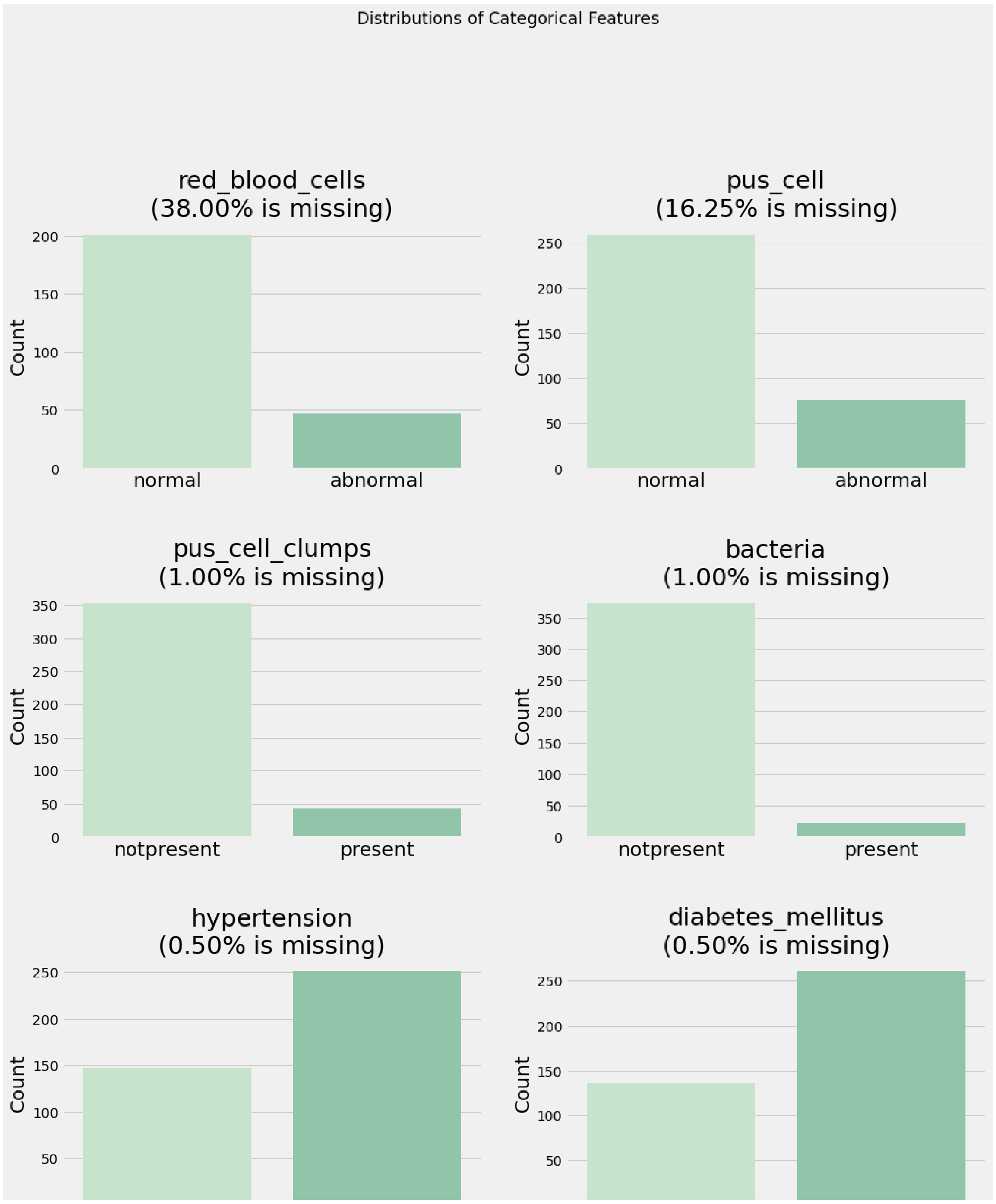


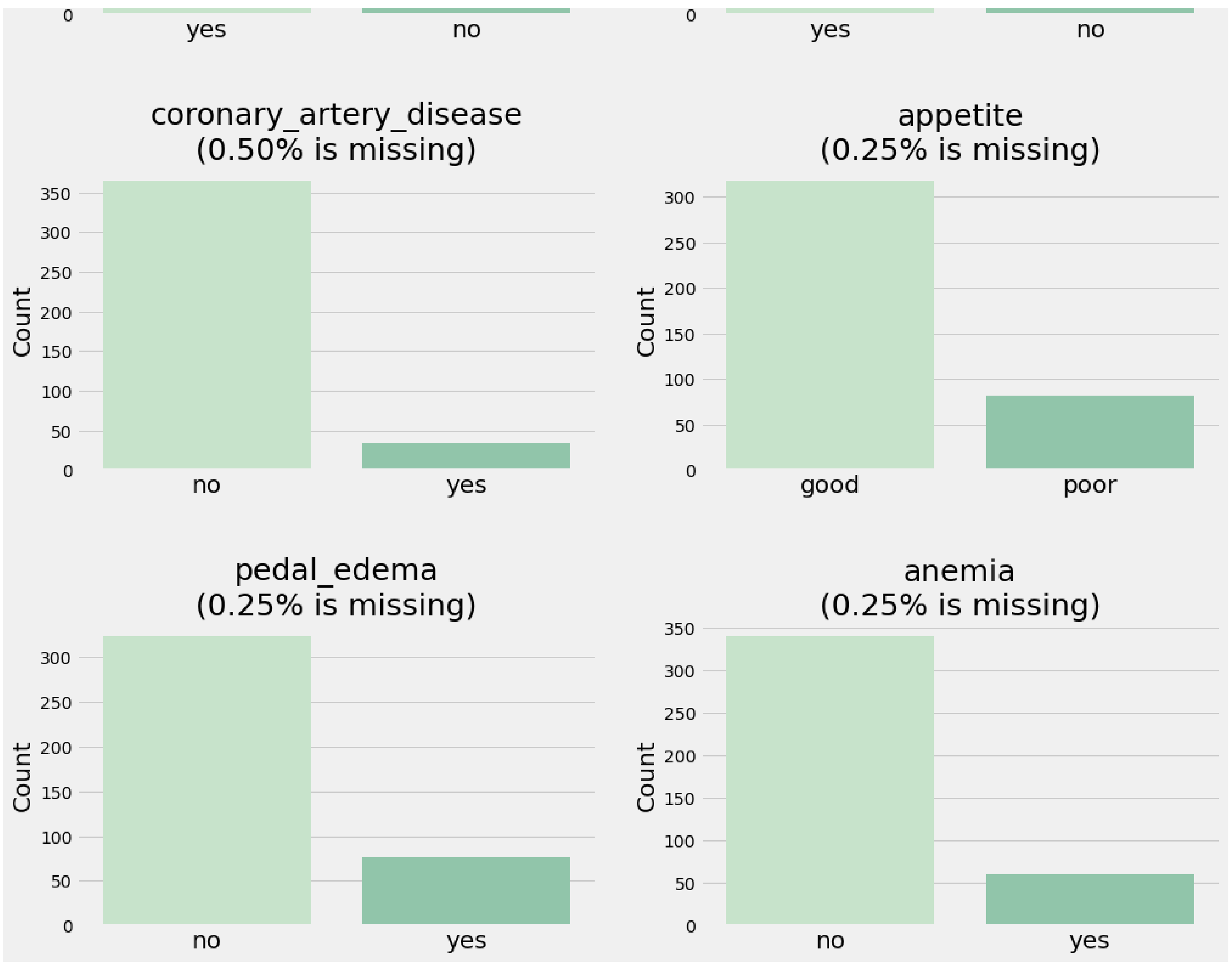
Numeric features:-

While diving into detailed EDA we could see that some of the features represent good distributions, some are skewed by right & left and shows us positive and negative insights.

Checking distribution of the Categorical features

In [15]:
```
style.use('fivethirtyeight')

fig, axes = plt.subplots(nrows=5, ncols=2, figsize=(15,30))
fig.subplots_adjust(hspace=0.5)
fig.suptitle('Distributions of Categorical Features')

n_rows, n_cols = (5,2)

for index, column in enumerate(categoricals):

    i,j = index // n_cols, index % n_cols
    miss_perc="%.2f"%(100*(1-(ckd_df[column].dropna().shape[0])/ckd_df.shape[0]))
    collabel=column+"\n({}% is missing)".format(miss_perc)
    fig = sns.countplot(x=column, data=ckd_df,label=collabel,
                        palette=sns.cubehelix_palette(rot=-.4,light=0.85,hue=1), ax=axes[i,j])

    axes[i,j].set_title(collabel,fontsize=25)
    axes[i,j].set_xlabel(None)
    axes[i,j].set_ylabel("Count",fontsize=20)
    axes[i,j].set_xticklabels(axes[i,j].get_xticklabels(), Fontsize=20)

plt.show()
```

