

Data Collection and Preprocessing Phase

Date	18 June 2025
Team ID	SWTID1749641473
Project Title	Early Prediction for Chronic Kidney Disease Detection: A Progressive Approach to Health Management
Maximum Marks	6 Marks

Data Exploration and Preprocessing Template

Identifies data sources, assesses quality issues like missing values and duplicates, and implements resolution plans to ensure accurate and reliable analysis.

Section	Description																																																																																																												
Data Overview	<u>Dimensions:</u> 400 rows × 26 columns																																																																																																												
	<u>Descriptive statistics:</u>																																																																																																												
	<table><thead><tr><th></th><th>age</th><th>bp</th><th>sg</th><th>al</th><th>su</th><th>bgr</th><th>bu</th><th>sc</th><th>sod</th><th>pot</th><th>hemo</th></tr></thead><tbody><tr><td>count</td><td>391.000000</td><td>388.000000</td><td>353.000000</td><td>354.000000</td><td>351.000000</td><td>356.000000</td><td>381.000000</td><td>383.000000</td><td>313.000000</td><td>312.000000</td><td>348.000000</td></tr><tr><td>mean</td><td>51.483376</td><td>76.469072</td><td>1.017408</td><td>1.016949</td><td>0.450142</td><td>148.036517</td><td>57.425722</td><td>3.072454</td><td>137.528754</td><td>4.627244</td><td>12.526437</td></tr><tr><td>std</td><td>17.169714</td><td>13.683637</td><td>0.005717</td><td>1.352679</td><td>1.099191</td><td>79.281714</td><td>50.503006</td><td>5.741126</td><td>10.408752</td><td>3.193904</td><td>2.912587</td></tr><tr><td>min</td><td>2.000000</td><td>50.000000</td><td>1.005000</td><td>0.000000</td><td>0.000000</td><td>22.000000</td><td>1.500000</td><td>0.400000</td><td>4.500000</td><td>2.500000</td><td>3.100000</td></tr><tr><td>25%</td><td>42.000000</td><td>70.000000</td><td>1.010000</td><td>0.000000</td><td>0.000000</td><td>99.000000</td><td>27.000000</td><td>0.900000</td><td>135.000000</td><td>3.800000</td><td>10.300000</td></tr><tr><td>50%</td><td>55.000000</td><td>80.000000</td><td>1.020000</td><td>0.000000</td><td>0.000000</td><td>121.000000</td><td>42.000000</td><td>1.300000</td><td>138.000000</td><td>4.400000</td><td>12.650000</td></tr><tr><td>75%</td><td>64.500000</td><td>80.000000</td><td>1.020000</td><td>2.000000</td><td>0.000000</td><td>163.000000</td><td>66.000000</td><td>2.800000</td><td>142.000000</td><td>4.900000</td><td>15.000000</td></tr><tr><td>max</td><td>90.000000</td><td>180.000000</td><td>1.025000</td><td>5.000000</td><td>5.000000</td><td>490.000000</td><td>391.000000</td><td>76.000000</td><td>163.000000</td><td>47.000000</td><td>17.800000</td></tr></tbody></table>		age	bp	sg	al	su	bgr	bu	sc	sod	pot	hemo	count	391.000000	388.000000	353.000000	354.000000	351.000000	356.000000	381.000000	383.000000	313.000000	312.000000	348.000000	mean	51.483376	76.469072	1.017408	1.016949	0.450142	148.036517	57.425722	3.072454	137.528754	4.627244	12.526437	std	17.169714	13.683637	0.005717	1.352679	1.099191	79.281714	50.503006	5.741126	10.408752	3.193904	2.912587	min	2.000000	50.000000	1.005000	0.000000	0.000000	22.000000	1.500000	0.400000	4.500000	2.500000	3.100000	25%	42.000000	70.000000	1.010000	0.000000	0.000000	99.000000	27.000000	0.900000	135.000000	3.800000	10.300000	50%	55.000000	80.000000	1.020000	0.000000	0.000000	121.000000	42.000000	1.300000	138.000000	4.400000	12.650000	75%	64.500000	80.000000	1.020000	2.000000	0.000000	163.000000	66.000000	2.800000	142.000000	4.900000	15.000000	max	90.000000	180.000000	1.025000	5.000000	5.000000	490.000000	391.000000	76.000000	163.000000	47.000000	17.800000
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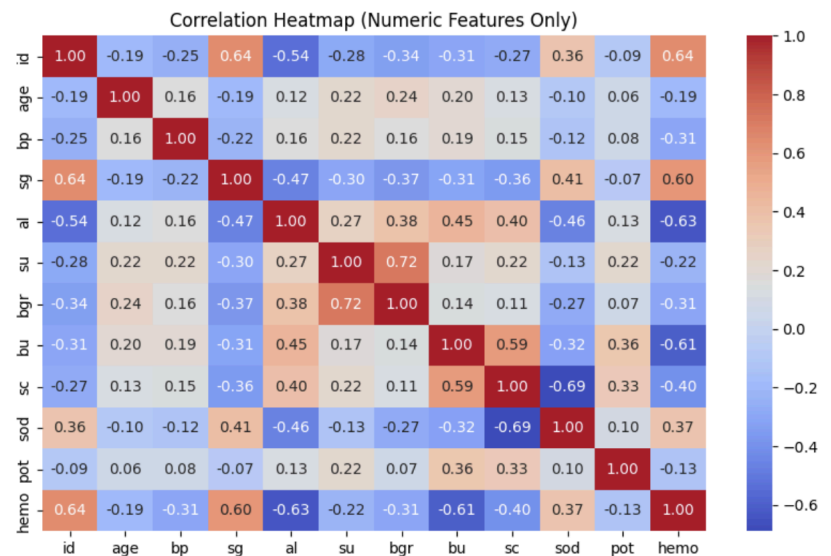
Univariate Analysis

