Ai - Data Preprocessing & Analysis

FOR CHRONIC KIDNEY DISEASE DATASET

DR SUBRAMANI SURESH

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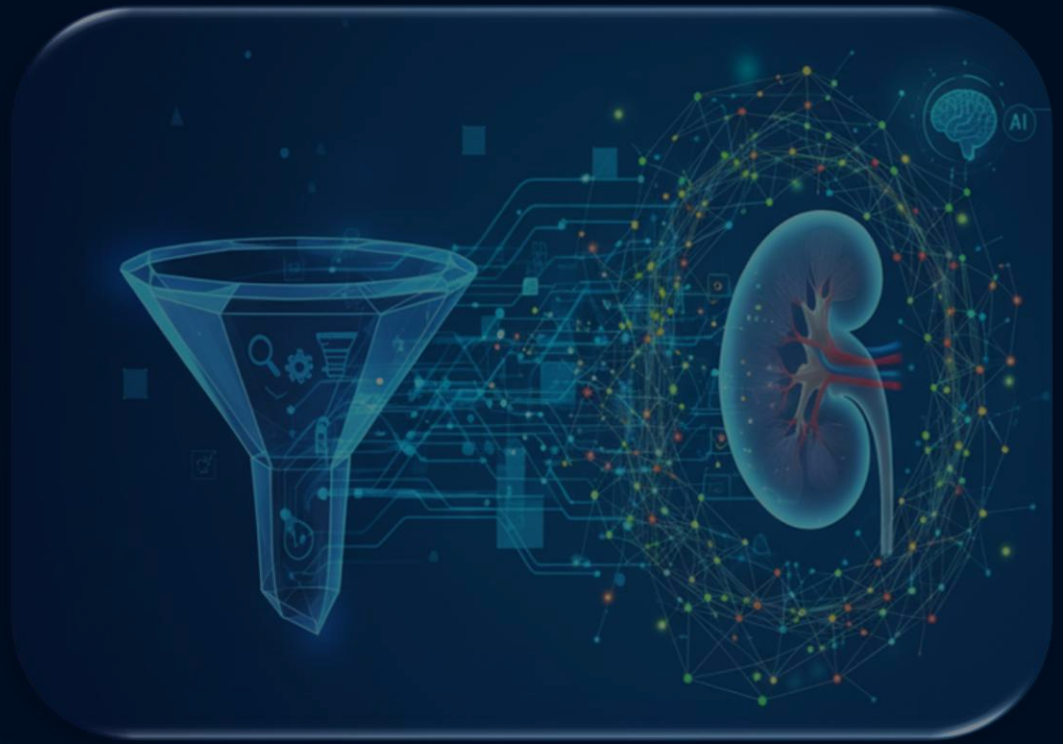
Overview

- This presentation covers loading Chronic Kidney Disease Dataset (CKD) dataset
- Cleaning
- Imputing
- Analyzing
- Building predictive models
- Python code



Dataset Overview

- Loaded from "kidney_disease.csv" using Pandas.
- 400 rows x 26 columns (e.g., id, age, bp, sg, classification).
- Initial data snippet: Shows patient IDs, features like bp, sg, al, and classifications (ckd/notckd).

	id	age	bp	sg	al	su	rbc	pc	pcc	ba
0	0	48.0	80.0	1.020	1.0	0.0	NaN	Normal	notpresent	notpresent
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notPresent	notpresent
2	2	62.0	80.0	1.010	2.0	3.0	Normal	normal	notpresent	notpresent
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent

Column Renaming & Types

- Renamed for clarity: e.g., 'bp' → 'blood_pressure', 'classification' → 'ckd_class' , rbc → 'red_blood_cells'.
- Data types: int64 (patient_id), float64 (age, bp), object (rbc, pc).
- Descriptive stats: Mean age 51.48, bp 76.47; highlights central tendency & dispersion.

	patient_id	age	blood_pressure	specific_gravity	albumin	sugar	red_blood_cells	pus_cell
0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal

Cleaning Text Data

- Converted to lowercase; no uppercase after.
  - eg. Ckd -> cdk , Normal -> normal
- Checked unique values:
  - e.g diabetes_mellitus ['yes' 'no' ' yes' '\tno' '\tyes' nan]
- Cleaned: Removed tabs, spaces, '\t?', replaced empty /'nan' with NaN.
- Post-clean uniques:
  - e.g., diabetes_mellitus ['yes', 'no’, NaN].

Missing Values

Column removal:
drop columns if >70–80% missing.

Row removal:
drop rows if >50% missing values
(depends on dataset size).

Otherwise: use imputation
(mean, median, mode, regression, KNN, etc.).

Imputation with KNNImputer

- KNNImputer (from sklearn.impute) fills missing values using the k nearest neighbors (rows), replacing them with the mean, median, or weighted average of their neighbors.
- Method: KNNImputer (n_neighbors=5) for mixed data.
- Benefits of KNNImputer
  - Uses similar rows (neighbors) instead of global mean/median.
  - Preserves data patterns and variability.
  - Works for both numeric & categorical (after encoding).
  - Makes no strong assumptions about distribution.
  - Adaptive → imputes differently for different groups.
- Process: Encode categoricals, impute, decode.
- Validation: KNN Classifier accuracy 0.97, F1 0.97.
- No missing post-imputation.

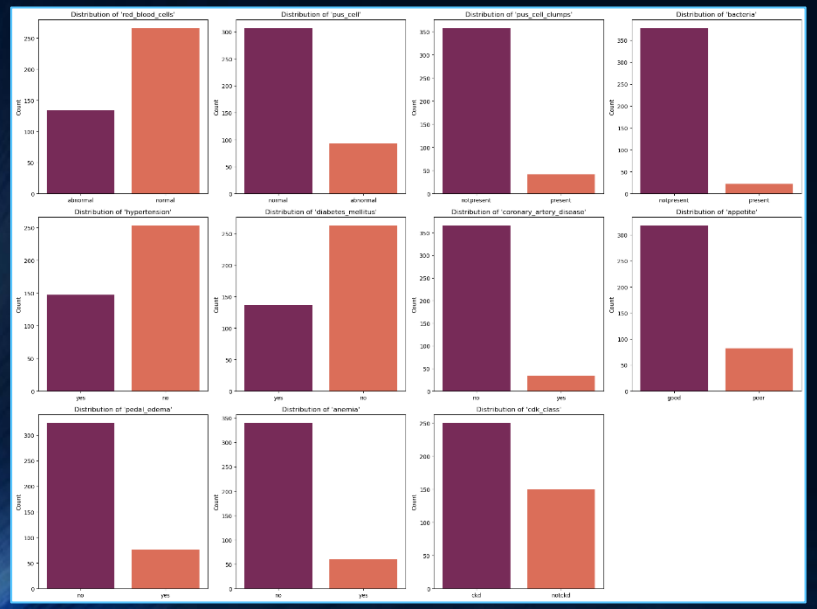
	Missing	% Missing (null)
red_blood_cells	152	38.00
red_blood_cell_count	131	32.75
white_blood_cell_count	106	26.50
potassium	88	22.00
sodium	87	21.75
packed_cell_volume	71	17.75
pus_cell	65	16.25
hemoglobin	52	13.00

```
Imputation Validation: Based on KNN model
Train Set:
Model accuracy: 0.96
Test Set:
Accuracy: 0.97
F1_score: 0.97
ROC-AUC : 0.98
Model Cross-Validation (10-fold) score: 0.9
```