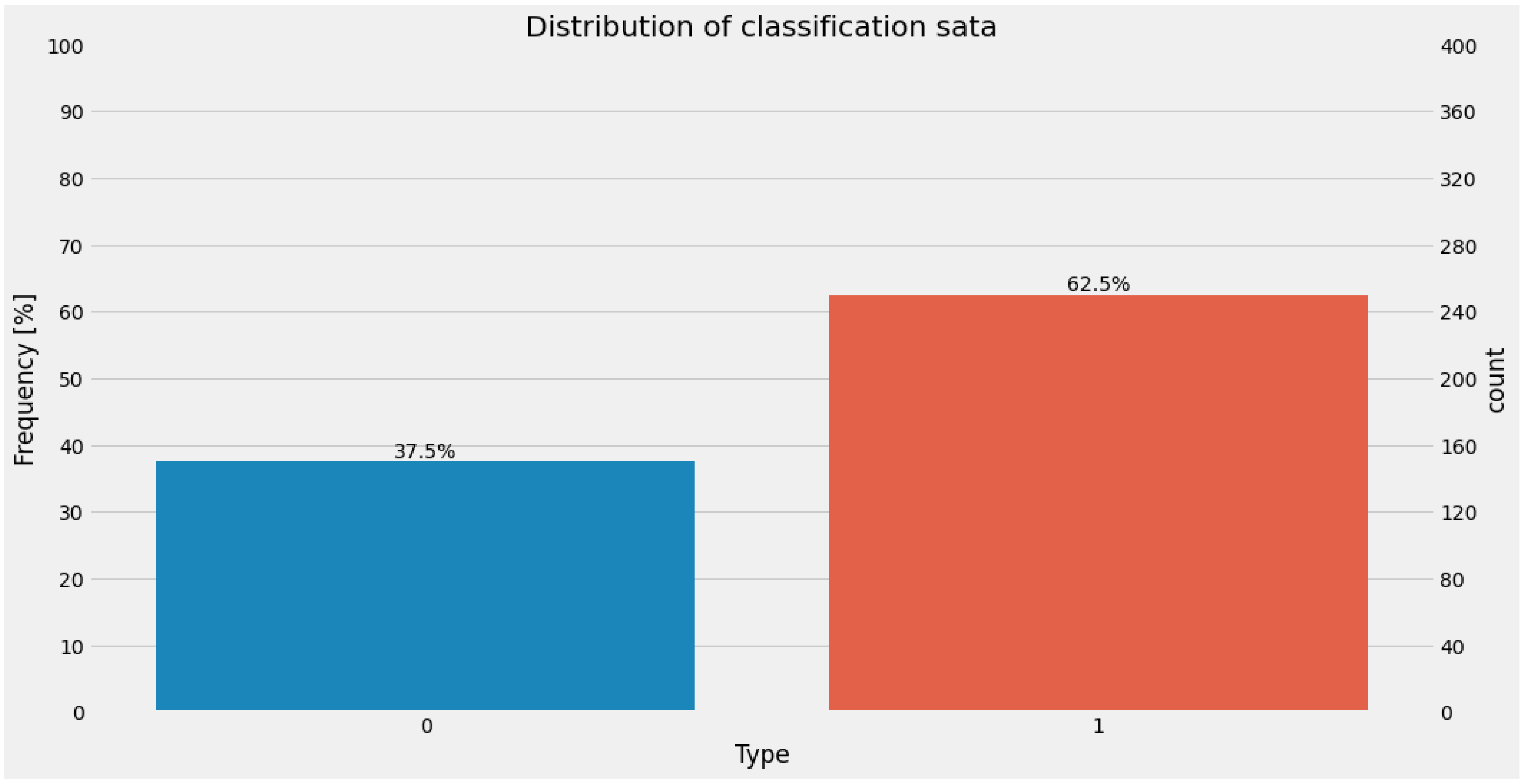




Categorical features:-

Bar graph is used to analysis categorical values. Since it’s an binary classification dataset, we could see that Most of the uniques features in categorical data we’re ‘good’, ‘poor’, ‘yes’, ‘no’, ‘normal’, ‘abnormal’ and finally our classification label ‘ckd’ and ‘notckd’.

In [16]:
```
import matplotlib.ticker as ticker
style.use('fivethirtyeight')
# Some random data
ncount = 400

plt.figure(figsize=(15,8))
ax = sns.countplot(x="classification", data=ckd_df)
plt.title('Distribution of classification sata')
plt.xlabel('Type')

# Make twin axis
ax2=ax.twinx()

# Switch so count axis is on right, frequency on left
ax2.yaxis.tick_left()
ax.yaxis.tick_right()

# Also switch the labels over
ax.yaxis.set_label_position('right')
ax2.yaxis.set_label_position('left')

ax2.set_ylabel('Frequency [%]')

for p in ax.patches:
    x=p.get_bbox().get_points()[:,0]
    y=p.get_bbox().get_points()[1,1]
    ax.annotate('{:.1f}%'.format(100.*y/ncount), (x.mean(), y),
            ha='center', va='bottom') # set the alignment of the text

# Use a LinearLocator to ensure the correct number of ticks
ax.yaxis.set_major_locator(ticker.LinearLocator(11))

# Fix the frequency range to 0-100
ax2.set_ylim(0,100)
ax.set_ylim(0,ncount)

# And use a MultipleLocator to ensure a tick spacing of 10
ax2.yaxis.set_major_locator(ticker.MultipleLocator(10))

# Need to turn the grid on ax2 off, otherwise the gridlines end up on top of the bars
ax2.grid(None)
```



After required taking acting on Missing values using Sklearn package, Outliers were found by checking uniqueness values of each features.

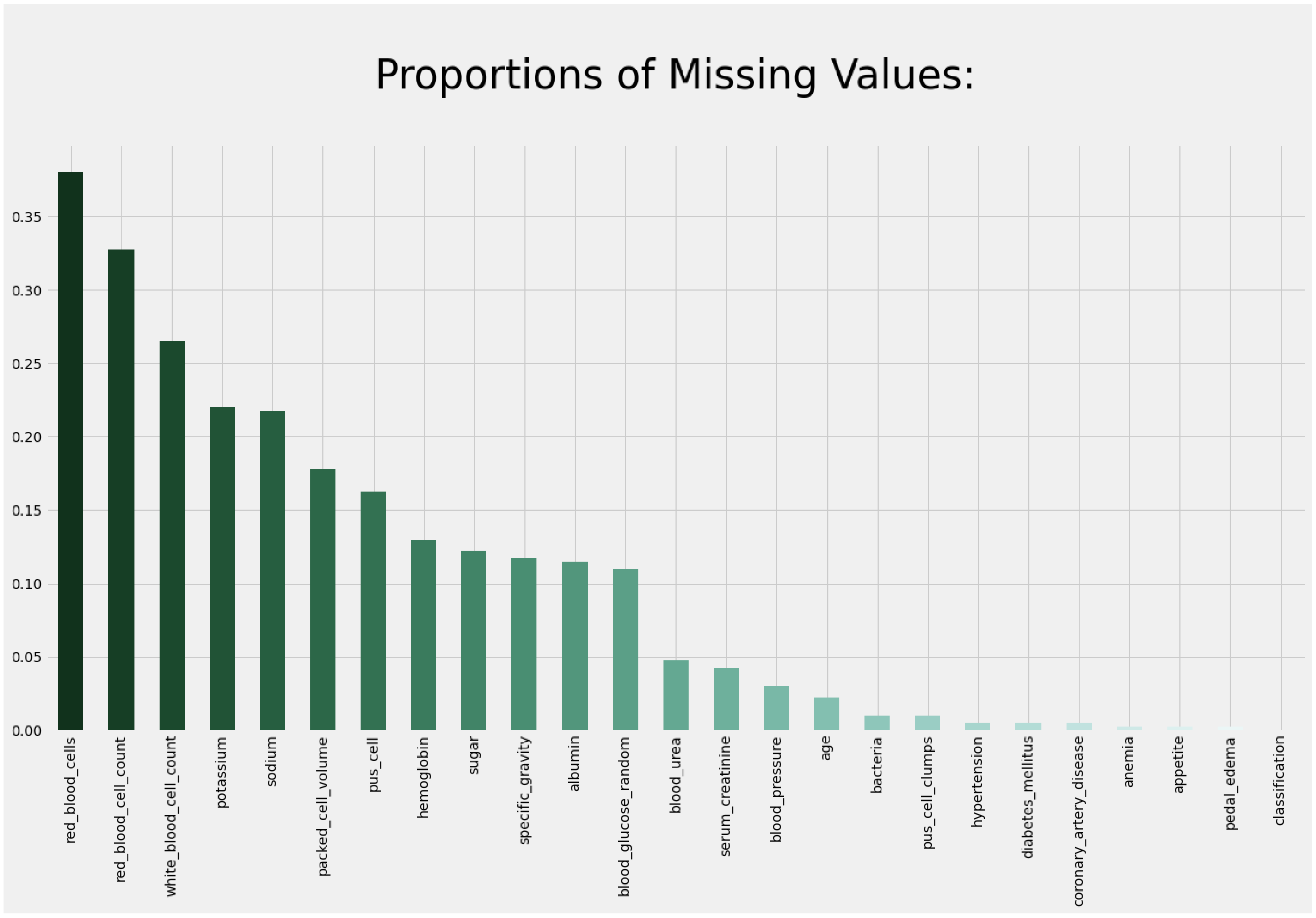
Outliers removal:-

```
-Since we don’t have higher level of data outliers.
-We took necessary outliers fix based on the domain knowledge by updating invalid data entry.
-Removing outliers will help to improve our data quality, which will be resulting in the model performa
nce.
```

In [17]:
```
for i in range(ckd_df.shape[0]):
    if ckd_df.iloc[i,24]=='ckd':
        ckd_df.iloc[i,24]='1'
    if ckd_df.iloc[i,24]=='notckd':
        ckd_df.iloc[i,24]='0'
```

Missing Values

```
In [18]: style.use('fivethirtyeight')

         d=((ckd_df.isnull().sum()/ckd_df.shape[0])).sort_values(ascending=False)
         d.plot(kind='bar',
                color=sns.cubehelix_palette(start=2,
                                             rot=0.15,
                                             dark=0.15,
                                             light=0.95,
                                             reverse=True,
                                             n_colors=24),
                 figsize=(20,10))
         plt.title("\nProportions of Missing Values:\n",fontsize=40)
         plt.show()
```



Data cleaning

```
    Data cleaningprocess were the key to projecting model quality and good accuracy score.
    In CKD dataset we can clearly view the percentage of Missing values. Which is later handled using S
klearn missing value imputer.
    Sklearn is one of the best library for imputation.
```

In [19]:
```
ckd_df.head(10).T
```

Out[19]:

