



## **Data Collection and Preprocessing Phase**

Date	16 June 2025
Team ID	SWTID1749709635
Project Title	Mental Health Prediction
Maximum Marks	6 Marks

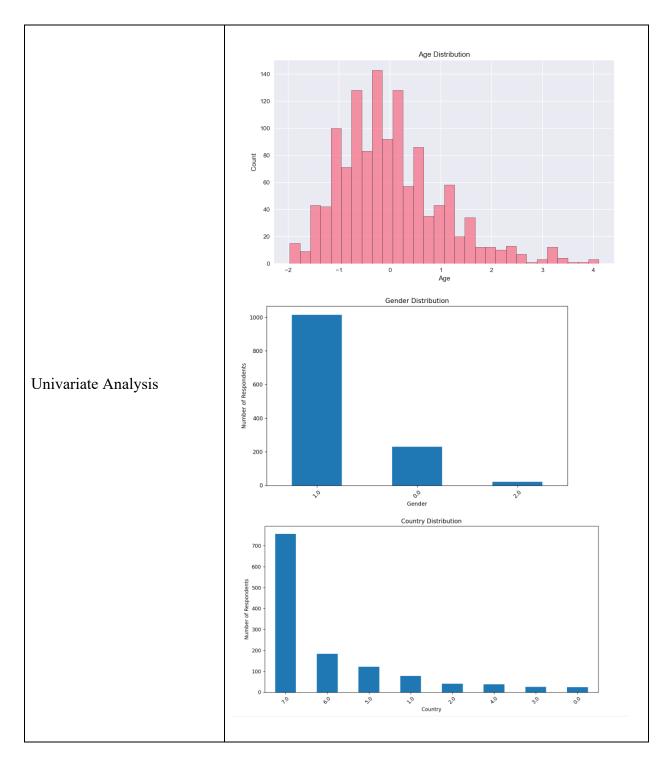
## **Data Exploration and Preprocessing Template**

Dataset variables will be statistically analyzed to identify patterns and outliers, with Python employed for preprocessing tasks such as normalization and feature engineering. Data cleaning will address missing values, duplicates, and inconsistencies, ensuring quality for subsequent analysis and modeling, and forming a strong foundation for actionable insights and accurate mental health risk predictions.

Section	Description
	Dimension: 1260 rows x 27 columns Descriptive statistics:
Data Overview	Count 1245.000000 mean 32.060241 std 7.352870 min 5.000000 25% 27.000000 50% 31.000000 75% 36.000000 max 72.000000