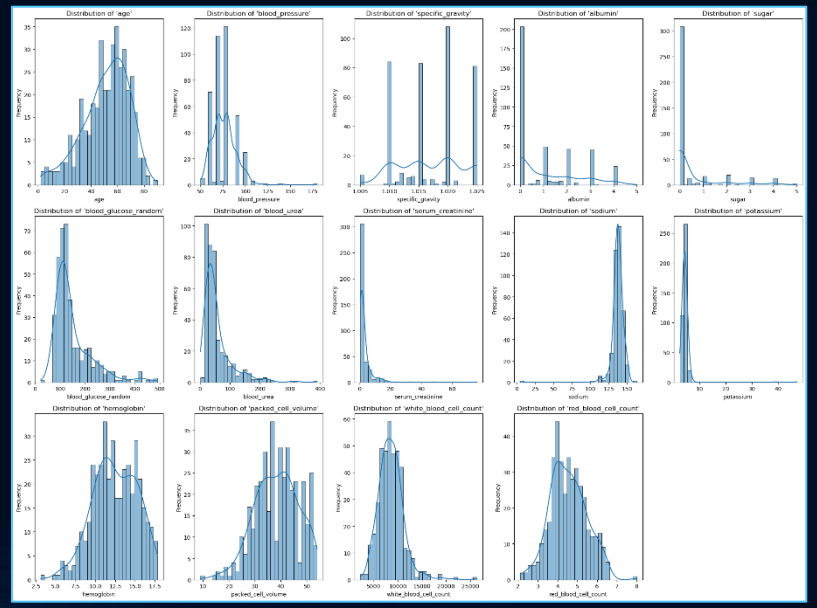
Data Analysis

- Categorical (11 cols): Count plots e.g., more 'normal' rbc; balanced hypertension.
- Numeric (14 cols): Histplots e.g., age skewed ~50s; univariate table (mean, median, IQR).
- Key stats: Hemoglobin mean 12.53, blood_urea 57.43

Categorical



Numeric



Model Prediction & Save

- DOMAIN PREDICTION: MACHINE LEARNING
  - Predicted Value: **cdk_class** Yes (cdk) / No (notcdk) (1 or 0)
  - Input: Numerical & Categorical Data.
- LEARNING PREDICTION: SUPERVISED LEARNING
  - Requirement clear.
  - Both input and output data are available
- ALGORITHM PREDICTION: CLASSIFICATION
  - Prediction is Yes/No → Classification Problem
  - Inputs: 24 features
  - Output: 1 target
- CLASSIFICATION ALGORITHMS USED
  - K-Nearest Neighbour Classification, Logistic Regression, Decision Tree Classification, Random Forest Classification, XGBoost

```
Logistic Regression Accuracy: 1.00
Logistic Regression f1_score: 1.00
Logistic Regression ROC-AUC : 1.00

Decision Tree Accuracy: 0.99
Decision Tree f1_score: 0.99
Decision Tree ROC-AUC : 0.99

Random Forest Accuracy: 1.00
Random Forest f1_score: 1.00
Random Forest ROC-AUC : 1.00

XGBoost Accuracy: 0.99
XGBoost f1_score: 0.99
XGBoost ROC-AUC : 0.99
```

