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Problem Statement

Objective

The goal of this project is to create a model that can predict the presence of diabetes in individuals by analyzing data from the Behavioral Risk Factor Surveillance System (BRFSS) 2015 survey. The main objective is to accurately forecast whet prediabetes (*Outcome* = 1) or no diabetes (*Outcome* = 0) based on specific health measurements and indicators.

Background

Diabetes poses a significant challenge to public health, impacting numerous Americans and leading to severe health complications and considerable financial strains. Timely identification and intervention can greatly enhance patient outcomes t appropriate treatments.

This initiative intends to harness machine learning methods to bolster the early recognition of diabetes, potentially assisting healthcare professionals in making well informed choices and enhancing patient well being.

Health Indicators and Indicators for Diagnosis

The model will consider a range of health indicators, such as high blood pressure, elevated cholesterol levels, recent cholesterol screenings, BMI, smoking habits, history of stroke or heart disease/attack, level of physical activity, consumption o access to healthcare services, financial obstacles hindering doctor visits, overall health condition perception, number of days with mental or physical health issues, mobility difficulties, gender identity, age groupings education attainment levels a

These signs offer a detailed overview of a person's well being and habits, which are essential for predicting the likelihood of developing diabetes.

Data Overview

The information utilized in this study is a refined and organized version of the BRFSS 2015 survey data found on Kaggle. It encompasses responses from more than 253,680 individuals and incorporates various health related measurements. Tl indicates whether an individual does not have diabetes (0), has prediabetes (1) or has diabetes (2).

The dataset named "diabetes_012_health_indicators_BRFSS2015.csv" was selected for specific reasons:

- **Diverse Target Variable:** This dataset offers a three class target variable (no diabetes, prediabetes and diabetes), enabling a thorough examination and forecasting of different diabetes stages.
- **Substantial Sample Size:** With 253,680 survey responses, this dataset presents a significant sample size that boosts the trustworthiness and applicability of the predictive model.
- **Extensive Health Indicators:** Featuring 21 feature variables encompassing various health indicators, this dataset establishes a comprehensive foundation for predictive analysis.
- **Natural Class Imbalance:** In contrast to the "diabetes_binary_5050split_health_indicators_BRFSS2015.csv" dataset with an even split, this dataset mirrors the typical class imbalance observed in real world settings. This characteristic sup performance assessment.

Research Inquiries

This project seeks to investigate several primary research queries;

1. Can survey data effectively forecast an individual's diabetes status?
2. What are the most influential risk factors for diabetes prediction?
3. Can a subset of the characteristics accurately predict the likelihood of developing diabetes?
4. Is it possible to develop a concise set of survey questions for efficient screening of diabetes risk?

Significance

Developing a dependable model for diagnosing diabetes can significantly impact public health. It can aid in identifying high risk individuals, enabling prompt intervention and ultimately leading to improved disease management. This endeavor nc model but also aims to comprehend the fundamental elements contributing to diabetes risk, offering valuable insights for healthcare professionals and policymakers.

In [6]:
```
# pip install -r Requirements.txt
```

In [8]:
```
pip install dataprep --quiet
```

```
^C
Note: you may need to restart the kernel to use updated packages.
```

In [72]:
```
import random
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
import warnings
from sklearn.model_selection import train_test_split, GridSearchCV, cross_val_score, cross_validate
from sklearn.preprocessing import StandardScaler, LabelEncoder
from sklearn.impute import SimpleImputer
from sklearn.decomposition import PCA
from sklearn.utils.class_weight import compute_class_weight
from sklearn.ensemble import RandomForestClassifier
from sklearn.naive_bayes import MultinomialNB, GaussianNB
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
from sklearn.metrics import classification_report, mean_squared_error, r2_score, f1_score, accuracy_score, precision_score, recall_score, confusion_matrix, ConfusionMatrixDisplay, roc_auc_score, roc_curve, auc, precision_recall_curve
from xgboost import XGBClassifier
from imblearn.over_sampling import SMOTE
from imblearn.under_sampling import RandomUnderSampler
from imblearn.combine import SMOTEENN
from yellowbrick.classifier import ROCAUC
from scipy.stats import chi2_contingency, ttest_ind
import optuna

# supress warnings
warnings.filterwarnings("ignore")

# from dataprep.eda import *
# from dataprep.datasets import load_dataset
# from dataprep.eda import plot, plot_correlation, plot_missing, plot_diff, create_report #

# Apply the seaborn theme
sns.set_theme() #overwrite default Matplotlib styling parameters
```