	0	1	2	3	4	5	6	7	8	9
age	48	7	62	48	51	60	68	24	52	53
blood_pressure	80	50	80	70	80	90	70	NaN	100	90
specific_gravity	1.02	1.02	1.01	1.005	1.01	1.015	1.01	1.015	1.015	1.02
albumin	1	4	2	4	2	3	0	2	3	2
sugar	0	0	3	0	0	0	0	4	0	0
red_blood_cells	NaN	NaN	normal	normal	normal	NaN	NaN	normal	normal	abnormal
pus_cell	normal	normal	normal	abnormal	normal	NaN	normal	abnormal	abnormal	abnormal
pus_cell_clumps	notpresent	notpresent	notpresent	present	notpresent	notpresent	notpresent	notpresent	present	present
bacteria	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent	notpresent
blood_glucose_random	121	NaN	423	117	106	74	100	410	138	70
blood_urea	36	18	53	56	26	25	54	31	60	107
serum_creatinine	1.2	0.8	1.8	3.8	1.4	1.1	24	1.1	1.9	7.2
sodium	NaN	NaN	NaN	111	NaN	142	104	NaN	NaN	114
potassium	NaN	NaN	NaN	2.5	NaN	3.2	4	NaN	NaN	3.7
hemoglobin	15.4	11.3	9.6	11.2	11.6	12.2	12.4	12.4	10.8	9.5
packed_cell_volume	44	38	31	32	35	39	36	44	33	29
white_blood_cell_count	7800	6000	7500	6700	7300	7800	NaN	6900	9600	12100
red_blood_cell_count	5.2	NaN	NaN	3.9	4.6	4.4	NaN	5	4	3.7
hypertension	yes	no	no	yes	no	yes	no	no	yes	yes
diabetes_mellitus	yes	no	yes	no	no	yes	no	yes	yes	yes
coronary_artery_disease	no	no	no	no	no	no	no	no	no	no
appetite	good	good	poor	poor	good	good	good	good	good	poor
pedal_edema	no	no	no	yes	no	yes	no	yes	no	no
anemia	no	no	yes	yes	no	no	no	no	yes	yes
classification	1	1	1	1	1	1	1	1	1	1

One-Hot Encoding

In [20]:
```python
onehotdata=pd.get_dummies(ckd_df,drop_first=True,prefix_sep=': ')
onehotdata.head(13).T
```
Out[20]:

	0	1	2	3	4	5	6	7	8	9	10	11	12
age	48.00	7.00	62.00	48.000	51.00	60.000	68.00	24.000	52.000	53.00	50.00	63.00	68.000
blood_pressure	80.00	50.00	80.00	70.000	80.00	90.000	70.00	NaN	100.000	90.00	60.00	70.00	70.000
specific_gravity	1.02	1.02	1.01	1.005	1.01	1.015	1.01	1.015	1.015	1.02	1.01	1.01	1.015
albumin	1.00	4.00	2.00	4.000	2.00	3.000	0.00	2.000	3.000	2.00	2.00	3.00	3.000
sugar	0.00	0.00	3.00	0.000	0.00	0.000	0.00	4.000	0.000	0.00	4.00	0.00	1.000
blood_glucose_random	121.00	NaN	423.00	117.000	106.00	74.000	100.00	410.000	138.000	70.00	490.00	380.00	208.000
blood_urea	36.00	18.00	53.00	56.000	26.00	25.000	54.00	31.000	60.000	107.00	55.00	60.00	72.000
serum_creatinine	1.20	0.80	1.80	3.800	1.40	1.100	24.00	1.100	1.900	7.20	4.00	2.70	2.100
sodium	NaN	NaN	NaN	111.000	NaN	142.000	104.00	NaN	NaN	114.00	NaN	131.00	138.000
potassium	NaN	NaN	NaN	2.500	NaN	3.200	4.00	NaN	NaN	3.70	NaN	4.20	5.800
hemoglobin	15.40	11.30	9.60	11.200	11.60	12.200	12.40	12.400	10.800	9.50	9.40	10.80	9.700
packed_cell_volume	44.00	38.00	31.00	32.000	35.00	39.000	36.00	44.000	33.000	29.00	28.00	32.00	28.000
white_blood_cell_count	7800.00	6000.00	7500.00	6700.000	7300.00	7800.000	NaN	6900.000	9600.000	12100.00	NaN	4500.00	12200.000
red_blood_cell_count	5.20	NaN	NaN	3.900	4.60	4.400	NaN	5.000	4.000	3.70	NaN	3.80	3.400
classification	1.00	1.00	1.00	1.000	1.00	1.000	1.00	1.000	1.000	1.00	1.00	1.00	1.000
red_blood_cells: normal	0.00	0.00	1.00	1.000	1.00	0.000	0.00	1.000	1.000	0.00	0.00	0.00	0.000
pus_cell: normal	1.00	1.00	1.00	0.000	1.00	0.000	1.00	0.000	0.000	0.00	0.00	0.00	1.000
pus_cell_clumps: present	0.00	0.00	0.00	1.000	0.00	0.000	0.00	0.000	1.000	1.00	1.00	1.00	1.000
bacteria: present	0.00	0.00	0.00	0.000	0.00	0.000	0.00	0.000	0.000	0.00	0.00	0.00	0.000
hypertension: yes	1.00	0.00	0.00	1.000	0.00	1.000	0.00	0.000	1.000	1.00	1.00	1.00	1.000
diabetes_mellitus: yes	1.00	0.00	1.00	0.000	0.00	1.000	0.00	1.000	1.000	1.00	1.00	1.00	1.000
coronary_artery_disease: yes	0.00	0.00	0.00	0.000	0.00	0.000	0.00	0.000	0.000	0.00	0.00	0.00	1.000
appetite: poor	0.00	0.00	1.00	1.000	0.00	0.000	0.00	0.000	0.000	1.00	0.00	1.00	1.000
pedal_edema: yes	0.00	0.00	0.00	1.000	0.00	1.000	0.00	1.000	0.000	0.00	0.00	1.00	1.000
anemia: yes	0.00	0.00	1.00	1.000	0.00	0.000	0.00	0.000	1.000	1.00	1.00	0.00	0.000

In [21]:
```python
# define imputer
from sklearn.impute import KNNImputer

imputer = KNNImputer(n_neighbors=5, weights='uniform', metric='nan_euclidean')

impute_columns=list(set(onehotdata.columns)-set(["classification"]))
print(impute_columns)
```
```
['coronary_artery_disease: yes', 'pedal_edema: yes', 'albumin', 'blood_pressure', 'hemoglobin', 'sugar', 'whi
te_blood_cell_count', 'bacteria: present', 'serum_creatinine', 'potassium', 'hypertension: yes', 'red_blood_c
ells: normal', 'specific_gravity', 'packed_cell_volume', 'red_blood_cell_count', 'sodium', 'diabetes_mellitu
s: yes', 'appetite: poor', 'pus_cell_clumps: present', 'blood_urea', 'blood_glucose_random', 'pus_cell: norma
l', 'age', 'anemia: yes']
```

In [22]:
```python
imputer.fit(onehotdata[impute_columns])
```
Out[22]:
```
KNNImputer()
```

In [23]:
```python
X_trans=pd.DataFrame(imputer.transform(onehotdata[impute_columns]), columns=impute_columns)
```

```
In [24]: X_trans.head(13).T
```

Out[24]:

	0	1	2	3	4	5	6	7	8	9	10	11	1
coronary_artery_disease: yes	0.00	0.00	0.00	0.000	0.00	0.000	0.00	0.000	0.000	0.00	0.00	0.00	1.00
pedal_edema: yes	0.00	0.00	0.00	1.000	0.00	1.000	0.00	1.000	0.000	0.00	0.00	1.00	1.00
albumin	1.00	4.00	2.00	4.000	2.00	3.000	0.00	2.000	3.000	2.00	2.00	3.00	3.00
blood_pressure	80.00	50.00	80.00	70.000	80.00	90.000	70.00	74.000	100.000	90.00	60.00	70.00	70.00
hemoglobin	15.40	11.30	9.60	11.200	11.60	12.200	12.40	12.400	10.800	9.50	9.40	10.80	9.70
sugar	0.00	0.00	3.00	0.000	0.00	0.000	0.00	4.000	0.000	0.00	4.00	0.00	1.00
white_blood_cell_count	7800.00	6000.00	7500.00	6700.000	7300.00	7800.000	10280.00	6900.000	9600.000	12100.00	9260.00	4500.00	12200.00
bacteria: present	0.00	0.00	0.00	0.000	0.00	0.000	0.00	0.000	0.000	0.00	0.00	0.00	0.00
serum_creatinine	1.20	0.80	1.80	3.800	1.40	1.100	24.00	1.100	1.900	7.20	4.00	2.70	2.10
potassium	4.20	3.92	4.20	2.500	3.98	3.200	4.00	4.200	4.960	3.70	4.56	4.20	5.80
hypertension: yes	1.00	0.00	0.00	1.000	0.00	1.000	0.00	0.000	1.000	1.00	1.00	1.00	1.00
red_blood_cells: normal	0.00	0.00	1.00	1.000	1.00	0.000	0.00	1.000	1.000	0.00	0.00	0.00	0.00
specific_gravity	1.02	1.02	1.01	1.005	1.01	1.015	1.01	1.015	1.015	1.02	1.01	1.01	1.01
packed_cell_volume	44.00	38.00	31.00	32.000	35.00	39.000	36.00	44.000	33.000	29.00	28.00	32.00	28.00
red_blood_cell_count	5.20	4.96	3.80	3.900	4.60	4.400	4.64	5.000	4.000	3.70	4.92	3.80	3.40
sodium	137.60	136.80	133.80	111.000	138.40	142.000	104.00	133.800	134.000	114.00	139.00	131.00	138.00
diabetes_mellitus: yes	1.00	0.00	1.00	0.000	0.00	1.000	0.00	1.000	1.000	1.00	1.00	1.00	1.00
appetite: poor	0.00	0.00	1.00	1.000	0.00	0.000	0.00	0.000	0.000	1.00	0.00	1.00	1.00
pus_cell_clumps: present	0.00	0.00	0.00	1.000	0.00	0.000	0.00	0.000	1.000	1.00	1.00	1.00	1.00
blood_urea	36.00	18.00	53.00	56.000	26.00	25.000	54.00	31.000	60.000	107.00	55.00	60.00	72.00
blood_glucose_random	121.00	113.00	423.00	117.000	106.00	74.000	100.00	410.000	138.000	70.00	490.00	380.00	208.00
pus_cell: normal	1.00	1.00	1.00	0.000	1.00	0.000	1.00	0.000	0.000	0.00	0.00	0.00	1.00
age	48.00	7.00	62.00	48.000	51.00	60.000	68.00	24.000	52.000	53.00	50.00	63.00	68.00
anemia: yes	0.00	0.00	1.00	1.000	0.00	0.000	0.00	0.000	1.000	1.00	1.00	0.00	0.00

```
In [25]: X_trans # final datset
```