Ai

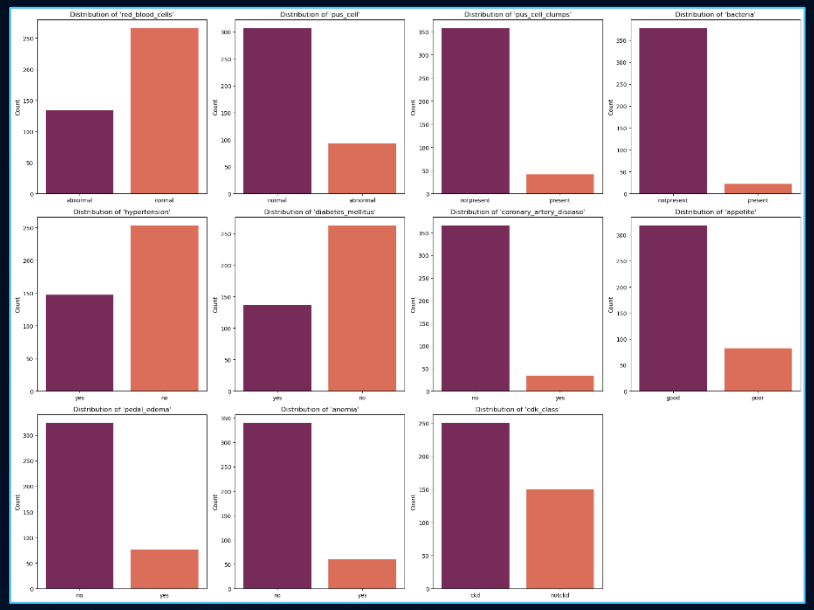
Python Code: Attached step by step

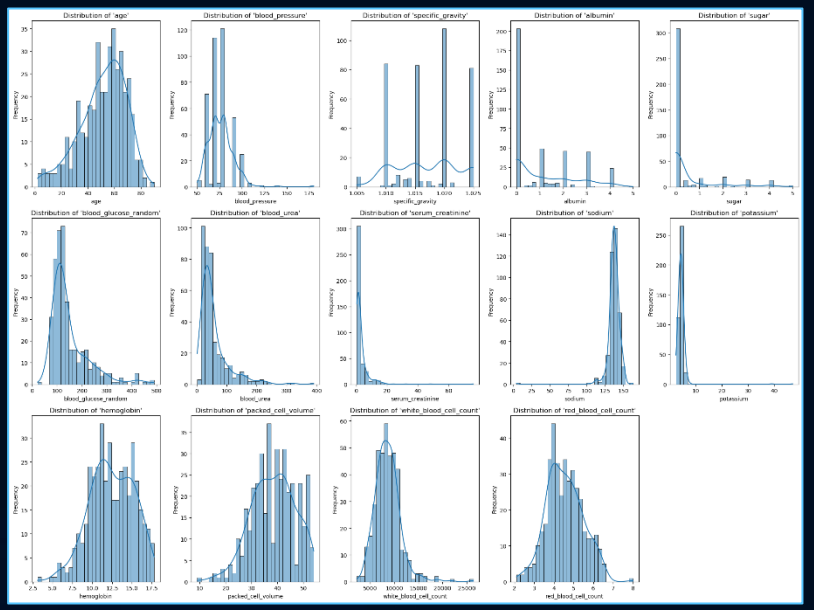
```
Logistic Regression Accuracy: 1.00
Logistic Regression f1_score: 1.00
Logistic Regression ROC-AUC : 1.00

Decision Tree Accuracy: 0.99
Decision Tree f1_score: 0.99
Decision Tree ROC-AUC : 0.99

Random Forest Accuracy: 1.00
Random Forest f1_score: 1.00
Random Forest ROC-AUC : 1.00

XGBoost Accuracy: 0.99
XGBoost f1_score: 0.99
XGBoost ROC-AUC : 0.99
```





Data_Preprocessing_Clean_Analysis

September 29, 2025

1 Chronic Kidney Disease dataset

Data Preprocessing & Analysis with Model Prediction Dr. Subramani Suresh

[176]:
```
#Data collection
import pandas as pd
import numpy as np
import warnings
# Ignore FutureWarning
warnings.simplefilter(action='ignore', category=FutureWarning)

dataset=pd.read_csv("kidney_disease.csv")
#orginal dataset
dataset
```

[176]:

	id	age	bp	sg	al	su	rbc	pc	pcc	\
0	0	48.0	80.0	1.020	1.0	0.0	NaN	Normal	notpresent	
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notPresent	
2	2	62.0	80.0	1.010	2.0	3.0	Normal	normal	notpresent	
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	
..	…	…	…	…	…	…	…	…	…	
395	395	55.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	
396	396	42.0	70.0	1.025	0.0	0.0	normal	normal	notpresent	
397	397	12.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	
398	398	17.0	60.0	1.025	0.0	0.0	normal	normal	notpresent	
399	399	58.0	80.0	1.025	0.0	0.0	normal	normal	notpresent	

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

```
398  notpresent  …   51  7200  5.9   no   no   no  good   no   no
399  notpresent  …   53  6800  6.1   no   no   no  good   no   no

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

[400 rows x 26 columns]
```

2 Data Preprocessing

[177]:
```
# columns name
dataset.dtypes
```

[177]:
```
id                int64
age             float64
bp              float64
sg              float64
al              float64
su              float64
rbc              object
pc               object
pcc              object
ba               object
bgr             float64
bu              float64
sc              float64
sod             float64
pot             float64
hemo            float64
pcv              object
wc               object
rc               object
htn              object
dm               object
cad              object
appet            object
```

```
pe                  object
ane                 object
classification      object
dtype: object
```

[178]:
```
# renames columns into more meaningful
dataset.rename(columns={
    "id": "patient_id",
    "age": "age",
    "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",
    "classification": "cdk_class"
}, inplace=True)
# after renamed
dataset.dtypes
```

[178]:
```
patient_id                  int64
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
hemoglobin                 float64
packed_cell_volume          object
white_blood_cell_count      object
red_blood_cell_count        object
hypertension                object
diabetes_mellitus           object
coronary_artery_disease     object
appetite                    object
pedal_edema                 object
anemia                      object
cdk_class                   object
dtype: object
```

[179]:
```
'''Descriptive statistics include those that summarize the central
tendency, dispersion and shape of a
dataset's distribution, excluding ``NaN`` values.'''
dataset.describe()
```

[179]:

	patient_id	age	blood_pressure	specific_gravity	albumin	\
count	400.000000	391.000000	388.000000	353.000000	354.000000	
mean	199.500000	51.483376	76.469072	1.017408	1.016949	
std	115.614301	17.169714	13.683637	0.005717	1.352679	
min	0.000000	2.000000	50.000000	1.005000	0.000000	
25%	99.750000	42.000000	70.000000	1.010000	0.000000	
50%	199.500000	55.000000	80.000000	1.020000	0.000000	
75%	299.250000	64.500000	80.000000	1.020000	2.000000	
max	399.000000	90.000000	180.000000	1.025000	5.000000	

	sugar	blood_glucose_random	blood_urea	serum_creatinine	\
count	351.000000	356.000000	381.000000	383.000000	
mean	0.450142	148.036517	57.425722	3.072454	
std	1.099191	79.281714	50.503006	5.741126	
min	0.000000	22.000000	1.500000	0.400000	
25%	0.000000	99.000000	27.000000	0.900000	
50%	0.000000	121.000000	42.000000	1.300000	
75%	0.000000	163.000000	66.000000	2.800000	
max	5.000000	490.000000	391.000000	76.000000	

	sodium	potassium	hemoglobin
count	313.000000	312.000000	348.000000
mean	137.528754	4.627244	12.526437
std	10.408752	3.193904	2.912587

```
min      4.500000    2.500000    3.100000
25%    135.000000    3.800000   10.300000
50%    138.000000    4.400000   12.650000
75%    142.000000    4.900000   15.000000
max    163.000000   47.000000   17.800000
```

[180]:
```
# Check each categorical (object) if uppercase exists
def df_check_uppercase(df):
    print("\nuppercase present 'yes'/'no'\n----------------------------")
    for col in df.select_dtypes(include="object").columns:
        has_upper = df[col].str.contains(r'[A-Z]').any()
        print(f"{col}: {"uppercase present 'yes'" if has_upper else 'no'}")
    print("\ndataset = uppercase present 'yes'" if has_upper else '\ndataset =␣
 ↪uppercase not present')

#check_uppercase in dataset
df_check_uppercase(dataset)
```

```
uppercase present 'yes'/'no'
----------------------------
red_blood_cells: uppercase present 'yes'
pus_cell: uppercase present 'yes'
pus_cell_clumps: uppercase present 'yes'
bacteria: no
packed_cell_volume: no
white_blood_cell_count: no
red_blood_cell_count: no
hypertension: no
diabetes_mellitus: no
coronary_artery_disease: no
appetite: no
pedal_edema: no
anemia: no
cdk_class: uppercase present 'yes'

dataset = uppercase present 'yes'
```