Data understanding (EDA)

In [10]:
```
# Load data and print dataframe shape
file_path = "diabetes_012_health_indicators_BRFSS2015.csv"
df = pd.read_csv(file_path)

shape = df.shape
print("Shape of the dataframe (row, col):",shape,"\r\n")

# Show the dataframe
pd.set_option('display.max_columns', None)
df
```

```
Shape of the dataframe (row, col): (253680, 22)
```

Out[10]:

	Diabetes_012	HighBP	HighChol	CholCheck	BMI	Smoker	Stroke	HeartDiseaseorAttack	PhysActivity	Fruits	Veggies	HvyAlcoholConsump	AnyHealthcare	NoDocbcCost	GenHlth	MentHlth	PhysHlth	DiffWalk	Sex	Age	Education
0	0.0	1.0	1.0	1.0	40.0	1.0	0.0	0.0	0.0	0.0	1.0	0.0	1.0	0.0	5.0	18.0	15.0	1.0	0.0	9.0	4.0
1	0.0	0.0	0.0	0.0	25.0	1.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	1.0	3.0	0.0	0.0	0.0	0.0	7.0	6.0
2	0.0	1.0	1.0	1.0	28.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	1.0	1.0	5.0	30.0	30.0	1.0	0.0	9.0	4.0
3	0.0	1.0	0.0	1.0	27.0	0.0	0.0	0.0	1.0	1.0	1.0	0.0	1.0	0.0	2.0	0.0	0.0	0.0	0.0	11.0	3.0
4	0.0	1.0	1.0	1.0	24.0	0.0	0.0	0.0	1.0	1.0	1.0	0.0	1.0	0.0	2.0	3.0	0.0	0.0	0.0	11.0	5.0
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
253675	0.0	1.0	1.0	1.0	45.0	0.0	0.0	0.0	0.0	1.0	1.0	0.0	1.0	0.0	3.0	0.0	5.0	0.0	1.0	5.0	6.0
253676	2.0	1.0	1.0	1.0	18.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	4.0	0.0	0.0	1.0	0.0	11.0	2.0
253677	0.0	0.0	0.0	1.0	28.0	0.0	0.0	0.0	1.0	1.0	0.0	0.0	1.0	0.0	1.0	0.0	0.0	0.0	0.0	2.0	5.0
253678	0.0	1.0	0.0	1.0	23.0	0.0	0.0	0.0	0.0	1.0	1.0	0.0	1.0	0.0	3.0	0.0	0.0	0.0	1.0	7.0	5.0
253679	2.0	1.0	1.0	1.0	25.0	0.0	0.0	1.0	1.0	1.0	0.0	0.0	1.0	0.0	2.0	0.0	0.0	0.0	0.0	9.0	6.0

253680 rows × 22 columns

In [ ]:
```
display(df.info())
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 253680 entries, 0 to 253679
Data columns (total 22 columns):
 #   Column                Non-Null Count   Dtype  
---  ------                --------------   -----  
 0   Diabetes_012          253680 non-null  float64
 1   HighBP                253680 non-null  float64
 2   HighChol              253680 non-null  float64
 3   CholCheck             253680 non-null  float64
 4   BMI                   253680 non-null  float64
 5   Smoker                253680 non-null  float64
 6   Stroke                253680 non-null  float64
 7   HeartDiseaseorAttack  253680 non-null  float64
 8   PhysActivity          253680 non-null  float64
 9   Fruits                253680 non-null  float64
 10  Veggies               253680 non-null  float64
 11  HvyAlcoholConsump     253680 non-null  float64
 12  AnyHealthcare         253680 non-null  float64
 13  NoDocbcCost           253680 non-null  float64
 14  GenHlth               253680 non-null  float64
 15  MentHlth              253680 non-null  float64
 16  PhysHlth              253680 non-null  float64
 17  DiffWalk              253680 non-null  float64
 18  Sex                   253680 non-null  float64
 19  Age                   253680 non-null  float64
 20  Education             253680 non-null  float64
 21  Income                253680 non-null  float64
dtypes: float64(22)
memory usage: 42.6 MB
None
```