Out[25]:

	coronary_artery_disease: yes	pedal_edema: yes	albumin	blood_pressure	hemoglobin	sugar	white_blood_cell_count	bacteria: present	serum_creatinine	potass
0	0.0	0.0	1.0	80.0	15.4	0.0	7800.0	0.0	1.2	
1	0.0	0.0	4.0	50.0	11.3	0.0	6000.0	0.0	0.8	
2	0.0	0.0	2.0	80.0	9.6	3.0	7500.0	0.0	1.8	
3	0.0	1.0	4.0	70.0	11.2	0.0	6700.0	0.0	3.8	
4	0.0	0.0	2.0	80.0	11.6	0.0	7300.0	0.0	1.4	
...	...	...	...	...	...	...	...	...	...	
395	0.0	0.0	0.0	80.0	15.7	0.0	6700.0	0.0	0.5	
396	0.0	0.0	0.0	70.0	16.5	0.0	7800.0	0.0	1.2	
397	0.0	0.0	0.0	80.0	15.8	0.0	6600.0	0.0	0.6	
398	0.0	0.0	0.0	60.0	14.2	0.0	7200.0	0.0	1.0	
399	0.0	0.0	0.0	80.0	15.8	0.0	6800.0	0.0	1.1	

400 rows × 24 columns

Modelling

In [26]:
```
X=X_trans
y=ckd_df["classification"]



X_prod=X_trans
print(X.shape)
print(y.shape)
print(X_prod.shape)
```

```
(400, 24)
(400,)
(400, 24)
```

Predictive Models with hyperparameter tuning Section

In [27]:
```
from sklearn.metrics import classification_report
from sklearn.metrics import accuracy_score
from sklearn.metrics import confusion_matrix

from sklearn.model_selection import GridSearchCV
```

In [28]:
```
def display_confusion_matrix(y_test,y_pred):

    cm = confusion_matrix(y_test, y_pred_lr)
    group_names = ["True Neg","False Pos","False Neg","True Pos"]
    group_counts = ["{0:0.0f}".format(value) for value in cm.flatten()]
    group_percentages = ["{0:.2%}".format(value) for value in cm.flatten()/np.sum(cm)]

    labels = [f"{v1}\n{v2}\n{v3}" for v1, v2, v3 in zip(group_names,group_counts,group_percentages)]
    labels = np.asarray(labels).reshape(2,2)

    sns.heatmap(cm, annot=labels, fmt="", cmap="Blues")
    print(classification_report(y_test, y_pred))
```

In [29]:
```
def plot_roc_curve(fpr, tpr):
    plt.plot(fpr, tpr, label='ROC')
    plt.plot([0, 1], linestyle='--')
    plt.xlabel('False Positive Rate')
    plt.ylabel('True Positive Rate')
    plt.legend()
    plt.show()
```

In [30]:
```
##Split train and test
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.20, random_state = 4658)

print(X_train.shape)
print(X_test.shape)
print(y_train.shape)
print(y_test.shape)
```

```
(320, 24)
(80, 24)
(320,)
(80,)
```

StandardScaler data with PCA implementation

#performing preprocessing part from sklearn.preprocessing import StandardScaler sc = StandardScaler()

X_train = sc.fit_transform(X_train) X_test = sc.transform(X_test)

#Applying PCA function on training and testing set of X component from sklearn.decomposition import PCA

pca = PCA(n_components = 2)

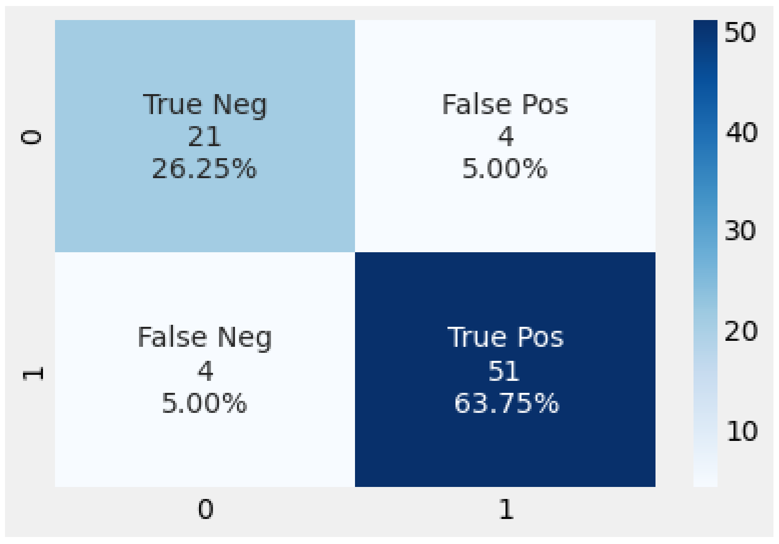
X_train = pca.fit_transform(X_train) X_test = pca.transform(X_test)

explained_variance = pca.explained_variance_ratio_ explained_variance

Logistic Regression Hyper parameter tuning

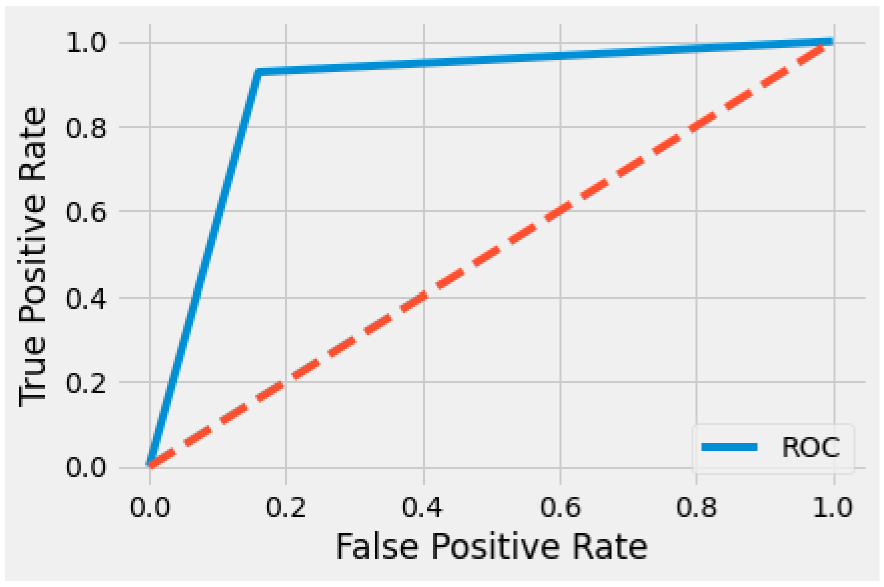
In [31]:
```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import roc_curve
from sklearn.metrics import roc_auc_score

c_space = np.logspace(-5, 8, 15)
param_grid = {'C': c_space}

start_lr = time.time()
lr = GridSearchCV(LogisticRegression(),
                  param_grid,
                  cv = 5)
lr.fit(X_train, y_train)
end_lr = time.time()
final_lr = end_lr - start_lr
final_lr = round(final_lr,3)
final_lr

# Print the tuned parameters and score
print("Tuned Logistic Regression Parameters: {}".format(lr.best_params_))
print("Best score is {}".format(lr.best_score_))
print("Best estimator is {} \n\n".format(lr.best_estimator_))

y_pred_lr = lr.predict(X_test)
display_confusion_matrix(y_test, y_pred_lr)
accuracy_lr=lr.best_score_
print("\nAccuracy of Logistic Regression is :", accuracy_lr)
print("Computation time {} - Sec".format(final_lr))
```

```
Tuned Logistic Regression Parameters: {'C': 2275.845926074791}
Best score is 0.9
Best estimator is LogisticRegression(C=2275.845926074791)


              precision    recall  f1-score   support

           0       0.84      0.84      0.84        25
           1       0.93      0.93      0.93        55

    accuracy                           0.90        80
   macro avg       0.88      0.88      0.88        80
weighted avg       0.90      0.90      0.90        80


Accuracy of Logistic Regression is : 0.9
Computation time 3.003 - Sec
```



In [32]:
```
auc = roc_auc_score(y_test, y_pred_lr)
print('AUC: %.2f' % auc)

fpr, tpr, thresholds = roc_curve(y_test, y_pred_lr)
plot_roc_curve(fpr, tpr)
```