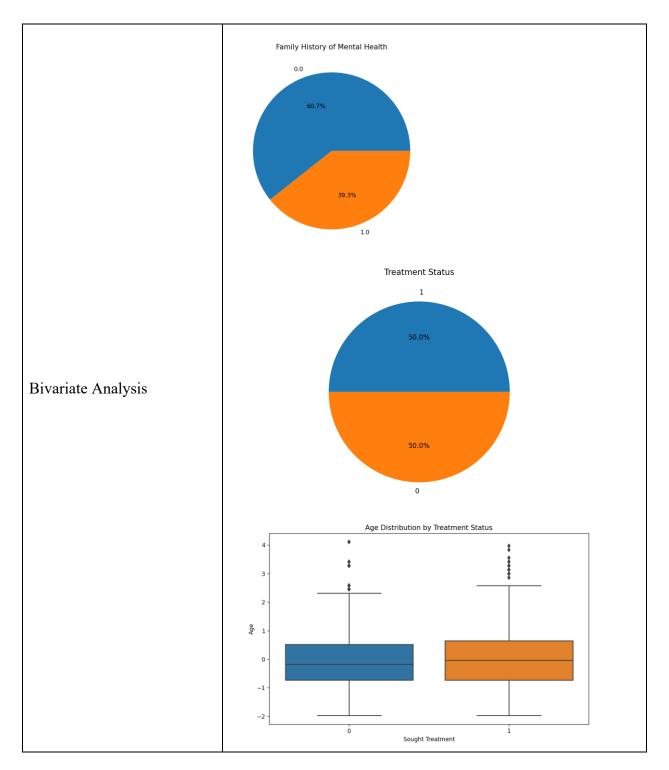






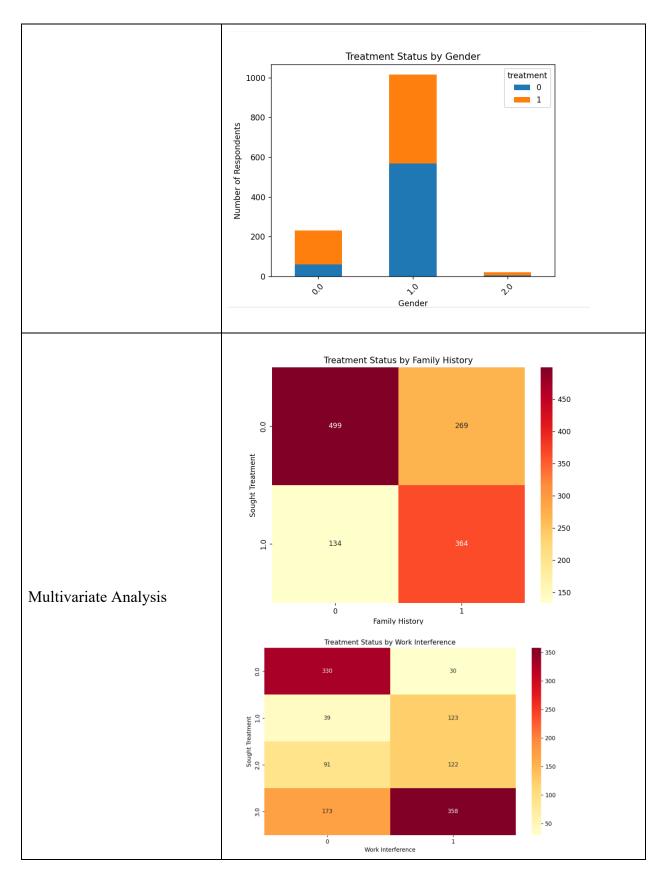






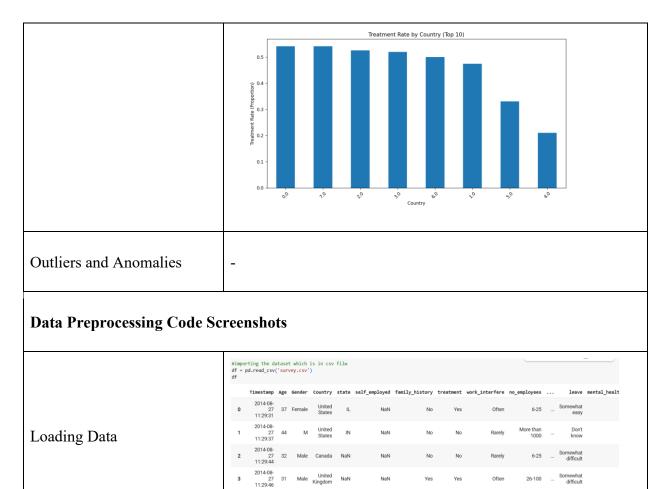












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Handling Missing Data

# Drop irrelevant columns
df\_processed = df\_processed.drop(columns=['Timestamp', 'comments'])

# Handle missing values
df\_processed['state'] = df\_processed['state'].fillna('Unknown')
df\_processed['self\_employed'] = df\_processed['self\_employed'].fillna('No')
df\_processed['work\_interfere'] = df\_processed['work\_interfere'].fillna('Never')

df\_processed = df\_processed[(df\_processed['Age'] >= 0) & (df\_processed['Age'] <= 100)]
df\_processed['Gender'] = df\_processed['Gender'].str.strip() # Remove any leading or trailing spaces</pre>





	# Standardize entries
Data Transformation	# Standardize entries gender mapping = {     Wh: "Male, "male': "Male', "Male-ish': "Male', "maile': "Male',     "Trans-female': 'Trans', 'Cis Female'; 'Female', 'Female',     "Something kinda male': 'Other', 'Cis Fale': "Male', 'Male', 'Male', 'Male', 'Male', 'Male', 'Male', 'Male', 'Wale', 'Gender', 'Wake': 'Male',     "Nah': 'Other', 'All': 'Other', 'Enby': 'Other', 'Filuid': 'Other',     "Genderqueer': 'Non-binary', 'Female' ': 'Female', 'Marogyne': 'Other',     "Agender': Non-binary', 'Female ': 'Female', 'Marogyne': 'Other',     "male leaning androgynous': 'Male', 'Male': 'Male', 'Male
	<pre># Encode target le_target = LabelEncoder() y_encoded = le_target.fit_transform(df_processed['treatment'])</pre>
Feature Engineering	Attached the codes in final submission.
Save Processed Data	-