Detailed Variable Descriptions

1. **Diabetes_012** :
   - Categorical: 0 = No diabetes, 1 = Prediabetes, 2 = Diabetes.
2. **HighBP** :
   - Binary: 0 = No high blood pressure, 1 = High blood pressure.
3. **HighChol** :
   - Binary: 0 = No high cholesterol, 1 = High cholesterol.
4. **CholCheck** :
   - Binary: 0 = No cholesterol check in the last 5 years, 1 = Cholesterol check in the last 5 years.
5. **BMI** (Body Mass Index):
   - Continuous: A key indicator of body fat based on height and weight.
6. **Smoker** :
   - Binary: 0 = Non-smoker, 1 = Smoker (100+ cigarettes in life).
7. **Stroke** :
   - Binary: 0 = No stroke, 1 = Stroke.
8. **HeartDiseaseorAttack** :
   - Binary: 0 = No heart disease or attack, 1 = Heart disease or attack.
9. **PhysActivity** :
   - Binary: 0 = No physical activity, 1 = Physical activity.
10. **Fruits** :
    - Binary: 0 = Less than once per day, 1 = One or more times per day.
11. **Veggies** :
    - Binary: 0 = Less than once per day, 1 = One or more times per day.
12. **HvyAlcoholConsump** :
    - Binary: 0 = Not a heavy drinker, 1 = Heavy drinker (adult men >14 drinks/week, women >7 drinks/week).
13. **AnyHealthcare** :
    - Binary: 0 = No healthcare coverage, 1 = Healthcare coverage.
14. **NoDocbcCost** :
    - Binary: 0 = No cost barriers to healthcare, 1 = Cost barriers to healthcare.
15. **GenHlth** :
    - Ordinal (1-5): 1 = Excellent, 5 = Poor general health.
16. **MentHlth** :
    - Continuous (0-30 days): Number of days with poor mental health.
17. **PhysHlth** :
    - Continuous (0-30 days): Number of days with poor physical health.
18. **DiffWalk** :
    - Binary: 0 = No difficulty walking/climbing stairs, 1 = Difficulty.
19. **Sex** :
    - Binary: 0 = Female, 1 = Male.
20. **Age** :
    - Categorical (1-13 age groups): 1 = 18-24 years, 9 = 60-64 years, 13 = 80 or older.
21. **Education** :
    - Ordinal (1-6): 1 = No schooling, 6 = College graduate.
22. **Income** :
    - Ordinal (1-8): 1 = Less than 10, 000, 8 = 75,000 or more.

In [ ]:

In [ ]:
```
print(df.describe())
```

```
       Diabetes_012        HighBP      HighChol     CholCheck  \
count  253680.000000  253680.000000  253680.000000  253680.000000
mean        0.296921       0.429001       0.424121       0.962670
std         0.698160       0.494934       0.494210       0.189571
min         0.000000       0.000000       0.000000       0.000000
25%         0.000000       0.000000       0.000000       1.000000
50%         0.000000       0.000000       0.000000       1.000000
75%         0.000000       1.000000       1.000000       1.000000
max         2.000000       1.000000       1.000000       1.000000

                BMI         Smoker         Stroke  HeartDiseaseorAttack  \
count  253680.000000  253680.000000  253680.000000         253680.000000
mean       28.382364       0.443169       0.040571              0.094186
std         6.608694       0.496761       0.197294              0.292087
min        12.000000       0.000000       0.000000              0.000000
25%        24.000000       0.000000       0.000000              0.000000
50%        27.000000       0.000000       0.000000              0.000000
75%        31.000000       1.000000       0.000000              0.000000
max        98.000000       1.000000       1.000000              1.000000

       PhysActivity         Fruits        Veggies  HvyAlcoholConsump  \
count  253680.000000  253680.000000  253680.000000      253680.000000
mean        0.756544       0.634256       0.811420           0.056197
std         0.429169       0.481639       0.391175           0.230302
min         0.000000       0.000000       0.000000           0.000000
25%         1.000000       0.000000       1.000000           0.000000
50%         1.000000       1.000000       1.000000           0.000000
75%         1.000000       1.000000       1.000000           0.000000
max         1.000000       1.000000       1.000000           1.000000

       AnyHealthcare    NoDocbcCost        GenHlth       MentHlth  \
count  253680.000000  253680.000000  253680.000000  253680.000000
mean        0.951053       0.084177       2.511392       3.184772
std         0.215759       0.277654       1.068477       7.412847
min         0.000000       0.000000       1.000000       0.000000
25%         1.000000       0.000000       2.000000       0.000000
50%         1.000000       0.000000       2.000000       0.000000
75%         1.000000       0.000000       3.000000       2.000000
max         1.000000       1.000000       5.000000      30.000000

            PhysHlth       DiffWalk            Sex            Age  \
count  253680.000000  253680.000000  253680.000000  253680.000000
mean        4.242081       0.168224       0.440342       8.032119
std         8.717951       0.374066       0.496429       3.054220
min         0.000000       0.000000       0.000000       1.000000
25%         0.000000       0.000000       0.000000       6.000000
50%         0.000000       0.000000       0.000000       8.000000
75%         3.000000       0.000000       1.000000      10.000000
max        30.000000       1.000000       1.000000      13.000000

          Education         Income
count  253680.000000  253680.000000
mean        5.050434       6.053875
std         0.985774       2.071148
min         1.000000       1.000000
25%         4.000000       5.000000
50%         5.000000       7.000000
75%         6.000000       8.000000
max         6.000000       8.000000
```

In [ ]:
```
print(df.shape)
```

```
(253680, 22)
```

Initial Plot for EDA

In [ ]:
```
plot(df)
```

Out[ ]:

Show Stats and Insights

Number of plots per page: - +

Diabetes_012 HighBP HighChol CholCheck BMI Smoker Stroke HeartDiseaseorAttack PhysActivity Fruits Veggies HvyAlcoholConsump AnyHealthcare NoDocbcCost GenHlth MentHlth PhysHlth DiffWalk Sex Age Education Income

Dataset Overview

Total Variables: 22 Total Rows: 253,680 Missing Data: None reported Duplicate Rows: 23,899 (9.4%) Memory Usage: 42.6 MB Data Types: All variables are numeric but largely categorical by nature.

Variable Descriptions

Categorical (Binary or Multi-Class): Most of the variables are categorical, with binary encoding (e.g., HighBP, Smoker, PhysActivity) except Diabetes_012, which is a multi-class categorical variable. Numerical: BMI is a true continuous variable a category. Key Insights and Considerations No Missing Values: This indicates that the dataset is complete, which simplifies preprocessing but should be verified for correctness (e.g., no improper imputation).

Duplicates: The presence of about 9.4% duplicate rows should be addressed. Determine if these duplicates are due to data entry errors or if they represent legitimate repeated measurements.

Variable Characteristics:

Diabetes Status (Diabetes_012) : Captures the absence or presence of diabetes and its stage, useful for detailed health-related analyses. Lifestyle and Health Checks (Smoker, CholCheck) : Reflect lifestyle choices and adherence to health n Health Metrics (BMI, PhysActivity) : Directly measures aspects of physical health and activity, crucial for studying correlations with health outcomes.

Data Skewness and Distribution:

Skewed Variables (MentHlth, PhysHlth) : High zero count suggests many participants report no issues, which might require special modeling techniques like zero-inflated models if predicting these conditions. BMI Distribution: Given its role as (e.g., normality, presence of outliers) is important for understanding population health metrics. Binary Variables: Many variables are binary, indicating conditions like high blood pressure, smoking status, or having had a stroke. These will be par statistical tests to determine risk factors for various health conditions.