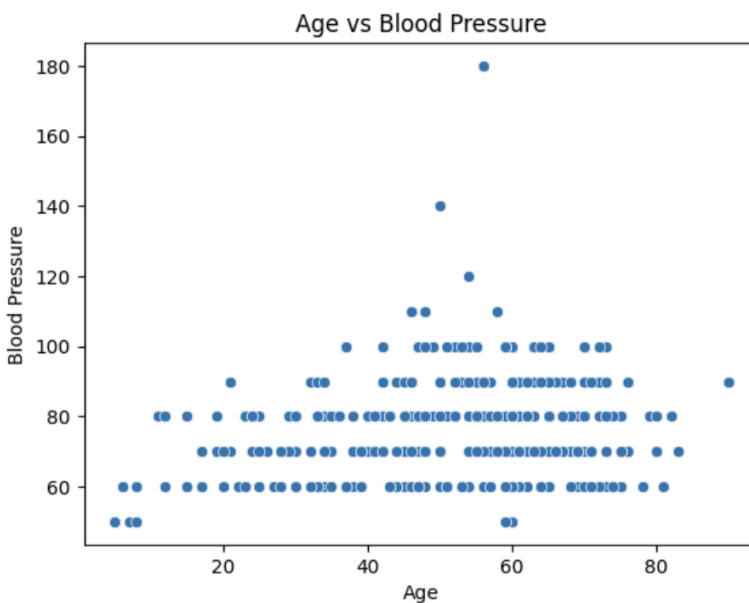
Mean age: 51.48337595907928
Median age: 55.0
Mode age: 60.0
Standard Deviation: 17.16971408926224