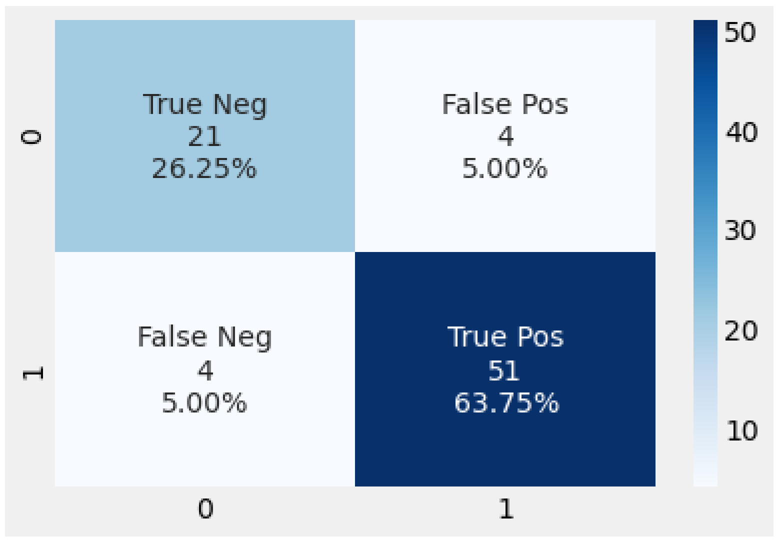
```
AUC: 0.88
```



Decision Tree Hyper parameter tuning

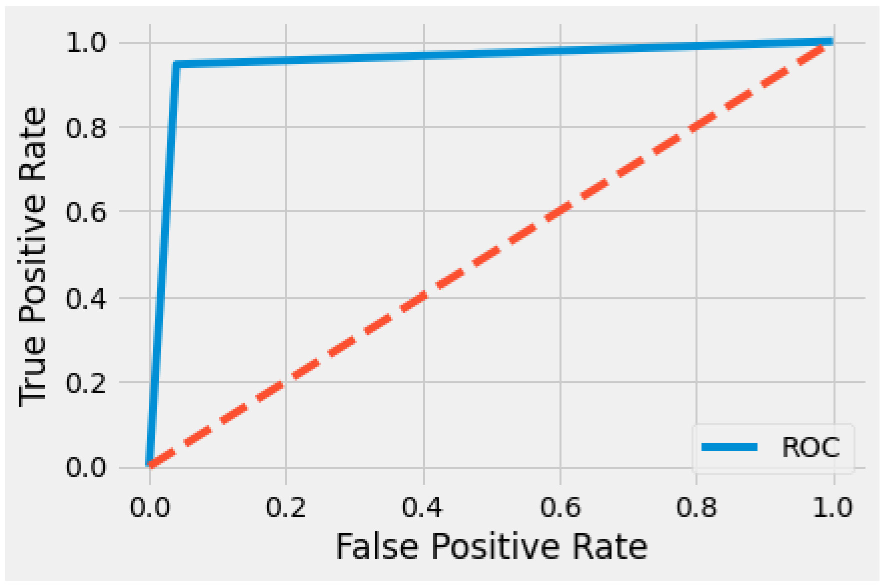
```
In [33]: from sklearn.tree import DecisionTreeClassifier
         from sklearn.model_selection import RandomizedSearchCV

         hyperparam_combs = {
             'max_depth': [4, 6, 8, 10, 12],
             'criterion': ['gini', 'entropy'],
             'min_samples_split': [2, 10, 20, 30, 40],
             'max_features': [0.2, 0.4, 0.6, 0.8, 1],
             'max_leaf_nodes': [8, 16, 32, 64, 128],
             'class_weight': [{0: 1, 1: 1}, {0: 1, 1: 2}, {0: 1, 1: 3}, {0: 1, 1: 4}, {0: 1, 1: 5}]
         }

         start_dt = time.time()
         clf = RandomizedSearchCV(DecisionTreeClassifier(),
                                  hyperparam_combs,
                                  scoring='f1',
                                  random_state=1,
                                  n_iter=20)

         dt_model = clf.fit(X_train, y_train)
         end_dt = time.time()
         final_dt = end_dt - start_dt
         final_dt = round(final_dt,3)
         final_dt

         # Print the tuned parameters and score
         print("Tuned Decision Tree Parameters: {}".format(dt_model.best_params_))
         print("Best score is {}".format(dt_model.best_score_))
         print("Best estimator is {}".format(dt_model.best_estimator_))

         y_pred_dt = dt_model.predict(X_test)
         display_confusion_matrix(y_test, y_pred_dt)
         accuracy_dt=dt_model.best_score_
         print("Accuracy of Decision Tree is :", accuracy_dt)
         print("Computation time {} - Sec".format(final_dt))
```

```
Tuned Decision Tree Parameters: {'min_samples_split': 2, 'max_leaf_nodes': 128, 'max_features': 0.2, 'max_dep
th': 10, 'criterion': 'gini', 'class_weight': {0: 1, 1: 3}}
Best score is 0.9687584678257564
Best estimator is DecisionTreeClassifier(class_weight={0: 1, 1: 3}, max_depth=10,
                       max_features=0.2, max_leaf_nodes=128)
              precision    recall  f1-score   support

           0       0.89      0.96      0.92        25
           1       0.98      0.95      0.96        55

    accuracy                           0.95        80
   macro avg       0.94      0.95      0.94        80
weighted avg       0.95      0.95      0.95        80

Accuracy of Decision Tree is : 0.9687584678257564
Computation time 0.609 - Sec
```



```
In [34]: auc = roc_auc_score(y_test, y_pred_dt)
         print('AUC: %.2f' % auc)

         fpr, tpr, thresholds = roc_curve(y_test, y_pred_dt)
         plot_roc_curve(fpr, tpr)
```

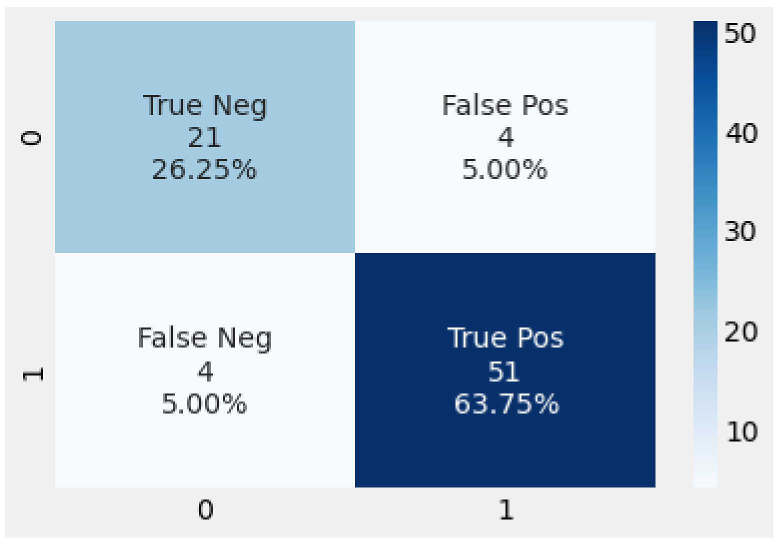
```
AUC: 0.95
```



Random Forest Hyper parameter tuning

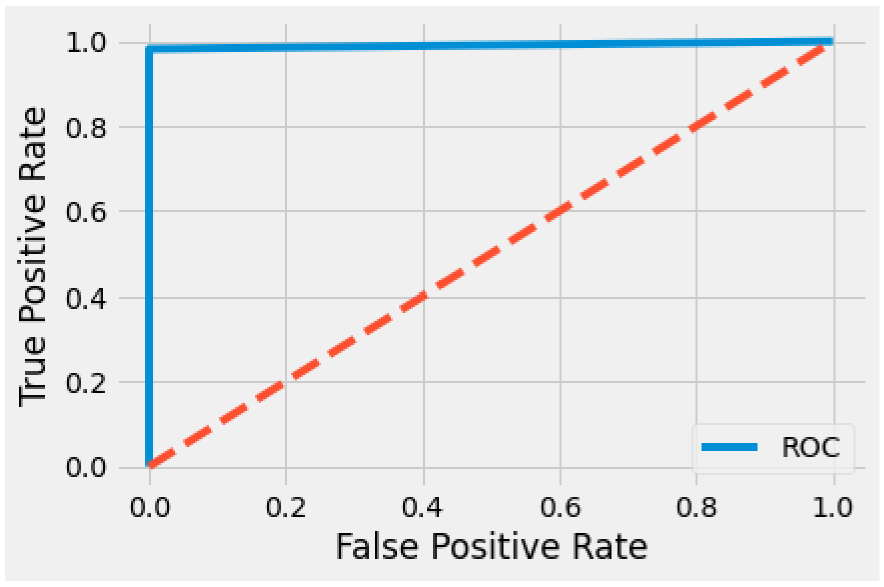
```
In [35]: from sklearn.ensemble import RandomForestClassifier

         param_grid = {"n_estimators": np.arange(2, 300, 2),
                       "max_depth": np.arange(1, 28, 1),
                       "min_samples_split": np.arange(1,150,1),
                       "min_samples_leaf": np.arange(1,60,1),
                       "max_leaf_nodes": np.arange(2,60,1),
                       "min_weight_fraction_leaf": np.arange(0.1,0.4, 0.1)}

         start_rf = time.time()
         rf = RandomizedSearchCV(RandomForestClassifier(),
                                 param_grid,
                                 scoring='f1',
                                 random_state=4658,
                                 n_iter=20)

         rf_model = rf.fit(X_train, y_train)
         end_rf = time.time()
         final_rf = end_rf - start_rf
         final_rf = round(final_rf,3)
         final_rf

         # Print the tuned parameters and score
         print("Tuned Random Tree Parameters: {}".format(rf_model.best_params_))
         print("Best score is {}".format(rf_model.best_score_))
         print("Best estimator is {}".format(rf_model.best_estimator_))

         y_pred_rf = rf_model.predict(X_test)
         display_confusion_matrix(y_test, y_pred_rf)
         accuracy_rf=rf_model.best_score_
         print("Accuracy of Random Forests model is :", accuracy_rf)
         print("Computation time {} - Sec".format(final_rf))
```

```
Tuned Random Tree Parameters: {'n_estimators': 240, 'min_weight_fraction_leaf': 0.1, 'min_samples_split': 52,
'min_samples_leaf': 38, 'max_leaf_nodes': 39, 'max_depth': 26}
Best score is 0.9740925740925741
Best estimator is RandomForestClassifier(max_depth=26, max_leaf_nodes=39, min_samples_leaf=38,
                       min_samples_split=52, min_weight_fraction_leaf=0.1,
                       n_estimators=240)
              precision    recall  f1-score   support

           0       0.96      1.00      0.98        25
           1       1.00      0.98      0.99        55

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

Accuracy of Random Forests model is : 0.9740925740925741
Computation time 22.088 - Sec
```



In [36]:
```
auc = roc_auc_score(y_test, y_pred_rf)
print('AUC: %.2f' % auc)

fpr, tpr, thresholds = roc_curve(y_test, y_pred_rf)
plot_roc_curve(fpr, tpr)
```

```
AUC: 0.99
```



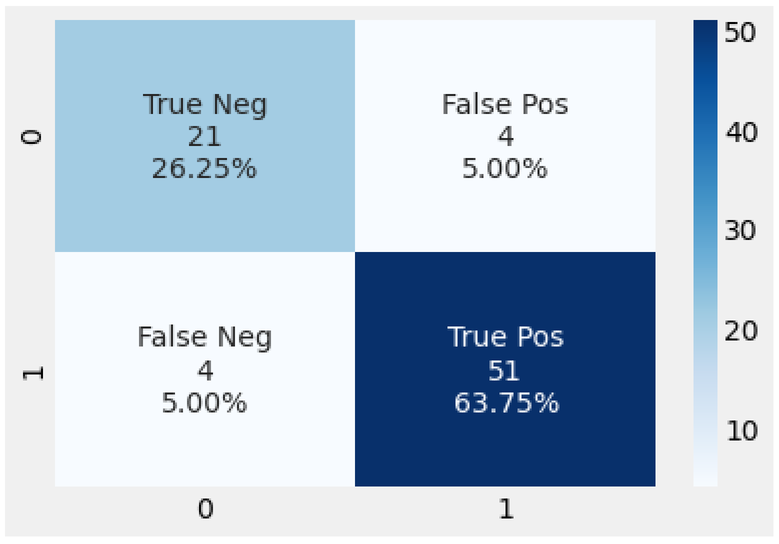
Support Vector Machine Hyper parameter tuning