[181]:
```
# Check each categorical (object) column and convert all text values to␣
 ↪lowercase
def df_convert_lowercase(df):
    for col in df.select_dtypes(include="object").columns:
        df[col] = df[col].str.lower()
    return df
#convert_lowercase in dataset
dataset=df_convert_lowercase(dataset)
#check_uppercase in dataset
```

```
df_check_uppercase(dataset)
```

```
uppercase present 'yes'/'no'
-----------------------------
red_blood_cells: no
pus_cell: no
pus_cell_clumps: no
bacteria: no
packed_cell_volume: no
white_blood_cell_count: no
red_blood_cell_count: no
hypertension: no
diabetes_mellitus: no
coronary_artery_disease: no
appetite: no
pedal_edema: no
anemia: no
cdk_class: no

dataset = uppercase not present
```

[182]:
```
#Detect missing values.
dataset.isnull().sum()
```

[182]:
```
patient_id                0
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
hemoglobin               52
packed_cell_volume       70
white_blood_cell_count  105
red_blood_cell_count    130
hypertension              2
diabetes_mellitus         2
coronary_artery_disease   2
appetite                  1
```

```
pedal_edema                 1
anemia                      1
cdk_class                   0
dtype: int64
```

[183]:
```
#Detect missing values with order and %
def df_missing_info(df):
    missing_info = df.isnull().sum().to_frame(name='Missing')
    missing_info['% Missing (null)'] = (missing_info['Missing'] / len(df) *␣
 ↪100).round(2)
    missing_info = missing_info[missing_info['Missing'] > 0].
 ↪sort_values(by='Missing', ascending=False)
    print(missing_info)

df_missing_info(dataset)
```

```
                          Missing  % Missing (null)
red_blood_cells               152             38.00
red_blood_cell_count          130             32.50
white_blood_cell_count        105             26.25
potassium                      88             22.00
sodium                         87             21.75
packed_cell_volume             70             17.50
pus_cell                       65             16.25
hemoglobin                     52             13.00
sugar                          49             12.25
specific_gravity               47             11.75
albumin                        46             11.50
blood_glucose_random           44             11.00
blood_urea                     19              4.75
serum_creatinine               17              4.25
blood_pressure                 12              3.00
age                             9              2.25
pus_cell_clumps                 4              1.00
bacteria                        4              1.00
hypertension                    2              0.50
diabetes_mellitus               2              0.50
coronary_artery_disease         2              0.50
appetite                        1              0.25
pedal_edema                     1              0.25
anemia                          1              0.25
```

[184]:
```
# looking at unique values in columns
def df_uni_val_info(df):
    for col in df:
        print(f"{col} {df[col].unique()} unique values | Type :{df[col].
 ↪dtype}\n")
```

```
df_uni_val_info(dataset)
```

```
patient_id [  0   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16
17
  18  19  20  21  22  23  24  25  26  27  28  29  30  31  32  33  34  35
  36  37  38  39  40  41  42  43  44  45  46  47  48  49  50  51  52  53
  54  55  56  57  58  59  60  61  62  63  64  65  66  67  68  69  70  71
  72  73  74  75  76  77  78  79  80  81  82  83  84  85  86  87  88  89
  90  91  92  93  94  95  96  97  98  99 100 101 102 103 104 105 106 107
 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125
 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143
 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161
 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179
 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197
 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215
 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233
 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251
 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269
 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287
 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305
 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323
 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341
 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359
 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377
 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395
 396 397 398 399] unique values | Type :int64

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 | Type :float64

blood_pressure [ 80.  50.  70.  90.  nan 100.  60. 110. 140. 180. 120.] unique
values | Type :float64

specific_gravity [1.02  1.01  1.005 1.015   nan 1.025] unique values | Type
:float64

albumin [ 1.  4.  2.  3.  0. nan  5.] unique values | Type :float64

sugar [ 0.  3.  4.  1. nan  2.  5.] unique values | Type :float64

red_blood_cells [nan 'normal' 'abnormal'] unique values | Type :object

pus_cell ['normal' 'abnormal' nan] unique values | Type :object
```

```
pus_cell_clumps ['notpresent' 'present' nan] unique values | Type :object

bacteria ['notpresent' 'present' nan] unique values | Type :object

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 | Type :float64

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 | Type :float64

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 | Type :float64

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 | Type :float64

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
```

```
| Type :float64

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 | Type :float64

packed_cell_volume ['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'] unique values | Type :object

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' '\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'] unique values | Type :object

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'
 '\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'] unique values | Type :object

hypertension ['yes' 'no' nan] unique values | Type :object

diabetes_mellitus ['yes' 'no' ' yes' '\tno' '\tyes' nan] unique values | Type
:object

coronary_artery_disease ['no' 'yes' '\tno' nan] unique values | Type :object

appetite ['good' 'poor' nan] unique values | Type :object

pedal_edema ['no' 'yes' nan] unique values | Type :object
```

```
anemia ['no' 'yes' nan] unique values | Type :object

cdk_class ['ckd' 'ckd\t' 'notckd'] unique values | Type :object
```

[185]:
```
# Clean the data based unique values, replace incorrect values eg. '\t6200',␣
 ↪'\t?', '\tno','\tyes' etc
def df_clean_all(df):
    for col in df.columns:
        # convert everything to string
        df[col] = df[col].astype(str)
        # remove tabs
        df[col] = df[col].str.replace('\t', ' ', regex=False)
        # Step 3: remove newlines (\n newlines, \r carriage returns)
        df[col] = df[col].str.replace('\n', ' ', regex=False)
        df[col] = df[col].str.replace('\r', ' ', regex=False)
        # replace multiple spaces with a single space
        df[col] = df[col].str.replace(' +', ' ', regex=True)
        # strip leading and trailing spaces
        df[col] = df[col].str.strip()
        # replace empty or "nan" strings with real NaN
        df[col] = df[col].replace(['', ' ', 'nan', 'NaN', 'None'], np.nan)
        #Extra string remove
        df[col] = df[col].replace(['?'], np.nan)
        # try converting back to numeric if possible
        df[col] = pd.to_numeric(df[col], errors='ignore')
    return df

dataset=df_clean_all(dataset)
```