Bivariate Analysis

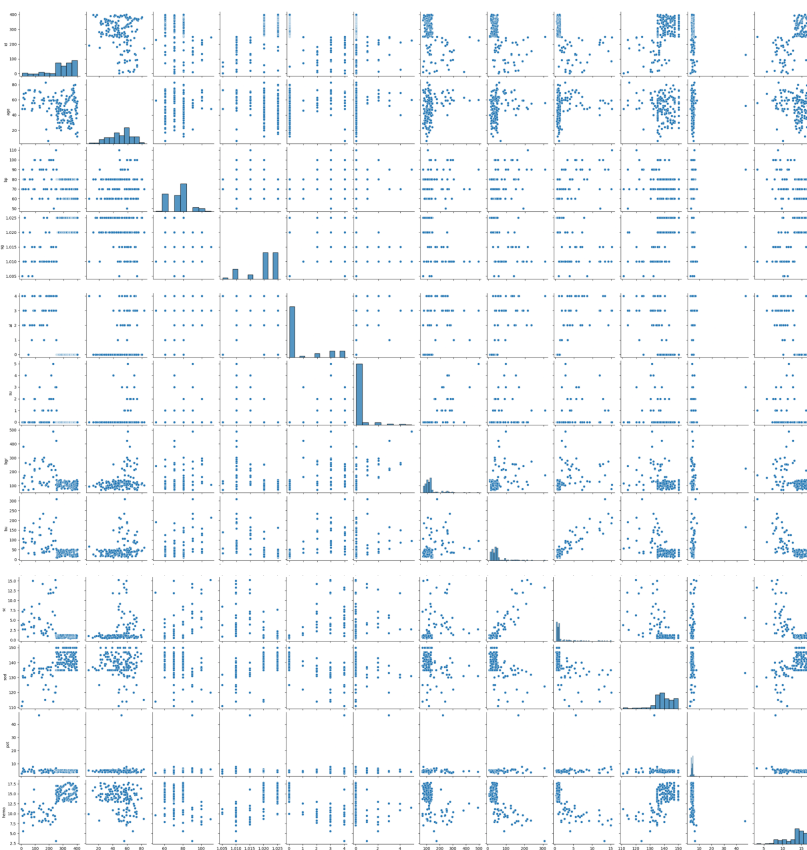
Correlation matrix:

	id	age	bp	sg	al	su	bgr	\
id	1.000000	-0.185308	-0.245744	0.642156	-0.541993	-0.283416	-0.338673	
age	-0.185308	1.000000	0.159480	-0.191096	0.122091	0.220866	0.244992	
bp	-0.245744	0.159480	1.000000	-0.218836	0.160689	0.222576	0.160193	
sg	0.642156	-0.191096	-0.218836	1.000000	-0.469760	-0.296234	-0.374710	
al	-0.541993	0.122091	0.160689	-0.469760	1.000000	0.269305	0.379464	
su	-0.283416	0.220866	0.222576	-0.296234	0.269305	1.000000	0.717827	
bgr	-0.338673	0.244992	0.160193	-0.374710	0.379464	0.717827	1.000000	
bu	-0.307175	0.196985	0.188517	-0.314295	0.453528	0.168583	0.143322	
sc	-0.268683	0.132531	0.146222	-0.361473	0.399198	0.223244	0.114875	
sod	0.364251	-0.100046	-0.116422	0.412190	-0.459896	-0.131776	-0.267848	
pot	-0.092347	0.058377	0.075151	-0.072787	0.129038	0.219450	0.066966	
hemo	0.640298	-0.192928	-0.306540	0.602582	-0.634632	-0.224775	-0.306189	
	bu	sc	sod	pot	hemo			
id	-0.307175	-0.268683	0.364251	-0.092347	0.640298			
age	0.196985	0.132531	-0.100046	0.058377	-0.192928			
bp	0.188517	0.146222	-0.116422	0.075151	-0.306540			
sg	-0.314295	-0.361473	0.412190	-0.072787	0.602582			
al	0.453528	0.399198	-0.459896	0.129038	-0.634632			
su	0.168583	0.223244	-0.131776	0.219450	-0.224775			
bgr	0.143322	0.114875	-0.267848	0.066966	-0.306189			
bu	1.000000	0.586368	-0.323054	0.357049	-0.610360			
sc	0.586368	1.000000	-0.690158	0.326107	-0.401670			
sod	-0.323054	-0.690158	1.000000	0.097887	0.365183			
pot	0.357049	0.326107	0.097887	1.000000	-0.133746			
hemo	-0.610360	-0.401670	0.365183	-0.133746	1.000000			