In [37]:
```
from sklearn.svm import SVC

# defining parameter range
param_grid = {'C': [0.1, 1, 10, 100, 1000],
              'gamma': [1, 0.1, 0.01, 0.001, 0.0001]}

start_svm = time.time()
svm = GridSearchCV(SVC(), param_grid, refit = True, verbose = 3)
# fitting the model for grid search
svm.fit(X_train, y_train)

end_svm = time.time()
final_svm = end_svm - start_svm
final_svm = round(final_svm,3)
final_svm

# Print the tuned parameters and score
print("Tuned Support Vector Machine Parameters: {}".format(svm.best_params_))
print("Best score is {}".format(svm.best_score_))
print("Best estimator is {}".format(svm.best_estimator_))
```

```
[CV] ....................... C=0.1, gamma=1, score=0.609, total=   0.0s
[CV] C=0.1, gamma=1 ..................................................
[CV] ....................... C=0.1, gamma=1, score=0.609, total=   0.0s
[CV] C=0.1, gamma=1 ..................................................
[CV] ....................... C=0.1, gamma=1, score=0.609, total=   0.0s
[CV] C=0.1, gamma=0.1 ................................................
[CV] ..................... C=0.1, gamma=0.1, score=0.609, total=   0.0s
[CV] C=0.1, gamma=0.1 ................................................
[CV] ..................... C=0.1, gamma=0.1, score=0.609, total=   0.0s
[CV] C=0.1, gamma=0.1 ................................................
[CV] ..................... C=0.1, gamma=0.1, score=0.609, total=   0.0s
[CV] C=0.1, gamma=0.1 ................................................
[CV] ..................... C=0.1, gamma=0.1, score=0.609, total=   0.0s
[CV] C=0.1, gamma=0.1 ................................................
[CV] ..................... C=0.1, gamma=0.1, score=0.609, total=   0.0s
[CV] C=0.1, gamma=0.01 ...............................................
[CV] .................... C=0.1, gamma=0.01, score=0.609, total=   0.0s
[CV] C=0.1, gamma=0.01 ...............................................
[CV] .................... C=0.1, gamma=0.01, score=0.609, total=   0.0s
[CV] C=0.1, gamma=0.01 ...............................................
```

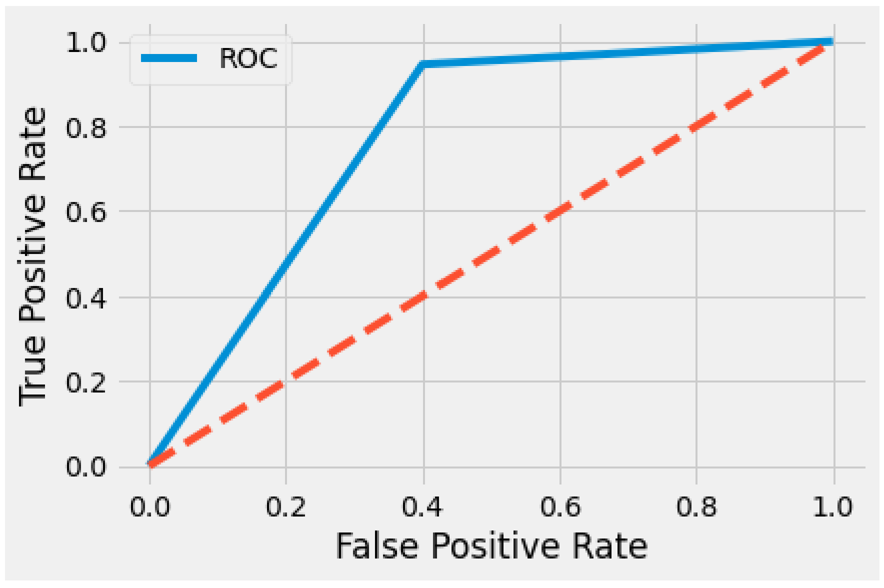
```
In [38]: y_pred_svm = svm.predict(X_test)
         display_confusion_matrix(y_test, y_pred_svm)
         accuracy_svm=svm.best_score_
         print("Accuracy of Support Vector Machine is :", accuracy_svm)
         print("Computation time {} - Sec".format(final_svm))
```

```
              precision    recall  f1-score   support

           0       0.83      0.60      0.70        25
           1       0.84      0.95      0.89        55

    accuracy                           0.84        80
   macro avg       0.84      0.77      0.79        80
weighted avg       0.84      0.84      0.83        80

Accuracy of Support Vector Machine is : 0.75625
Computation time 1.222 - Sec
```



```
In [39]: auc = roc_auc_score(y_test, y_pred_svm)
         print('AUC: %.2f' % auc)

         fpr, tpr, thresholds = roc_curve(y_test, y_pred_svm)
         plot_roc_curve(fpr, tpr)
```

```
AUC: 0.77
```



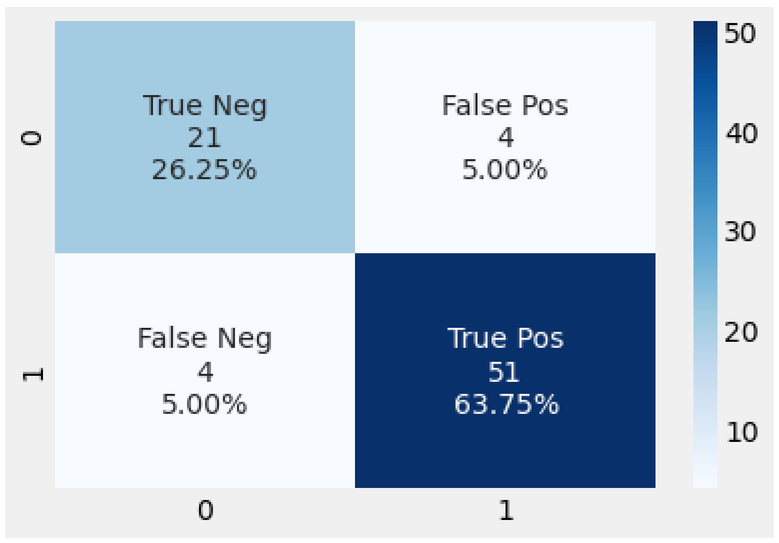
Artificial neural network

In [40]:
```
from sklearn.neural_network import MLPClassifier

# defining parameter range
param_grid = {
              'max_iter': [1000],
            }

start_mlp = time.time()
mlp = GridSearchCV(MLPClassifier(), param_grid, refit = True, verbose = 3)
# fitting the model for grid search
mlp.fit(X_train, y_train.values.ravel())

end_mlp = time.time()
final_mlp = end_mlp - start_mlp
final_mlp = round(final_mlp,3)
final_mlp

# Print the tuned parameters and score
print("Tuned Artificial neural network Parameters: {}".format(mlp.best_params_))
print("Best score is {}".format(mlp.best_score_))
print("Best estimator is {}".format(mlp.best_estimator_))
```

```
Fitting 5 folds for each of 1 candidates, totalling 5 fits
[CV] max_iter=1000 ..................................................
[CV] ....................... max_iter=1000, score=0.703, total=   0.2s
[CV] max_iter=1000 ..................................................

[Parallel(n_jobs=1)]: Using backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.2s remaining:    0.0s

[CV] ....................... max_iter=1000, score=0.859, total=   0.2s
[CV] max_iter=1000 ..................................................
[CV] ....................... max_iter=1000, score=0.875, total=   0.2s
[CV] max_iter=1000 ..................................................

[Parallel(n_jobs=1)]: Done   2 out of   2 | elapsed:    0.4s remaining:    0.0s

[CV] ....................... max_iter=1000, score=0.734, total=   0.2s
[CV] max_iter=1000 ..................................................
[CV] ....................... max_iter=1000, score=0.781, total=   0.4s

[Parallel(n_jobs=1)]: Done   5 out of   5 | elapsed:    1.2s finished

Tuned Artificial neural network Parameters: {'max_iter': 1000}
Best score is 0.790625
Best estimator is MLPClassifier(max_iter=1000)
```

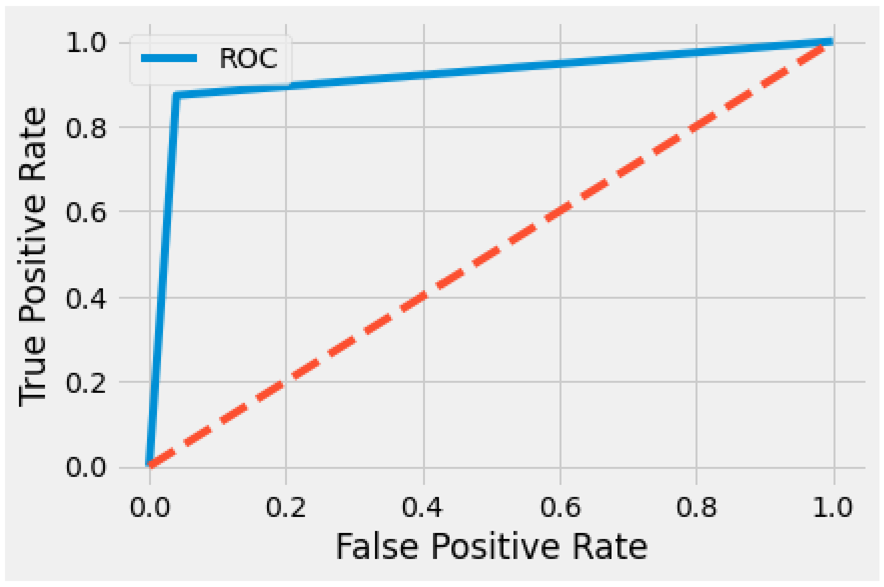
In [41]:
```
y_pred_mlp = mlp.predict(X_test)
display_confusion_matrix(y_test, y_pred_mlp)
accuracy_mlp=mlp.best_score_
print("Accuracy of Artificial neural network  is :", accuracy_mlp)
print("Computation time {} - Sec".format(final_mlp))
```

```
              precision    recall  f1-score   support

           0       0.77      0.96      0.86        25
           1       0.98      0.87      0.92        55

    accuracy                           0.90        80
   macro avg       0.88      0.92      0.89        80
weighted avg       0.92      0.90      0.90        80

Accuracy of Artificial neural network  is : 0.790625
Computation time 1.735 - Sec
```



```
In [42]: auc = roc_auc_score(y_test, y_pred_mlp)
         print('AUC: %.2f' % auc)

         fpr, tpr, thresholds = roc_curve(y_test, y_pred_mlp)
         plot_roc_curve(fpr, tpr)
```