[225]:
```
# looking at unique values after clean columns
df_uni_val_info(dataset[["diabetes_mellitus","red_blood_cell_count"]])
```

```
diabetes_mellitus ['yes' 'no'] unique values | Type :object

red_blood_cell_count [5.2  3.58 3.56 3.9  4.6  4.4  4.22 5.   4.   3.7  4.26 3.8
3.4  3.92
 2.6  2.8  4.36 4.3  3.2  3.6  3.64 4.1  4.12 4.02 3.52 3.76 3.48 4.9
 3.82 2.5  3.84 4.2  4.16 4.5  3.1  4.7  4.24 3.5  3.42 3.74 3.62 4.06
 3.72 4.76 4.12 4.04 6.   4.46 3.98 4.62 3.94 4.52 2.1  4.44 4.28 5.6
 4.42 4.82 2.3  4.68 3.96 4.52 4.14 4.48 4.46 4.34 3.26 3.28 3.98 2.9
 3.72 2.7  3.92 8.   4.54 5.1  3.52 3.3  3.   5.3  4.54 2.4  4.8  4.86
 5.4  4.08 3.18 4.88 4.32 4.06 3.76 4.16 4.02 3.46 4.14 4.68 5.26 5.32
 4.34 5.36 4.82 6.1  5.12 6.2  6.3  5.1  5.8  5.5  5.28 6.4  5.7  5.9
 5.44 6.5  4.86 5.42 4.94] unique values | Type :float64
```

[187]:
```
df_missing_info(dataset)
```

	Missing	% Missing (null)
red_blood_cells	152	38.00
red_blood_cell_count	131	32.75
white_blood_cell_count	106	26.50
potassium	88	22.00
sodium	87	21.75
packed_cell_volume	71	17.75
pus_cell	65	16.25
hemoglobin	52	13.00
sugar	49	12.25
specific_gravity	47	11.75
albumin	46	11.50
blood_glucose_random	44	11.00
blood_urea	19	4.75
serum_creatinine	17	4.25
blood_pressure	12	3.00
age	9	2.25
pus_cell_clumps	4	1.00
bacteria	4	1.00
hypertension	2	0.50
diabetes_mellitus	2	0.50
coronary_artery_disease	2	0.50
appetite	1	0.25
pedal_edema	1	0.25
anemia	1	0.25

2.1 Missing Values

When to Remove Nulls Based on % Rules of Thumb (Industry Practice) 1. Column removal: drop columns if >70–80% missing. 2. Row removal: drop rows if >50% missing values (depends on dataset size). 3. Otherwise: use imputation (mean, median, mode, regression, KNN, etc.).

2.2 Imputation : KNNImputer

Missing values max 38%, so use imputation method: KNNImputer. The KNNImputer (from sklearn.impute) fills missing values by finding the k nearest neighbors (rows) based on other feature values. It replaces the missing value with the mean (default), median, or weighted average of those neighbors.

n_neighbors (int, default=5) # we can tune 2,3,5,6,…. Number of neighboring samples to use for imputation.

2.3 Benefits of KNNImputer

1. Uses similar rows (neighbors) instead of global mean/median.
2. Preserves data patterns and variability.
3. Works for both numeric & categorical (after encoding).

4. Makes no strong assumptions about distribution.
5. Adaptive → imputes differently for different groups.
6. Often improves model accuracy compared to simple imputers.

[188]:
```python
# Handle missing values using the KNNImputer method
def df_fill_missing_values_knn(df):
    import pandas as pd
    import numpy as np
    from sklearn.preprocessing import LabelEncoder
    from sklearn.impute import KNNImputer
    from sklearn.model_selection import train_test_split,cross_val_score
    from sklearn.neighbors import KNeighborsClassifier
    from sklearn.metrics import accuracy_score, f1_score, roc_auc_score

    # --- STEP 1: Identify categorical and numeric columns ----
    cat_cols = df.select_dtypes(include=['object']).columns
    num_cols = df.select_dtypes(exclude=['object']).columns
    #print("Categorical columns:\n", list(cat_cols))
    #print("Numeric columns:\n", list(num_cols))

    # --- STEP 2: Encode categorical columns ----------------
    encoders = {}
    for col in cat_cols:
        le = LabelEncoder()
        df[col] = df[col].astype(str)  # ensure string
        df[col] = df[col].replace("nan", np.nan)
        mask = df[col].notna()
        if mask.sum() > 0:
            df.loc[mask, col] = le.fit_transform(df.loc[mask, col])
            encoders[col] = le

    # --- STEP 3: Apply KNN Imputer for categorical and numeric columns----
    df = df.apply(pd.to_numeric, errors='coerce')
    imputer = KNNImputer(n_neighbors=5)
    df_imputed = imputer.fit_transform(df)
    df_imputed = pd.DataFrame(df_imputed, columns=df.columns)

    #Encoded and imputed dataset (dataset contain numeric value only) for any␣
 ↪model creation
    df_imputed_encoded=df_imputed.copy()

    #--- STEP 4: Valiation with KNeighborsClassifier Model--------

    #traget columns for prediction
    # get the last column name as target
    target_col = df.columns[-1]
    # X, y split
```

```
    X=df_imputed.drop(target_col, axis=1)
    y=df_imputed[target_col]

    #split train and test set 20% test data 80% train data
    X_train,X_test,y_train,y_test=train_test_split(X,y,test_size=0.
 ↪20,random_state=42)

    #model creation
    model=KNeighborsClassifier(n_neighbors=5) #5
    model.fit(X_train,y_train)

    #y prediction for valitation
    y_pred = model.predict(X_test)

    # Valitation result
    print(f"\nImputation Validation: Based on KNN model\nTrain Set:")
    # Training set evaluation
    print(f"Model accuracy: {model.score(X_train,y_train):.2f}")
    # Test set evaluation
    print(f"Test Set:")
    print(f"Accuracy: {accuracy_score(y_test, y_pred):.2f}")
    print(f"F1_score: {f1_score(y_test, y_pred):.2f}")
    print(f"ROC-AUC : {roc_auc_score(y_test, y_pred):.2f}")
    # Cross-validation
    cv_scores = cross_val_score(model, X, y, cv=10)  # 10 cross-fold CV
    print("Model Cross-Validation (10-fold) score:", cv_scores.mean())

    # --- STEP 4: Decode categorical columns -------
    # Decode for data analysis
    for col in cat_cols:
        if col in encoders:
            df_imputed[col] = df_imputed[col].round().astype(int)
            df_imputed[col] = encoders[col].inverse_transform(df_imputed[col])

    # df_imputed_encoded = dataset after encoding all categorical and numerical␣
 ↪columns
    # df_imputed = dataset after decoding categorical columns back to original␣
 ↪labels
    return df_imputed, df_imputed_encoded
#
#call function
dataset,dataset_encoded=df_fill_missing_values_knn(dataset)
```

```
Imputation Validation: Based on KNN model
Train Set:
Model accuracy: 0.96
```

```
Test Set:
Accuracy: 0.97
F1_score: 0.97
ROC-AUC : 0.98
Model Cross-Validation (10-fold) score: 0.9
```

[226]:
```
# dataset after decoding categorical columns back to original labels
dataset
```