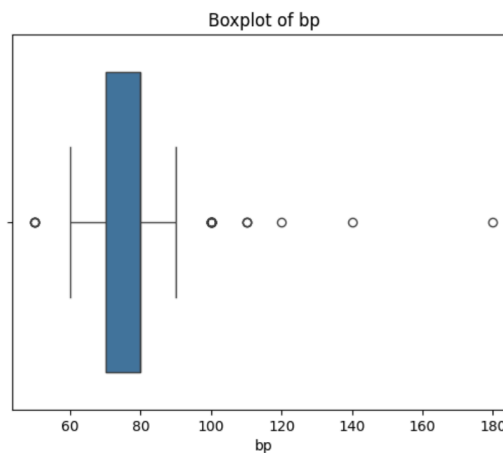
Multivariate Analysis



	id	age	bp	sg	al	\
classification						
ckd	124.427419	54.425000	79.705882	1.013937	1.721154	
ckd\t	133.500000	68.500000	70.000000	1.010000	2.000000	
notckd	324.500000	46.516779	71.351351	1.022414	0.000000	

	su	bgr	bu	sc	sod	\
classification						
ckd	0.770732	175.523810	72.656170	4.430720	133.882530	
ckd\t	0.000000	164.500000	41.000000	2.550000	135.500000	
notckd	0.000000	107.722222	32.798611	0.868966	141.731034	

	pot	hemo
classification		
ckd	4.883030	10.652217
ckd\t	4.500000	9.700000
notckd	4.337931	15.188194



Outliers and Anomalies

Outliers in 'bp':