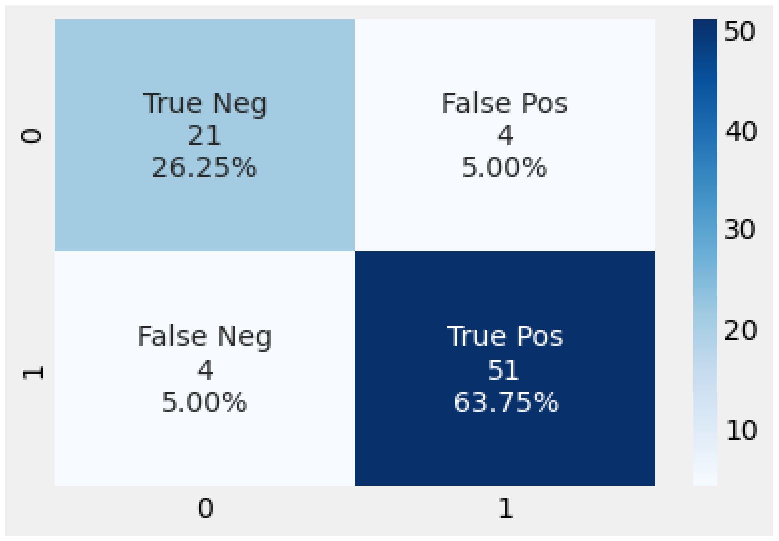
```
AUC: 0.92
```



k Nearest Neighbors

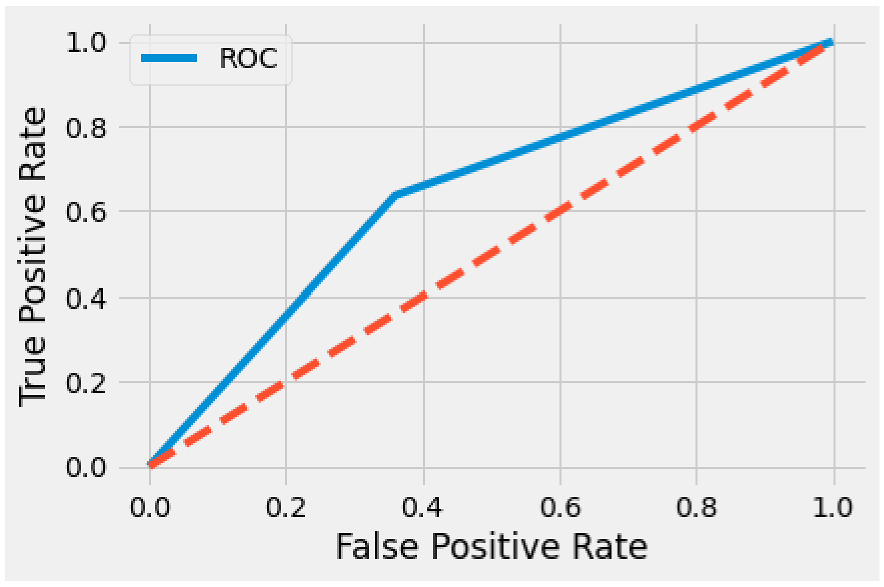
In [43]:
```
from sklearn.neighbors import KNeighborsClassifier

model = KNeighborsClassifier(n_jobs=-1)
params = {'n_neighbors':[5,6,7,8,9,10],
          'leaf_size':[1,2,3,5],
          'weights':['uniform', 'distance'],
          'algorithm':['auto', 'ball_tree','kd_tree','brute'],
          'n_jobs':[-1]}

start_knn = time.time()
model1 = GridSearchCV(model, param_grid=params, n_jobs=1)
model1.fit(X_train, y_train)
end_knn = time.time()
final_knn = end_knn - start_knn
final_knn = round(final_knn,3)
final_knn

# Print the tuned parameters and score
print("Tuned Logistic Regression Parameters: {}".format(model1.best_params_))
print("Best score is {}".format(model1.best_score_))
print("Best estimator is {} \n\n".format(model1.best_estimator_))

y_pred_knn = model1.predict(X_test)
display_confusion_matrix(y_test, y_pred_knn)
accuracy_knn=accuracy_score(y_test, y_pred_knn)
print("\nAccuracy of k Nearest Neighbors is \t:", accuracy_knn)
print("Best Accuracy of k Nearest Neighbors is : {}".format(model1.best_score_))
print("Computation time {} - Sec".format(final_knn))
```

```
Tuned Logistic Regression Parameters: {'algorithm': 'auto', 'leaf_size': 1, 'n_jobs': -1, 'n_neighbors': 7,
'weights': 'distance'}
Best score is 0.68125
Best estimator is KNeighborsClassifier(leaf_size=1, n_jobs=-1, n_neighbors=7, weights='distance')


              precision    recall  f1-score   support

           0       0.44      0.64      0.52        25
           1       0.80      0.64      0.71        55

    accuracy                           0.64        80
   macro avg       0.62      0.64      0.62        80
weighted avg       0.69      0.64      0.65        80


Accuracy of k Nearest Neighbors is      : 0.6375
Best Accuracy of k Nearest Neighbors is : 0.68125
Computation time 16.407 - Sec
```



```
In [44]: auc = roc_auc_score(y_test, y_pred_knn)
         print('AUC: %.2f' % auc)

         fpr, tpr, thresholds = roc_curve(y_test, y_pred_knn)
         plot_roc_curve(fpr, tpr)
```

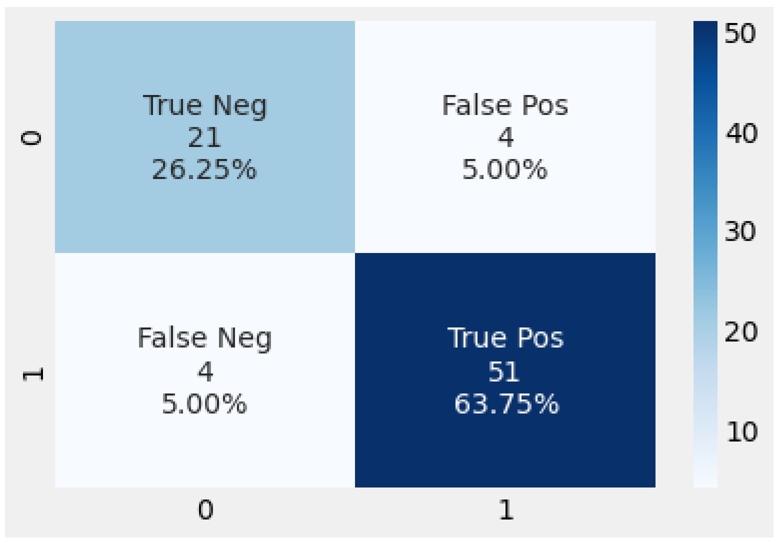
```
AUC: 0.64
```



Naive Bayes (NB) Classifier

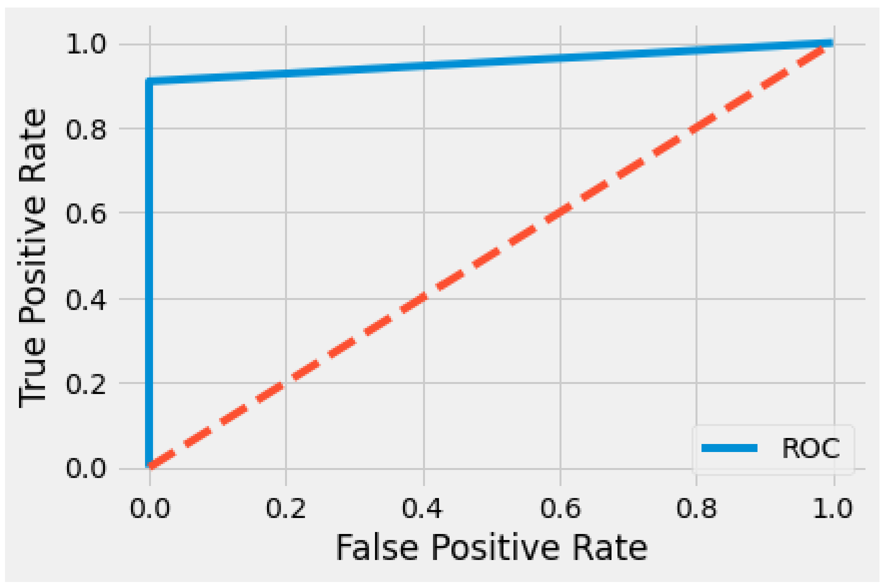
```
In [45]: from sklearn.naive_bayes import GaussianNB

         start_nb = time.time()
         gnb = GaussianNB()
         gnb.fit(X_train, y_train)
         nb_model = gnb.fit(X_train, y_train)
         end_nb = time.time()
         final_nb = end_nb - start_nb
         final_nb = round(final_nb,3)
         final_nb

         y_pred_nb = gnb.predict(X_test)

         display_confusion_matrix(y_test, y_pred_nb)
         accuracy_nb=accuracy_score(y_test, y_pred_nb)
         print("Gaussian Naive Bayes model accuracy :", accuracy_nb)
         print("Computation time {} - Sec".format(final_nb))
```

```
              precision    recall  f1-score   support

           0       0.83      1.00      0.91        25
           1       1.00      0.91      0.95        55

    accuracy                           0.94        80
   macro avg       0.92      0.95      0.93        80
weighted avg       0.95      0.94      0.94        80

Gaussian Naive Bayes model accuracy : 0.9375
Computation time 0.005 - Sec
```



In [46]:
```
auc = roc_auc_score(y_test, y_pred_nb)
print('AUC: %.2f' % auc)

fpr, tpr, thresholds = roc_curve(y_test, y_pred_nb)
plot_roc_curve(fpr, tpr)
```

```
AUC: 0.95
```

