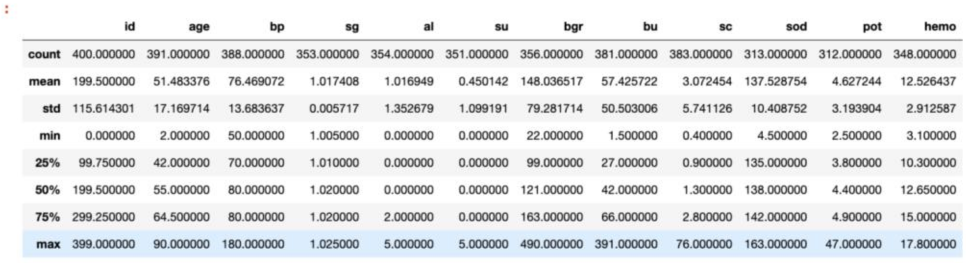
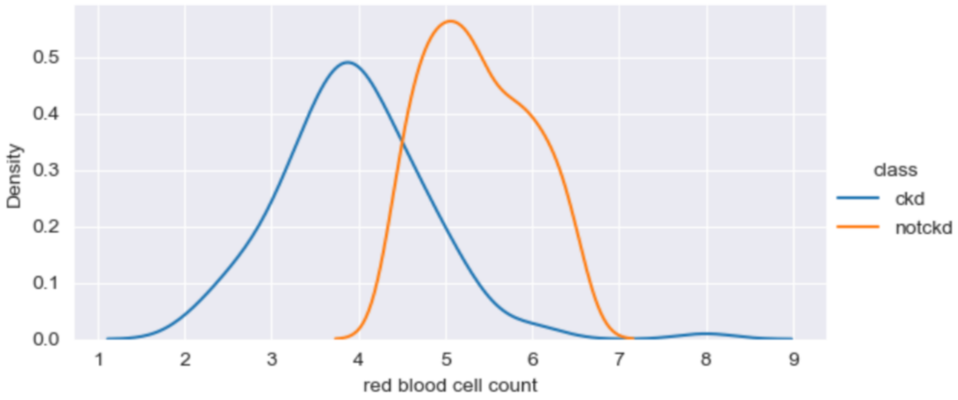
Data Collection and Preprocessing Phase

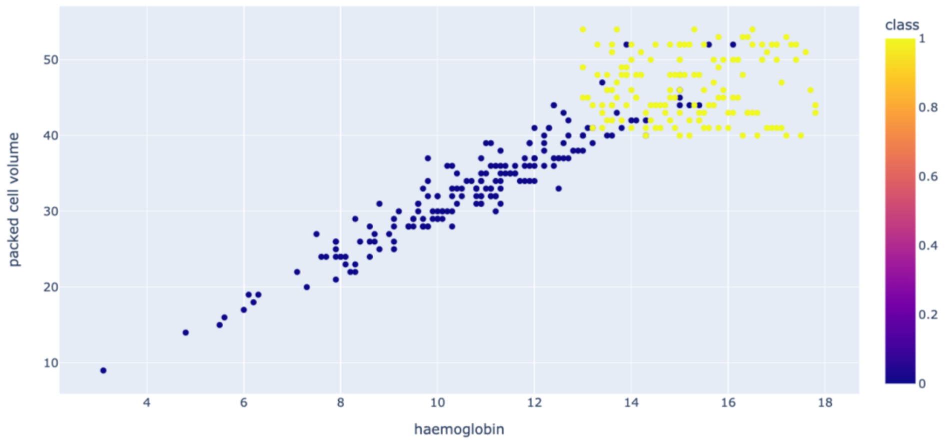
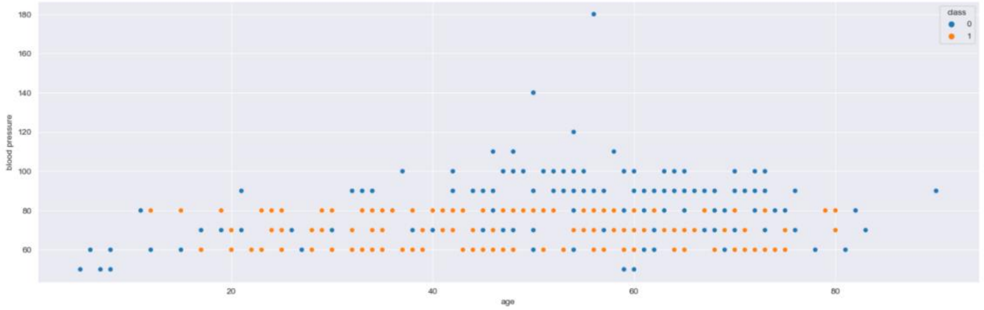
Date	08 July 2024
Team ID	SWTID1720174514
Project Title	Early Prediction Of Chronic Kidney Disease Using Machine Learning
Maximum Marks	6 Marks