	id	age	bp	sg	al	su	rbc	pc	pcc	\
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	
8	8	52.0	100.0	1.015	3.0	0.0	normal	abnormal	present	
18	18	60.0	100.0	1.025	0.0	3.0	NaN	normal	notpresent	
24	24	42.0	100.0	1.015	4.0	0.0	normal	abnormal	notpresent	
33	33	60.0	100.0	1.020	2.0	0.0	abnormal	abnormal	notpresent	
42	42	47.0	100.0	1.010	0.0	0.0	NaN	normal	notpresent	
51	51	54.0	100.0	1.015	3.0	0.0	NaN	normal	present	
59	59	59.0	100.0	NaN	NaN	NaN	NaN	NaN	notpresent	
73	73	NaN	100.0	1.015	2.0	0.0	abnormal	abnormal	notpresent	
87	87	70.0	100.0	1.005	1.0	0.0	normal	abnormal	present	
88	88	58.0	110.0	1.010	4.0	0.0	NaN	normal	notpresent	
90	90	63.0	100.0	1.010	2.0	2.0	normal	normal	notpresent	
93	93	73.0	100.0	1.010	3.0	2.0	abnormal	abnormal	present	
98	98	50.0	140.0	NaN	NaN	NaN	NaN	NaN	notpresent	
99	99	56.0	180.0	NaN	0.0	4.0	NaN	abnormal	notpresent	
107	107	55.0	100.0	1.015	1.0	4.0	normal	NaN	notpresent	
124	124	65.0	100.0	1.015	0.0	0.0	NaN	normal	notpresent	
131	131	5.0	50.0	1.010	0.0	0.0	NaN	normal	notpresent	
133	133	70.0	100.0	1.015	4.0	0.0	normal	normal	notpresent	
134	134	47.0	100.0	1.010	NaN	NaN	normal	NaN	notpresent	
146	146	53.0	100.0	1.010	1.0	3.0	abnormal	normal	notpresent	
175	175	60.0	50.0	1.010	0.0	0.0	NaN	normal	notpresent	
186	186	8.0	50.0	1.020	4.0	0.0	normal	normal	notpresent	
192	192	46.0	110.0	1.015	0.0	0.0	NaN	normal	notpresent	
196	196	49.0	100.0	1.010	3.0	0.0	abnormal	abnormal	notpresent	
198	198	59.0	100.0	1.020	4.0	2.0	normal	normal	notpresent	
210	210	59.0	100.0	1.015	4.0	2.0	normal	normal	notpresent	
211	211	54.0	120.0	1.015	0.0	0.0	NaN	normal	notpresent	
217	217	63.0	100.0	1.010	1.0	0.0	NaN	normal	notpresent	
226	226	64.0	100.0	1.015	4.0	2.0	abnormal	abnormal	notpresent	
229	229	59.0	50.0	1.010	3.0	0.0	normal	abnormal	notpresent	
233	233	51.0	100.0	1.015	2.0	0.0	normal	normal	notpresent	
234	234	37.0	100.0	1.010	0.0	0.0	abnormal	normal	notpresent	
238	238	72.0	100.0	NaN	NaN	NaN	NaN	NaN	notpresent	
245	245	48.0	100.0	NaN	NaN	NaN	NaN	NaN	notpresent	
246	246	48.0	110.0	1.015	3.0	0.0	abnormal	normal	present	

```

      ba ... pcv      wc      rc      htn      dm      cad      appet      pe      ane      \
1  notpresent ... 38      6000      NaN      no      no      no      good      no      no
8  notpresent ... 33      9600      4.0      yes      yes      no      good      no      yes
18 notpresent ... 37      11400      4.3      yes      yes      yes      good      no      no
24 present ... 39      8300      4.6      yes      no      no      poor      no      no
33 notpresent ... 29      NaN      NaN      yes      no      no      poor      no      no
42 notpresent ... 33      9200      4.5      yes      no      no      good      no      yes
51 notpresent ... 33      NaN      NaN      yes      yes      no      poor      yes      no
59 notpresent ... NaN      NaN      NaN      yes      yes      no      good      no      yes
73 notpresent ... 14      6300      NaN      yes      no      no      good      yes      yes
87 notpresent ... 32      5800      5      yes      yes      no      poor      no      no
88 notpresent ... NaN      13200      4.7      yes      \tyes      no      good      no      no
90 present ... 40      9800      4.2      yes      no      yes      good      no      no
93 notpresent ... 30      7000      3.2      yes      yes      yes      poor      no      no
98 notpresent ... 18      5800      2.3      yes      yes      no      poor      no      yes
99 notpresent ... 32      10400      4.2      yes      yes      no      poor      yes      no
107 notpresent ... 34      13600      4.4      yes      yes      no      good      no      no
124 notpresent ... 28      5500      3.6      yes      no      no      good      no      no
131 notpresent ... 36      12400      NaN      no      no      no      good      no      no
133 notpresent ... 37      \t8400      8.0      yes      no      no      good      no      no
134 notpresent ... 33      10200      3.8      no      yes      no      good      no      no
146 notpresent ... NaN      NaN      NaN      no      yes      no      good      no      no
175 notpresent ... NaN      4200      3.4      yes      no      no      good      no      no
186 notpresent ... NaN      NaN      NaN      no      no      no      good      yes      no
192 notpresent ... NaN      NaN      NaN      no      no      no      good      no      no
196 notpresent ... 24      9600      3.5      yes      yes      no      poor      yes      yes
198 notpresent ... 30      26400      3.9      yes      yes      no      poor      yes      no
210 notpresent ... 20      9800      3.9      yes      yes      yes      good      no      yes
211 notpresent ... NaN      NaN      NaN      no      no      no      good      no      no
217 notpresent ... 36      10500      4.3      no      yes      no      good      no      no
226 present ... 26      7500      3.4      yes      yes      no      good      yes      no
229 notpresent ... 31      15700      3.8      no      yes      no      good      yes      no
233 present ... NaN      NaN      NaN      no      no      no      poor      no      no
234 notpresent ... 44      4100      5.2      yes      no      no      good      no      no
238 notpresent ... 28      NaN      NaN      yes      yes      no      good      no      yes
245 notpresent ... 19      7200      2.6      yes      no      yes      poor      no      no
246 notpresent ... 26      5000      2.5      yes      no      yes      good      no      yes

