



Data Collection and Preprocessing Phase

Date	08 July 2024
Team ID	SWTID1720174640
Project Title	Early Prediction of Chronic Kidney Disease
Maximum Marks	6 Marks

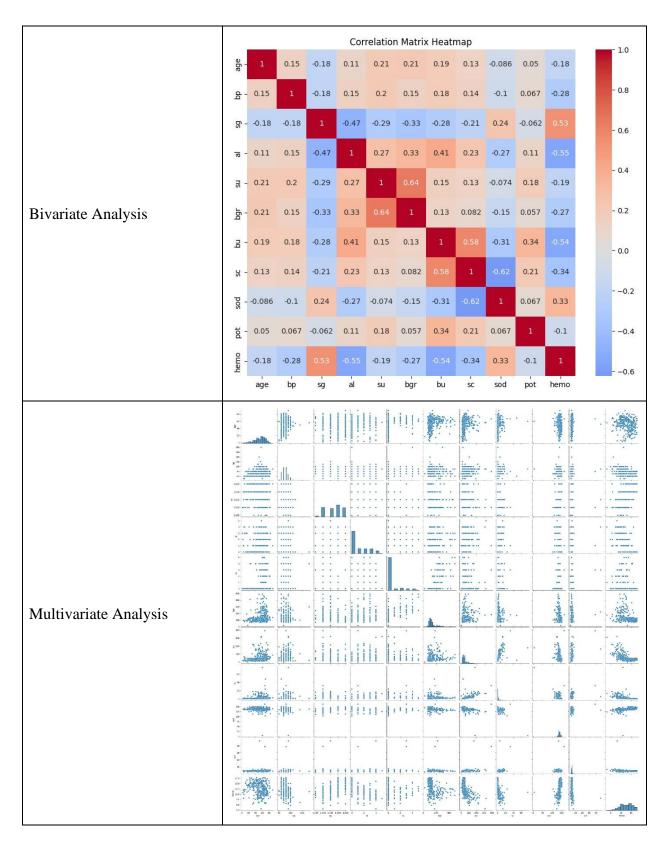
Data Exploration and Preprocessing Template

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	The dataset `chronickidneydisease.csv` has 400 rows and 26 columns, including both numerical and categorical data. It contains various patient attributes like age, blood pressure, specific gravity, albumin, sugar, red blood cells, hemoglobin, and more, along with a classification label indicating chronic kidney disease status. There are missing values in several columns. Basic statistics show that attributes like age, blood pressure, and others have varying ranges and distributions.	
Univariate Analysis	sns.countplot(data['classification']) **CAXes: xlabel='count', ylabel='classification'> /usr/local/lib/python3.l8/dist-packages/IPython/core/events.py:89: UserWarning: Glyph 9 () missing from current font. func('args, "'wargs) /usr/local/lib/python3.l8/dist-packages/IPython/core/pylabtools.py:151: UserWarning: Glyph 9 () missing from current font. fig.canvas.print_figure(bytes_lo, "*way) ckd - ckd - notckd - notckd - 0 50 100 150 200 250	











Data Preprocessing Code Screenshots Loading Data classification 0 dtype: int64 for i in data.columns: Handling Missing Data if data[i].dtype == 'object': data[i] = data[i].fillna(data[i].mode()[0]) data[i] = data[i].fillna(data[i].mean()) [] # Scaling from sklearn.preprocessing import StandardScaler sc = StandardScaler() **Data Transformation** x train = sc.fit transform(x train) x_test = sc.transform(x_test) [] # as id has no imp we can drop it Feature Engineering data.drop(['id'],axis = 1,inplace = True) # saving the result in a new datafram output_path = 'transformed_chronickidneydisease.csv' data.to_csv(output_path, index=False) Save Processed Data print(f"Transformed dataframe saved to {output_path}")

Transformed dataframe saved to transformed_chronickidneydisease