[226]:
```
     patient_id   age  blood_pressure  specific_gravity  albumin  sugar  \
0           0.0  48.0            80.0             1.020      1.0    0.0
1           1.0   7.0            50.0             1.020      4.0    0.0
2           2.0  62.0            80.0             1.010      2.0    3.0
3           3.0  48.0            70.0             1.005      4.0    0.0
4           4.0  51.0            80.0             1.010      2.0    0.0
..          …   …              …                 …       …    …
395       395.0  55.0            80.0             1.020      0.0    0.0
396       396.0  42.0            70.0             1.025      0.0    0.0
397       397.0  12.0            80.0             1.020      0.0    0.0
398       398.0  17.0            60.0             1.025      0.0    0.0
399       399.0  58.0            80.0             1.025      0.0    0.0

    red_blood_cells  pus_cell pus_cell_clumps    bacteria  …  \
0          abnormal    normal      notpresent  notpresent  …
1          abnormal    normal      notpresent  notpresent  …
2            normal    normal      notpresent  notpresent  …
3            normal  abnormal         present  notpresent  …
4            normal    normal      notpresent  notpresent  …
..              …       …              …          …  …
395          normal    normal      notpresent  notpresent  …
396          normal    normal      notpresent  notpresent  …
397          normal    normal      notpresent  notpresent  …
398          normal    normal      notpresent  notpresent  …
399          normal    normal      notpresent  notpresent  …

     packed_cell_volume  white_blood_cell_count  red_blood_cell_count  \
0                  44.0                  7800.0                  5.20
1                  38.0                  6000.0                  3.58
2                  31.0                  7500.0                  3.56
3                  32.0                  6700.0                  3.90
4                  35.0                  7300.0                  4.60
..                  …                     …                     …
395                47.0                  6700.0                  4.90
396                54.0                  7800.0                  6.20
397                49.0                  6600.0                  5.40
398                51.0                  7200.0                  5.90
399                53.0                  6800.0                  6.10
```

```
     hypertension  diabetes_mellitus  coronary_artery_disease  appetite  \
0             yes                yes                       no      good
1              no                 no                       no      good
2              no                yes                       no      poor
3             yes                 no                       no      poor
4              no                 no                       no      good
..            …                  …                        …       …
395            no                 no                       no      good
396            no                 no                       no      good
397            no                 no                       no      good
398            no                 no                       no      good
399            no                 no                       no      good

     pedal_edema  anemia cdk_class
0             no      no       ckd
1             no      no       ckd
2             no     yes       ckd
3            yes     yes       ckd
4             no      no       ckd
..           …     …       …
395           no      no    notckd
396           no      no    notckd
397           no      no    notckd
398           no      no    notckd
399           no      no    notckd

[400 rows x 26 columns]
```

[191]:
```
# cleaned dataset without null/missing values
df_missing_info(dataset)
```

```
Empty DataFrame
Columns: [Missing, % Missing (null)]
Index: []
```

3 Data Analysis

[227]:
```
#split categorical column names
cat_cals=[cal for cal in dataset if dataset[cal].dtype==object]
cat_cals
```

[227]:
```
['red_blood_cells',
 'pus_cell',
 'pus_cell_clumps',
 'bacteria',
 'hypertension',
```

```
 'diabetes_mellitus',
 'coronary_artery_disease',
 'appetite',
 'pedal_edema',
 'anemia',
 'cdk_class']
```