```

```

classification
1      ckd
8      ckd
18     ckd
24     ckd
33     ckd
42     ckd
51     ckd
59     ckd
73     ckd
87     ckd
88     ckd
90     ckd
93     ckd
98     ckd
99     ckd
107    ckd
124    ckd
131    ckd
133    ckd
134    ckd
146    ckd
175    ckd
186    ckd
192    ckd
196    ckd
198    ckd
210    ckd
211    ckd
217    ckd
226    ckd
229    ckd
233    ckd
234    ckd
238    ckd
245    ckd
246    ckd

[36 rows x 26 columns]

Original size: 400 rows
After removing outliers in 'bp': 352 rows

```

Data Preprocessing Code Screenshots

Loading Data

```
dataset_path = 'chronickidneydisease.csv'
try:
    df = pd.read_csv(dataset_path)
    print(f"\nDataset '{dataset_path}' loaded successfully.")
    print(f"Initial dataset shape: {df.shape}")
except FileNotFoundError:
    print(f"ERROR: Dataset '{dataset_path}' not found.")
    print("Please ensure you have downloaded 'chronickidneydisease.csv' and placed it in the 'CKD_Prediction_App/dataset/' folder.")
    exit()
except Exception as e:
    print(f"An error occurred while reading the dataset: {e}")
    exit()
```

Handling Missing Data

```
print("\n--- Missing Values Count per Column (After initial '?' handling) ---")
missing_values_count = df.isnull().sum()
missing_values_count = missing_values_count[missing_values_count > 0].sort_values(ascending=False)
print(missing_values_count)

print("\n--- Missing Values Percentage per Column (After initial '?' handling) ---")
missing_percentage = (df.isnull().sum() / len(df)) * 100
missing_percentage = missing_percentage[missing_percentage > 0].sort_values(ascending=False)
print(missing_percentage)

print("\n--- Visualizing Missing Value Pattern (Matrix) ---")
msno.matrix(df, figsize=(15, 7), color=(0.2, 0.4, 0.6))
plt.title('Missing Value Matrix', fontsize=20)
plt.show()
```

Data Transformation

```
from sklearn.preprocessing import MinMaxScaler

scaler = MinMaxScaler()

# Replace with your actual numeric columns
numeric_cols = ['age', 'bp', 'bgr', 'sc']

df[numeric_cols] = scaler.fit_transform(df[numeric_cols])
print("Min-Max scaling applied.")

from sklearn.preprocessing import StandardScaler

scaler = StandardScaler()
df[numeric_cols] = scaler.fit_transform(df[numeric_cols])
print("Standard scaling applied.")

Min-Max scaling applied.
Standard scaling applied.
```

Feature Engineering

```
# Creating a risk_score by averaging 'bp' and 'bgr'
df['risk_score'] = (df['bp'] + df['bgr']) / 2

df['age_group'] = pd.cut(df['age'], bins=[0, 30, 50, 100], labels=['Young', 'Middle-aged', 'Senior'])
```

Save Processed Data

```
df.to_csv('cleaned_ckd_data.csv', index=False)
print("Data saved to cleaned_ckd_data.csv")

Data saved to cleaned_ckd_data.csv
```