

## Data Collection and Preprocessing Phase

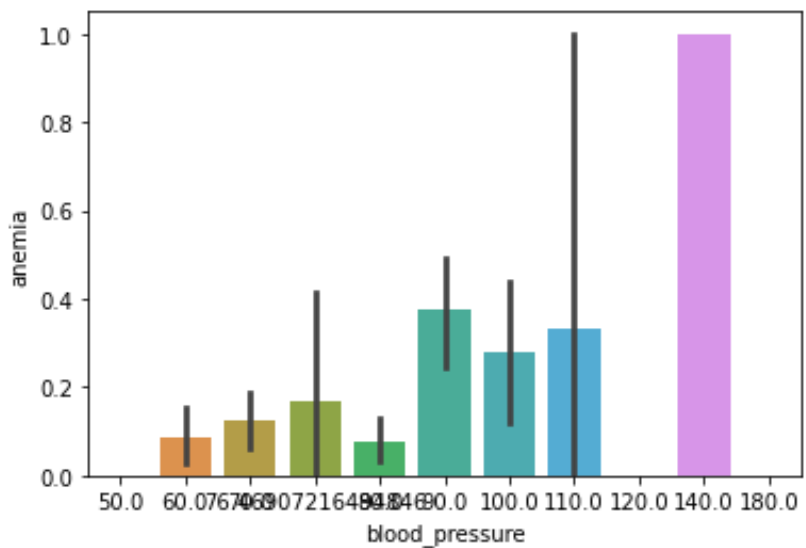
Date	15 July 2024
Team ID	739673
Project Title	Early Prediction Of Chronic Kidney Disease
Maximum Marks	6 Marks

## Data Exploration and Preprocessing Template

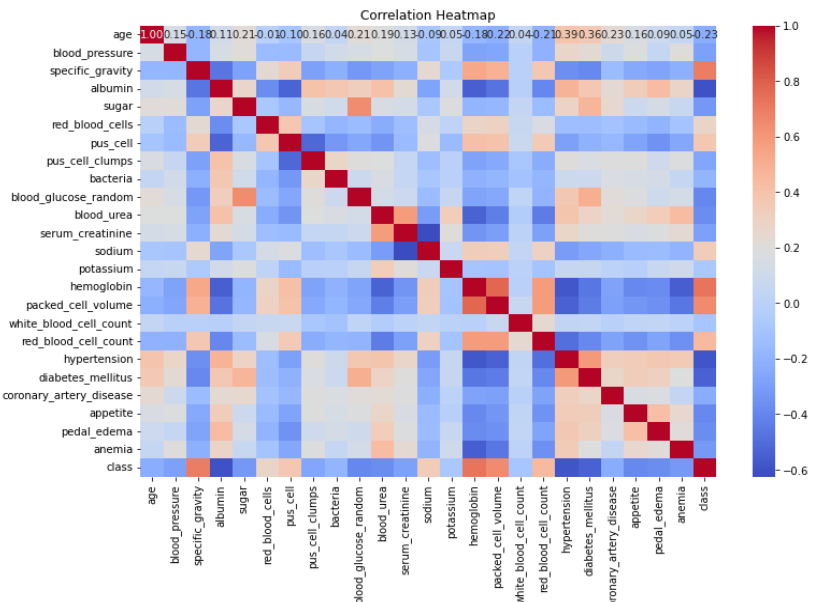
Identifies data sources, assesses quality issues like missing values and duplicates, and implements resolution plans to ensure accurate and reliable analysis.