4 categorical columns

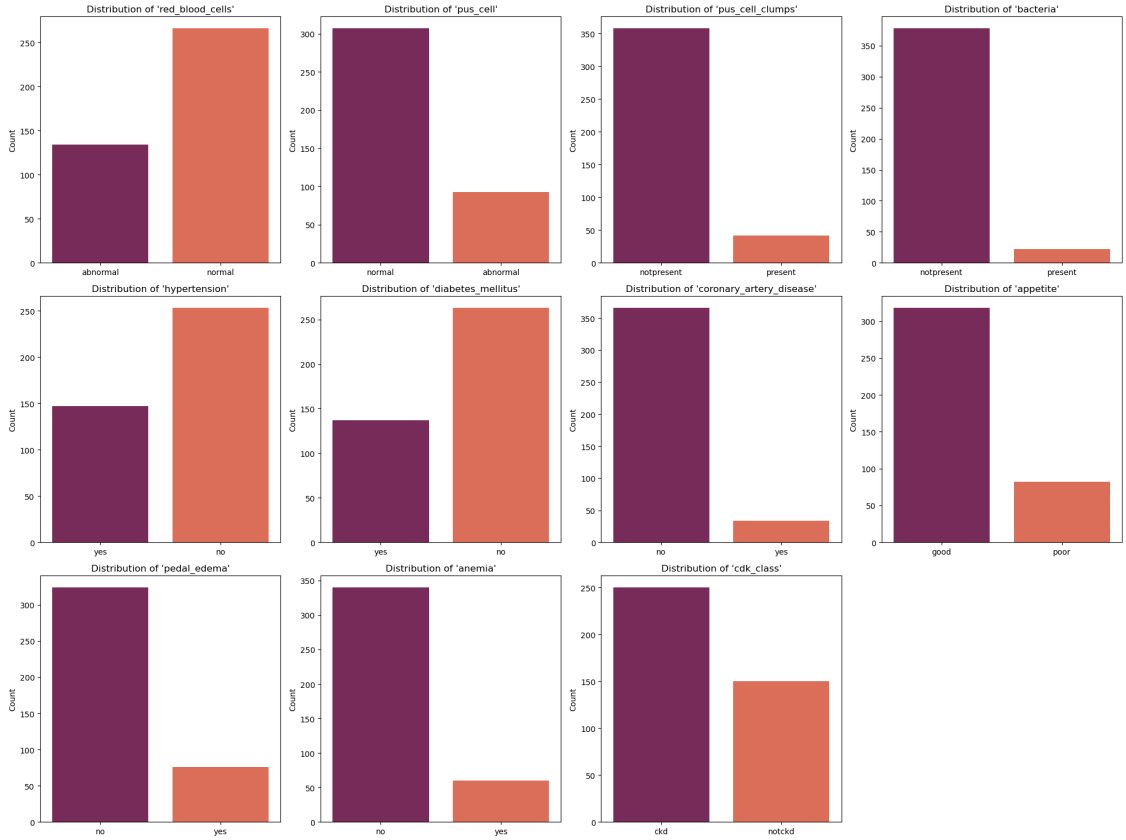
[209]:
```
#looking at categorical columns
import matplotlib.pyplot as plt
import seaborn as sns

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

for column in cat_cols:
    if plotnumber <= 11:
        ax = plt.subplot(3, 4, plotnumber)
        sns.countplot(x=dataset[column], palette='rocket', ax=ax)
        ax.set_title(f"Distribution of '{column}'")   # Title above each plot
        ax.set_xlabel("")  # optional: remove x-axis label if title is enough
        ax.set_ylabel("Count")

    plotnumber += 1

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



5 Numeric column

[216]:
```
#split numeric column names
num_cals=[cal for cal in dataset if dataset[cal].dtype!=object]
num_cals.remove("patient_id")
num_cals
```

[216]:
```
['age',
 'blood_pressure',
 'specific_gravity',
 'albumin',
 'sugar',
 'blood_glucose_random',
 'blood_urea',
 'serum_creatinine',
 'sodium',
 'potassium',
 'hemoglobin',
 'packed_cell_volume',
 'white_blood_cell_count',
```

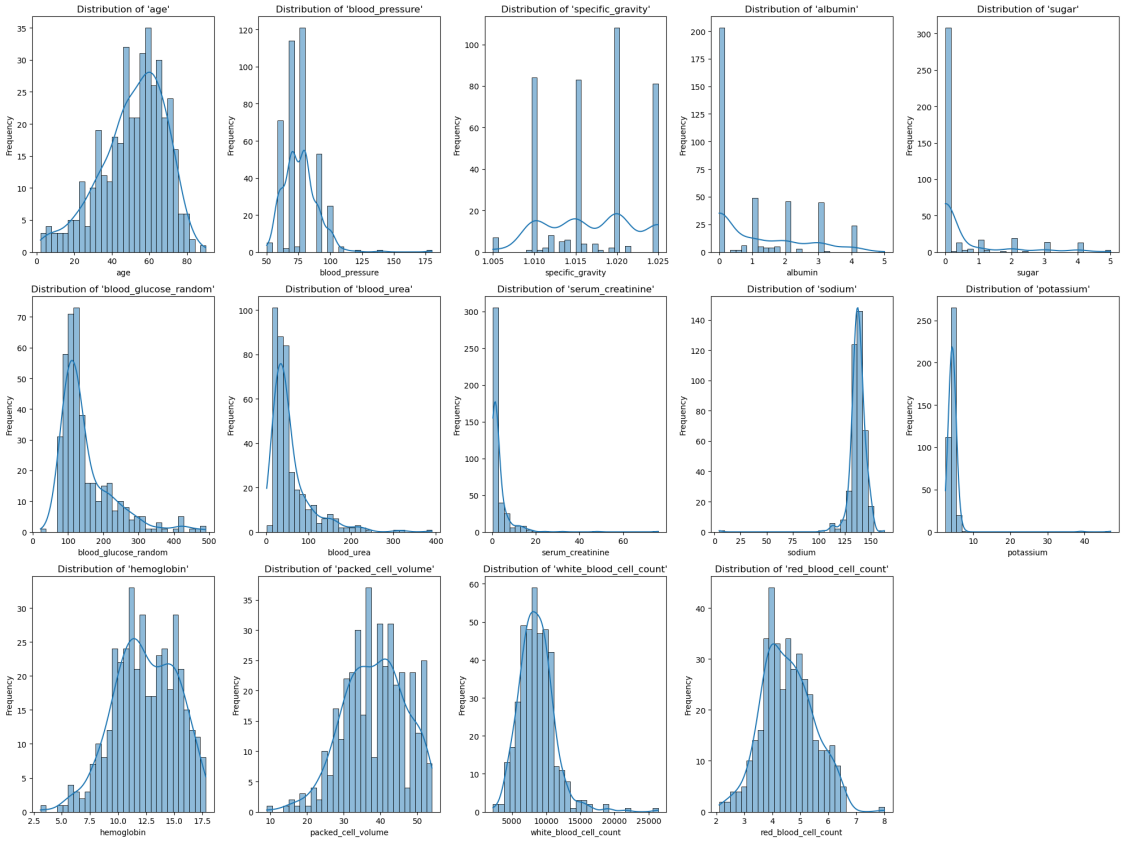
```
 'red_blood_cell_count']
```

[219]:
```
# checking numerical features distribution
plt.figure(figsize=(20, 15))
plotnumber = 1

for column in num_cals:
    if plotnumber <= 14:    # adjust subplot grid if you have more/less features
        ax = plt.subplot(3, 5, plotnumber)
        sns.histplot(dataset[column], kde=True, bins=30)  # kde=True adds␣
 ↪density curve
        ax.set_title(f"Distribution of '{column}'")   # Title above each plot
        plt.xlabel(column)
        plt.ylabel("Frequency")

    plotnumber += 1

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



[221]:
```
#looking at numeric column

#create New Table for central Tendency & descriptive
def UnivariateTable(df,num_cals):
    import pandas as pd
    import numpy as np
    descriptive=pd.DataFrame(index=["Mean","Median","Mode",
                                    "Min","Q1-25%","Q2-50%","Q3-75%","Max",
                                   "IQR","1.5-Rule","Lower-Bound","Upper-Bound"]
                             ,columns=num_cals)
    for cal in num_cals:
        #print(cal)
        descriptive.loc["Mean", cal] = round(df[cal].mean(), 2)
        descriptive.loc["Median", cal] = df[cal].median()
        descriptive.loc["Mode", cal] = round(df[cal].mode()[0], 2)
        descriptive.loc["Min",cal]=df.describe().loc['min',cal]
        descriptive.loc["Q1-25%",cal]=df.describe().loc['25%',cal]
        descriptive.loc["Q2-50%",cal]=df.describe().loc['50%',cal]
        descriptive.loc["Q3-75%",cal]=df.describe().loc['75%',cal]
        descriptive.loc["Max",cal]=df.describe().loc['max',cal]
        descriptive.loc["IQR",cal]=descriptive.loc["Q3-75%",cal]-descriptive.
 ↪loc["Q1-25%",cal]
        descriptive.loc["1.5-Rule",cal]=1.5*descriptive.loc["IQR",cal]
        descriptive.loc["Lower-Bound",cal]=descriptive.
 ↪loc["Q1-25%",cal]-descriptive.loc["1.5-Rule",cal]
        descriptive.loc["Upper-Bound",cal]=descriptive.
 ↪loc["Q3-75%",cal]+descriptive.loc["1.5-Rule",cal]
    return descriptive

UnivariateTable(dataset,num_cals)
```