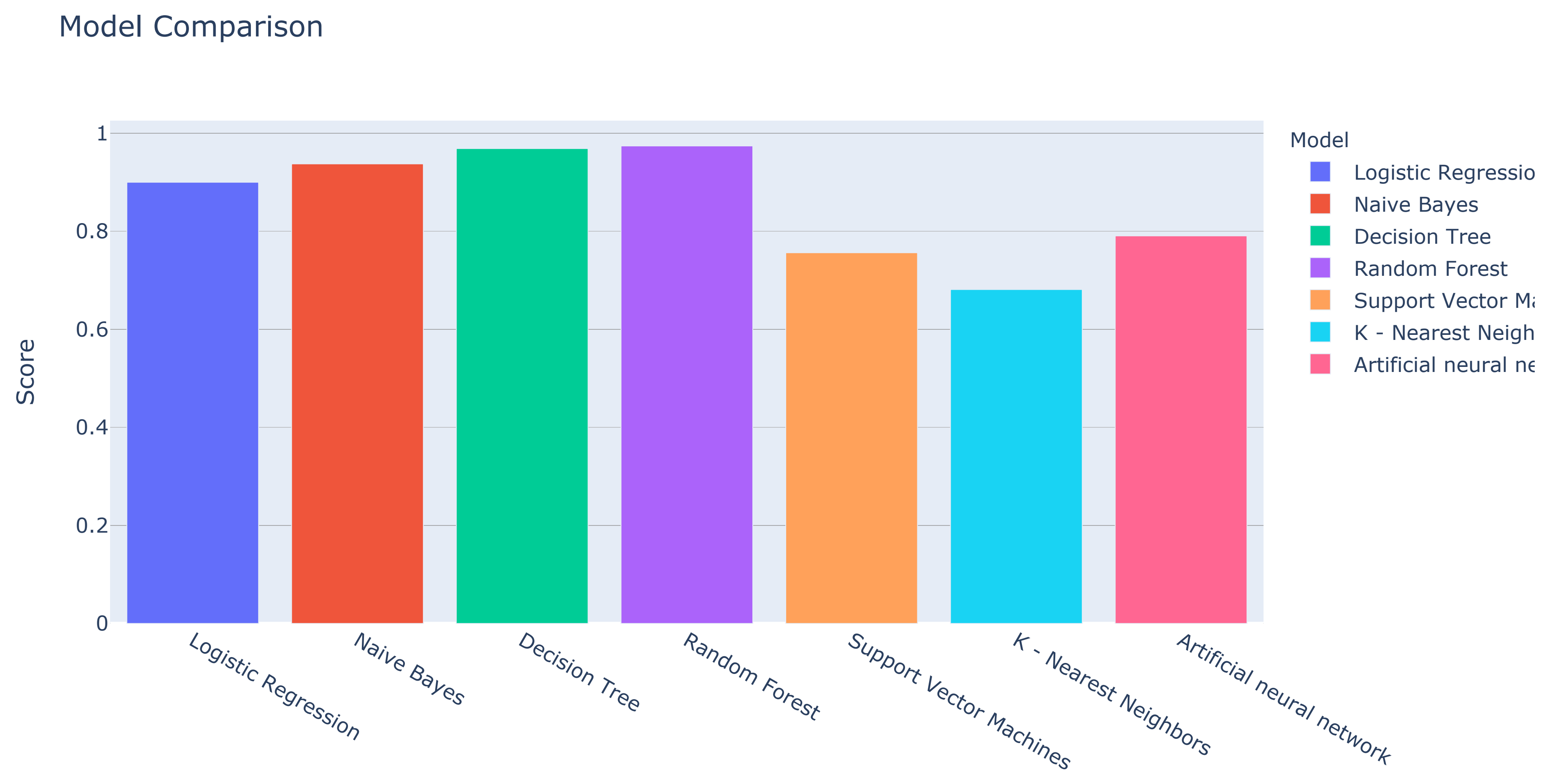


In [47]:
```
models = pd.DataFrame({
    'Model': ['Logistic Regression', 'Naive Bayes', 'Decision Tree', 'Random Forest', 'Support Vector Machines',
              'K - Nearest Neighbors', 'Artificial neural network'],
    'Score': [accuracy_lr, accuracy_nb , accuracy_dt, accuracy_rf, svm.best_score_, model1.best_score_, mlp.best
models.sort_values(by='Score', ascending=False)
```

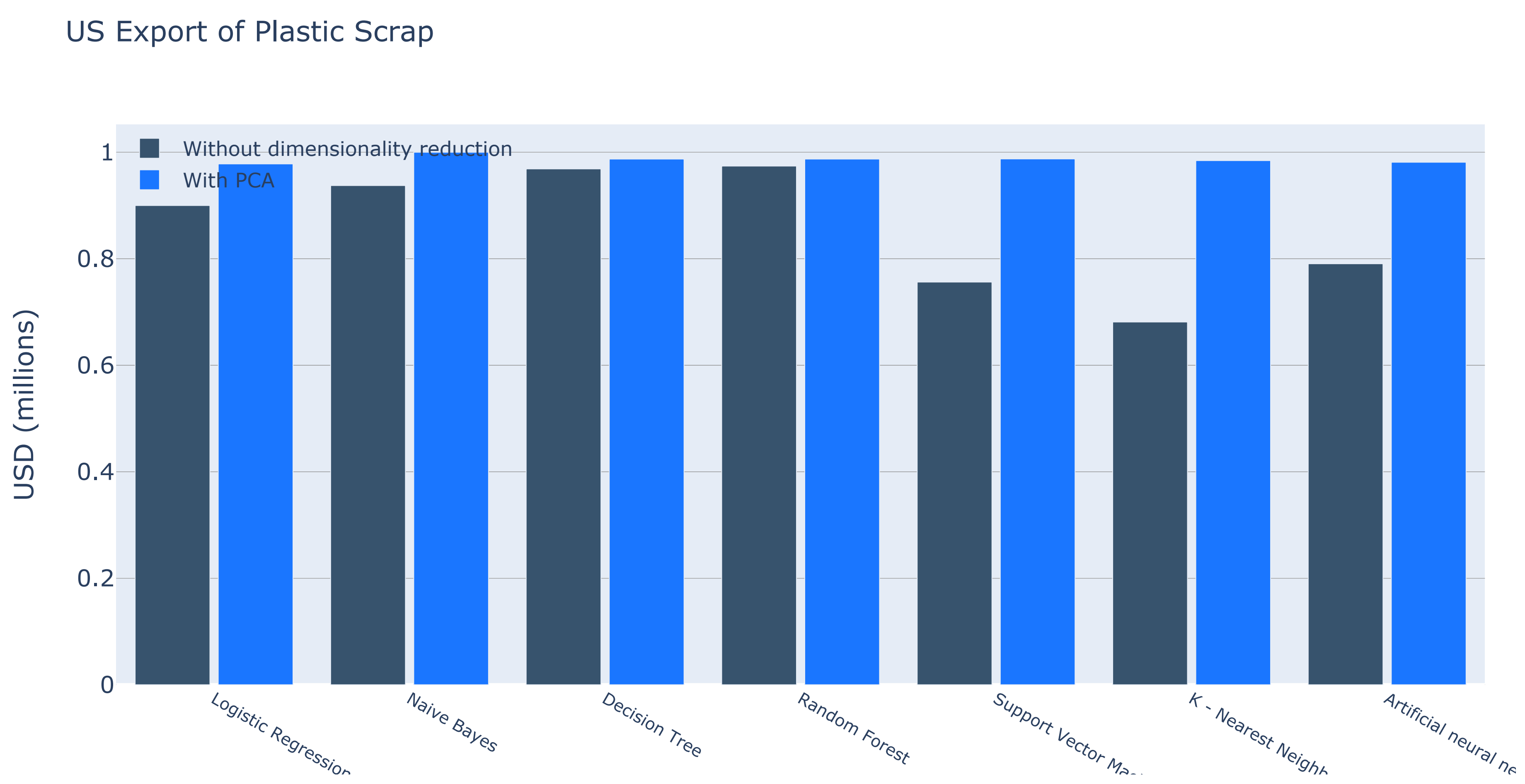
Out[47]:

	Model	Score
3	Random Forest	0.974093
2	Decision Tree	0.968758
1	Naive Bayes	0.937500
0	Logistic Regression	0.900000
6	Artificial neural network	0.790625
4	Support Vector Machines	0.756250
5	K - Nearest Neighbors	0.681250

In [48]:
```python
import plotly.express as px
import plotly.graph_objects as go

fig = px.bar(models, x='Model', y='Score', color="Model", title="Model Comparison")
fig.show()
```



```
In [49]: model = models["Model"]

fig = go.Figure()
fig.add_trace(go.Bar(x=model,
                y=models["Score"],
                name='Without dimensionality reduction',
                marker_color='rgb(55, 83, 109)'
                ))
fig.add_trace(go.Bar(x=model,
                y=[0.978125,1.000000, 0.987277, 0.987277, 0.987500, 0.984375, 0.981250],
                name='With PCA',
                marker_color='rgb(26, 118, 255)'
                ))

fig.update_layout(
    title='US Export of Plastic Scrap',
    xaxis_tickfont_size=10,
    yaxis=dict(
        title='USD (millions)',
        titlefont_size=16,
        tickfont_size=14,
    ),
    legend=dict(
        x=0,
        y=1.0,
        bgcolor='rgba(255, 255, 255, 0)',
        bordercolor='rgba(255, 255, 255, 0)'
    ),
    barmode='group',
    bargap=0.15, # gap between bars of adjacent location coordinates.
    bargroupgap=0.1 # gap between bars of the same location coordinate.
)
fig.show()
```



Insights,

24 data recording information of 400 people such as age, blood pressure, density, diabetes were used as attributes. Clinical records were examined to determine whether chronic kidney disease was present or not, and provided a high accuracy rate with machine learning methods.

Chronic kidney disease is a disease that hinders the normal functions of the kidney and damages the kidneys. It is one of the common diseases in the world and the prediction of the disease is one of the basic issues in medical diagnosis. Chronic kidney disease is one of the leading causes of death worldwide. Early detection of this disease is very important in terms of health and treatment costs. Many machine learning algorithms have been used in the literature to predict the disease.

Here, seven different classifiers were utilized in determining the targeted chronic kidney disease and the best performing classifier was tried to be found. These algorithms were compared on the basis of accuracy, sensitivity, sensitivity, recall and f1 score. When the results were evaluated with the data used in this study, it was seen that the **Random Forest and SVM** method (with an accuracy of 99.16%) performed better than other classification algorithms.

Here by concluding the **Naive Bayes** is normally giving good accuracy score with taken dataset and notably **Naive Bayes** is overfitting after implementing dimensionality reduction with PCA (2 components)