Understanding Correlation

1. Correlation Overview

In [ ]:
```
plot_correlation(df)
```

Out[ ]:

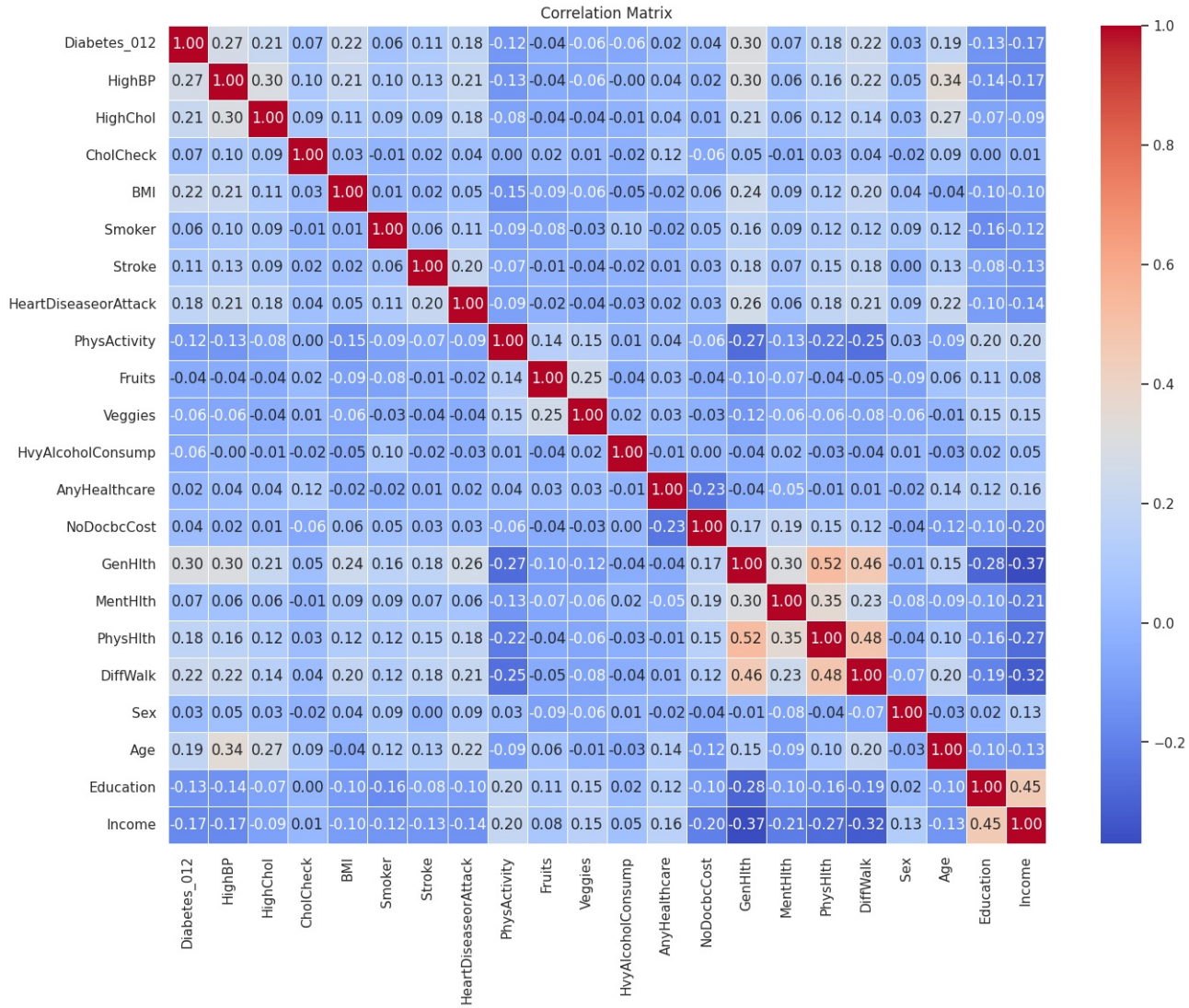
Stats	Pearson	Spearman	KendallTau
	Pearson	**Spearman**	**KendallTau**
Highest Positive Correlation	0.524	0.452	0.39
Highest Negative Correlation	-0.37	-0.354	-0.292
Lowest Correlation	0.002	0.003	0.003
Mean Correlation	0.032	0.03	0.028

In [ ]:
```
correlation = df.corr()
correlation
```

Out[ ]:

	Diabetes_012	HighBP	HighChol	CholCheck	BMI	Smoker	Stroke	HeartDiseaseorAttack	PhysActivity	Fruits	Veggies	HvyAlcoholConsump	AnyHealthcare	NoDocbcCost	GenHlth	MentHlth	PhysHlth
Diabetes_012	1.000000	0.271596	0.209085	0.067546	0.224379	0.062914	0.107179	0.180272	-0.121947	-0.042192	-0.058972	-0.057882	0.015410	0.035436	0.302587	0.073507	0.176287
HighBP	0.271596	1.000000	0.298199	0.098508	0.213748	0.096991	0.129575	0.209361	-0.125267	-0.040555	-0.061266	-0.003972	0.038425	0.017358	0.300530	0.056456	0.161212
HighChol	0.209085	0.298199	1.000000	0.085642	0.106722	0.091299	0.092620	0.180765	-0.078046	-0.040859	-0.039874	-0.011543	0.042230	0.013310	0.208426	0.062069	0.121751
CholCheck	0.067546	0.098508	0.085642	1.000000	0.034495	-0.009929	0.024158	0.044206	0.004190	0.023849	0.006121	-0.023730	0.117626	-0.058255	0.046589	-0.008366	0.031775
BMI	0.224379	0.213748	0.106722	0.034495	1.000000	0.013804	0.020153	0.052904	-0.147294	-0.087518	-0.062275	-0.048736	-0.018471	0.058206	0.239185	0.085310	0.121141
Smoker	0.062914	0.096991	0.091299	-0.009929	0.013804	1.000000	0.061173	0.114441	-0.087401	-0.077666	-0.030678	0.101619	-0.023251	0.048946	0.163143	0.092196	0.116460
Stroke	0.107179	0.129575	0.092620	0.024158	0.020153	0.061173	1.000000	0.203002	-0.069151	-0.013389	-0.041124	-0.016950	0.008776	0.034804	0.177942	0.070172	0.148944
HeartDiseaseorAttack	0.180272	0.209361	0.180765	0.044206	0.052904	0.114441	0.203002	1.000000	-0.087299	-0.019790	-0.039167	-0.028991	0.018734	0.031000	0.258383	0.064621	0.181698
PhysActivity	-0.121947	-0.125267	-0.078046	0.004190	-0.147294	-0.087401	-0.069151	-0.087299	1.000000	0.142756	0.153150	0.012392	0.035505	-0.061638	-0.266186	-0.125587	-0.219230
Fruits	-0.042192	-0.040555	-0.040859	0.023849	-0.087518	-0.077666	-0.013389	-0.019790	0.142756	1.000000	0.254342	-0.035288	0.031544	-0.044243	-0.103854	-0.068217	-0.044633
Veggies	-0.058972	-0.061266	-0.039874	0.006121	-0.062275	-0.030678	-0.041124	-0.039167	0.153150	0.254342	1.000000	0.021064	0.029584	-0.032232	-0.123066	-0.058884	-0.064290
HvyAlcoholConsump	-0.057882	-0.003972	-0.011543	-0.023730	-0.048736	0.101619	-0.016950	-0.028991	0.012392	-0.035288	0.021064	1.000000	-0.010488	0.004684	-0.036724	0.024716	-0.026415
AnyHealthcare	0.015410	0.038425	0.042230	0.117626	-0.018471	-0.023251	0.008776	0.018734	0.035505	0.031544	0.029584	-0.010488	1.000000	-0.232532	-0.040817	-0.052707	-0.008276
NoDocbcCost	0.035436	0.017358	0.013310	-0.058255	0.058206	0.048946	0.034804	0.031000	-0.061638	-0.044243	-0.032232	0.004684	-0.232532	1.000000	0.166397	0.192107	0.148998
GenHlth	0.302587	0.300530	0.208426	0.046589	0.239185	0.163143	0.177942	0.258383	-0.266186	-0.103854	-0.123066	-0.036724	-0.040817	0.166397	1.000000	0.301674	0.524364
MentHlth	0.073507	0.056456	0.062069	-0.008366	0.085310	0.092196	0.070172	0.064621	-0.125587	-0.068217	-0.058884	0.024716	-0.052707	0.192107	0.301674	1.000000	0.353619
PhysHlth	0.176287	0.161212	0.121751	0.031775	0.121141	0.116460	0.148944	0.181698	-0.219230	-0.044633	-0.064290	-0.026415	-0.008276	0.148998	0.524364	0.353619	1.000000
DiffWalk	0.224239	0.223618	0.144672	0.040585	0.197078	0.122463	0.176567	0.212709	-0.253174	-0.048352	-0.080506	-0.037668	0.007074	0.118447	0.456920	0.233688	0.478417
Sex	0.031040	0.052207	0.031205	-0.022115	0.042950	0.093662	0.002978	0.086096	0.032482	-0.091175	-0.064765	0.005740	-0.019405	-0.044931	-0.006091	-0.080705	-0.043137
Age	0.185026	0.344452	0.272318	0.090321	-0.036618	0.120641	0.126974	0.221618	-0.092511	0.064547	-0.009771	-0.034578	0.138046	-0.119777	0.152450	-0.092068	0.099130
Education	-0.130517	-0.141358	-0.070802	0.001510	-0.103932	-0.161955	-0.076009	-0.099600	0.199658	0.110187	0.154329	0.023997	0.122514	-0.100701	-0.284912	-0.101830	-0.155093
Income	-0.171483	-0.171235	-0.085459	0.014259	-0.100069	-0.123937	-0.128599	-0.141011	0.198539	0.079929	0.151087	0.053619	0.157999	-0.203182	-0.370014	-0.209806	-0.266799