[221]:

	age	blood_pressure	specific_gravity	albumin	sugar	\
Mean	51.38	76.36	1.02	1.05	0.46	
Median	54.0	80.0	1.016	0.0	0.0	
Mode	60.0	80.0	1.02	0.0	0.0	
Min	2.0	50.0	1.005	0.0	0.0	
Q1-25%	42.0	70.0	1.012	0.0	0.0	
Q2-50%	54.0	80.0	1.016	0.0	0.0	
Q3-75%	64.0	80.0	1.02	2.0	0.0	
Max	90.0	180.0	1.025	5.0	5.0	
IQR	22.0	10.0	0.008	2.0	0.0	
1.5-Rule	33.0	15.0	0.012	3.0	0.0	
Lower-Bound	9.0	55.0	1.0	-3.0	0.0	
Upper-Bound	97.0	95.0	1.032	5.0	0.0	

	blood_glucose_random	blood_urea	serum_creatinine	sodium	\
Mean	150.34	57.15	3.06	137.24	

```
Median                    123.0       42.0             1.3   137.3
Mode                       99.0       46.0             1.2   135.0
Min                        22.0        1.5             0.4     4.5
Q1-25%                    101.0       27.0             0.9   135.0
Q2-50%                    123.0       42.0             1.3   137.3
Q3-75%                    172.0       66.0             2.8   141.0
Max                       490.0      391.0            76.0   163.0
IQR                        71.0       39.0             1.9     6.0
1.5-Rule                  106.5       58.5            2.85     9.0
Lower-Bound                -5.5      -31.5           -1.95   126.0
Upper-Bound               278.5      124.5            5.65   150.0

            potassium hemoglobin packed_cell_volume white_blood_cell_count  \
Mean             4.56      12.44              38.35                8584.45
Median           4.34       12.3               39.0                 8300.0
Mode              3.5       15.0               41.0                 9800.0
Min               2.5        3.1                9.0                 2200.0
Q1-25%            3.9     10.515               32.4                 6900.0
Q2-50%           4.34       12.3               39.0                 8300.0
Q3-75%            4.9       14.8               44.0                 9800.0
Max              47.0       17.8               54.0                26400.0
IQR               1.0      4.285               11.6                 2900.0
1.5-Rule          1.5     6.4275               17.4                 4350.0
Lower-Bound       2.4     4.0875               15.0                 2550.0
Upper-Bound       6.4    21.2275               61.4                14150.0

            red_blood_cell_count
Mean                        4.54
Median                       4.5
Mode                         5.2
Min                          2.1
Q1-25%                       3.9
Q2-50%                       4.5
Q3-75%                       5.2
Max                          8.0
IQR                          1.3
1.5-Rule                    1.95
Lower-Bound                 1.95
Upper-Bound                 7.15
```

6 Model Prediction

[228]:
```
#dataset after encoding all categorical and numerical columns
dataset_encoded.head()
```

[228]:
```
   patient_id   age  blood_pressure  specific_gravity  albumin  sugar  \
0         0.0  48.0            80.0             1.020      1.0    0.0
1         1.0   7.0            50.0             1.020      4.0    0.0
2         2.0  62.0            80.0             1.010      2.0    3.0
3         3.0  48.0            70.0             1.005      4.0    0.0
4         4.0  51.0            80.0             1.010      2.0    0.0

   red_blood_cells  pus_cell  pus_cell_clumps  bacteria  …  \
0              0.2       1.0              0.0       0.0  …
1              0.4       1.0              0.0       0.0  …
2              1.0       1.0              0.0       0.0  …
3              1.0       0.0              1.0       0.0  …
4              1.0       1.0              0.0       0.0  …

   packed_cell_volume  white_blood_cell_count  red_blood_cell_count  \
0                44.0                  7800.0                  5.20
1                38.0                  6000.0                  3.58
2                31.0                  7500.0                  3.56
3                32.0                  6700.0                  3.90
4                35.0                  7300.0                  4.60

   hypertension  diabetes_mellitus  coronary_artery_disease  appetite  \
0           1.0                1.0                      0.0       0.0
1           0.0                0.0                      0.0       0.0
2           0.0                1.0                      0.0       1.0
3           1.0                0.0                      0.0       1.0
4           0.0                0.0                      0.0       0.0

   pedal_edema  anemia  cdk_class
0          0.0     0.0        0.0
1          0.0     0.0        0.0
2          0.0     1.0        0.0
3          1.0     1.0        0.0
4          0.0     0.0        0.0

[5 rows x 26 columns]
```

[222]:
```
# Model prediction for encoded dataset

#split X, y
target_col="cdk_class"
X=dataset_encoded.drop(target_col, axis=1)
y=dataset_encoded[target_col]

#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.
 ↪30,random_state=42, shuffle=True)

#model creation
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
import xgboost as xgb
from sklearn.metrics import accuracy_score, f1_score, roc_auc_score

models = {
    "Logistic Regression": LogisticRegression(),
    "Decision Tree": DecisionTreeClassifier(),
    "Random Forest": RandomForestClassifier(),
    "XGBoost": xgb.XGBClassifier()
}
# Evaluate models
for name, model in models.items():
    model.fit(X_train, y_train)
    y_pred = model.predict(X_test)
    print(f"\n{name} Accuracy: {accuracy_score(y_test, y_pred):.2f}")
    print(f"{name} f1_score: {f1_score(y_test, y_pred):.2f}")
    print(f"{name} ROC-AUC : {roc_auc_score(y_test, y_pred):.2f}")
```

```
C:\Anaconda3\envs\ssai\Lib\site-packages\sklearn\linear_model\_logistic.py:473:
ConvergenceWarning: lbfgs failed to converge after 100 iteration(s) (status=1):
STOP: TOTAL NO. OF ITERATIONS REACHED LIMIT

Increase the number of iterations to improve the convergence (max_iter=100).
You might also want to scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-
regression
  n_iter_i = _check_optimize_result(


Logistic Regression Accuracy: 1.00
Logistic Regression f1_score: 1.00
Logistic Regression ROC-AUC : 1.00

Decision Tree Accuracy: 0.99
Decision Tree f1_score: 0.99
Decision Tree ROC-AUC : 0.99

Random Forest Accuracy: 1.00
Random Forest f1_score: 1.00
Random Forest ROC-AUC : 1.00
```

```
XGBoost Accuracy: 0.99
XGBoost f1_score: 0.99
XGBoost ROC-AUC : 0.99
```

7 Save Cleaned Dataset

[223]:
```python
# ----------Save cleaned dataset ----------------
dataset.to_csv("ckd_dataset_imputed.csv", index=False)
dataset_encoded.to_csv("cdk_encoded_dataset_imputed.csv", index=False)
print("Cleaned dataset saved. Shape:", dataset.shape, dataset_encoded.shape)
```

```
Cleaned dataset saved. Shape: (400, 26) (400, 26)
```

[174]:
```python
# Dr. Subramani Suresh
```

[ ]:
```python

```