Section	Description																																																																																																																																				
Data Overview	<div>Dimensions</div> <div>399rows x 26columns</div> <table><tr><th></th><th>id</th><th>age</th><th>bp</th><th>sg</th><th>al</th><th>su</th><th>rbc</th><th>pc</th><th>pcc</th><th>ba</th><th>...</th><th>pcv</th><th>wc</th><th>rc</th><th>htn</th><th>dm</th><th>cad</th><th>appet</th><th>pe</th><th>ane</th><th>classification</th></tr><tr><td>0</td><td>0</td><td>48.0</td><td>80.0</td><td>1.020</td><td>1.0</td><td>0.0</td><td>NaN</td><td>normal</td><td>notpresent</td><td>notpresent</td><td>...</td><td>44</td><td>7800</td><td>5.2</td><td>yes</td><td>yes</td><td>no</td><td>good</td><td>no</td><td>no</td><td>ckd</td></tr><tr><td>1</td><td>1</td><td>7.0</td><td>50.0</td><td>1.020</td><td>4.0</td><td>0.0</td><td>NaN</td><td>normal</td><td>notpresent</td><td>notpresent</td><td>...</td><td>38</td><td>6000</td><td>NaN</td><td>no</td><td>no</td><td>no</td><td>good</td><td>no</td><td>no</td><td>ckd</td></tr><tr><td>2</td><td>2</td><td>62.0</td><td>80.0</td><td>1.010</td><td>2.0</td><td>3.0</td><td>normal</td><td>normal</td><td>notpresent</td><td>notpresent</td><td>...</td><td>31</td><td>7500</td><td>NaN</td><td>no</td><td>yes</td><td>no</td><td>poor</td><td>no</td><td>yes</td><td>ckd</td></tr><tr><td>3</td><td>3</td><td>48.0</td><td>70.0</td><td>1.005</td><td>4.0</td><td>0.0</td><td>normal</td><td>abnormal</td><td>present</td><td>notpresent</td><td>...</td><td>32</td><td>6700</td><td>3.9</td><td>yes</td><td>no</td><td>no</td><td>poor</td><td>yes</td><td>yes</td><td>ckd</td></tr><tr><td>4</td><td>4</td><td>51.0</td><td>80.0</td><td>1.010</td><td>2.0</td><td>0.0</td><td>normal</td><td>normal</td><td>notpresent</td><td>notpresent</td><td>...</td><td>35</td><td>7300</td><td>4.6</td><td>no</td><td>no</td><td>no</td><td>good</td><td>no</td><td>no</td><td>ckd</td></tr></table>		id	age	bp	sg	al	su	rbc	pc	pcc	ba	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane	classification	0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	...	44	7800	5.2	yes	yes	no	good	no	no	ckd	1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	...	38	6000	NaN	no	no	no	good	no	no	ckd	2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	...	31	7500	NaN	no	yes	no	poor	no	yes	ckd	3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32	6700	3.9	yes	no	no	poor	yes	yes	ckd	4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	...	35	7300	4.6	no	no	no	good	no	no	ckd
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Univariate Analysis	<div><div><div>Distribution of age</div></div><div><div>Distribution of blood pressure</div></div><div><div>Distribution of sugar</div></div></div>																																																																																																																																				

## Bivariate Analysis



## Multivariate Analysis



## Outliers and Anomalies

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## Data Preprocessing Code Screenshots

### Loading Data

```
# Load dataset
filename = "C:\\Users\\soumy\\OneDrive\\Desktop\\mini p\\data.csv"
data = pd.read_csv(filename)
```

Handling Missing Data	<pre># Handle missing values data = data.apply(lambda x: x.fillna(x.mean()) if x.dtype.kind in 'biufc' else x.fillna(x.mode().iloc[0]))</pre>
Data Transformation	<pre># Clean categorical variables with incorrect values data['class'] = data['class'].replace("ckd\t", "ckd") data['coronary_artery_disease'] = data['coronary_artery_disease'].replace("\tno", 'no') data['diabetes_mellitus'] = data['diabetes_mellitus'].replace(to_replace={"\tno": 'no', '\tyes': 'yes', 'yes': 'yes'})</pre> <pre># Encode categorical variables cat_cols = data.select_dtypes(include=['object']).columns label_encoders = {} for col in cat_cols:     le = LabelEncoder()     data[col] = le.fit_transform(data[col])     label_encoders[col] = le</pre>
Feature Engineering	Attached code in final submission.
Save Processed Data	-