Data Exploration and Preprocessing Template

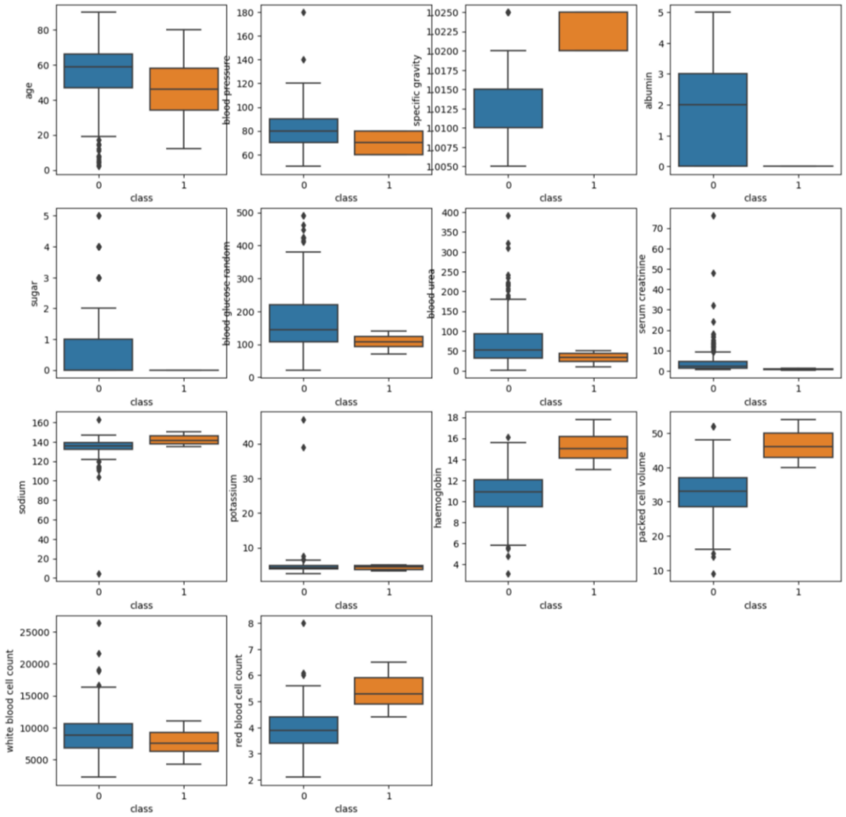
The variables of the dataset will be statistically examined to find general trends and extremes, and for this, a tool such as Python used for preprocessing like normalization and feature engineering activities. Data cleaning will find missing value analysis it determines the ways of handling missing values and outliers to improve the quality of the data in the upcoming analysis or modeling process.

Section	**Description**
Data Overview	
Univariate Analysis	

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

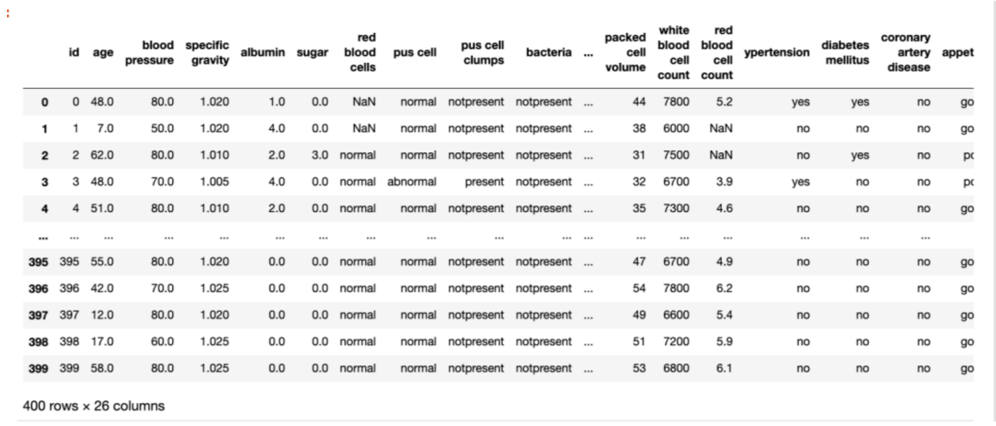
Bivariate Analysis	
Multivariate Analysis	`<Axes: xlabel='age', ylabel='blood pressure'>` 

Outliers and Anomalies



Data Preprocessing Code Screenshots

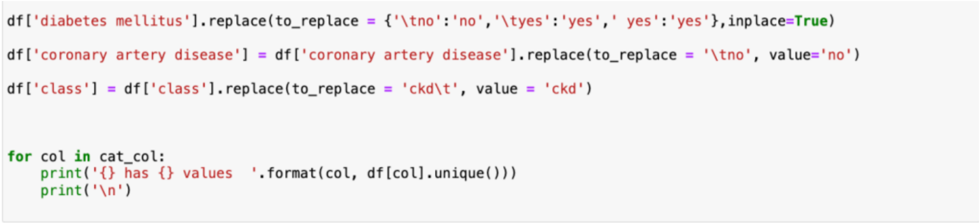
Loading Data



	id	age	blood pressure	specific gravity	albumin	sugar	red blood cells	pus cell	pus cell clumps	bacteria	...	packed cell volume	white blood cell count	red blood cell count	ypertension	diabetes mellitus	coronary artery disease	appet
0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	...	44	7800	5.2	yes	yes	no	go
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	...	38	6000	NaN	no	no	no	go
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	...	31	7500	NaN	no	yes	no	pc
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32	6700	3.9	yes	no	no	pc
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	...	35	7300	4.6	no	no	no	go
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
395	395	55.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	...	47	6700	4.9	no	no	no	go
396	396	42.0	70.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	54	7800	6.2	no	no	no	go
397	397	12.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	...	49	6600	5.4	no	no	no	go
398	398	17.0	60.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	51	7200	5.9	no	no	no	go
399	399	58.0	80.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	53	6800	6.1	no	no	no	go

400 rows × 26 columns

Handling Missing Data



```
df['diabetes mellitus'].replace(to_replace = {'\tno':'no','\tyes':'yes',' yes':'yes'},inplace=True)

df['coronary artery disease'] = df['coronary artery disease'].replace(to_replace = '\tno', value='no')

df['class'] = df['class'].replace(to_replace = 'ckd\t', value = 'ckd')



for col in cat_col:
    print('{} has {} values  '.format(col, df[col].unique()))
    print('\n')
```

Data Transformation	-
Feature Engineering	-
Save Processed Data	-