In [ ]:
```
# use sns heatmap to plot the correlation matrix
plt.figure(figsize=(16, 12))
sns.heatmap(correlation, annot=True, cmap='coolwarm', fmt=".2f", linewidths=.5)
plt.title('Correlation Matrix')
plt.show()
```



Notable Positive Correlations

- **Diabetes_012** and **GenHlth** **(0.302587)**: Higher diabetes categorization correlates with worse general health ratings. This suggests that as diabetes severity increases, overall health perceptions tend to decline.
- **HighBP** and **Age** **(0.344452)**: Older age groups tend to have higher incidences of high blood pressure.
- **PhysHlth** and **GenHlth** **(0.524364)**: More days with poor physical health correlate strongly with poorer general health ratings.
- **MentHlth** and **PhysHlth** **(0.353619)**: A significant positive correlation indicating that more days with mental health issues are associated with more days of poor physical health.
- **DiffWalk** and **PhysHlth** **(0.478417)**: Difficulty walking correlates with more days of poor physical health, suggesting mobility issues are associated with worse physical conditions.

Notable Negative Correlations

- **PhysActivity** and **GenHlth** **(-0.266186)**: Higher levels of physical activity correlate with better general health ratings.
- **Income** and **GenHlth** **(-0.370014)**: Higher income levels correlate with better general health, highlighting possible socioeconomic impacts on health.
- **Education** and **GenHlth** **(-0.284912)**: Higher education levels are associated with better general health ratings.

Implications for Analysis

- **Health Outcomes**: Variables like GenHlth , Diabetes_012 , HighBP , and HighChol can be used to model health outcomes, especially for understanding risk factors associated with chronic diseases.
- **Behavioral Factors**: The relationships between lifestyle choices (e.g., Smoker , PhysActivity , Fruits , Veggies) and health outcomes can inform public health interventions.
- **Socioeconomic Factors**: The strong correlations between Income , Education , and health variables suggest that socioeconomic factors are crucial determinants of health, which could be a focal point for deeper socioeconomic studies a

In [ ]:
```
%matplotlib inline

def plot_all_correlations_individual(dataframe):
    for column in dataframe.columns:
        # The function plot_correlation from dataprep to plot each column against all others
        plot_correlation(dataframe, column)
        print(f"Plotting correlations for: {column}")

# call the function with your DataFrame
plot_all_correlations_individual(df)
```

```
Plotting correlations for: Diabetes_012
Plotting correlations for: HighBP
Plotting correlations for: HighChol
Plotting correlations for: CholCheck
Plotting correlations for: BMI
Plotting correlations for: Smoker
Plotting correlations for: Stroke
Plotting correlations for: HeartDiseaseorAttack
Plotting correlations for: PhysActivity
Plotting correlations for: Fruits
Plotting correlations for: Veggies
Plotting correlations for: HvyAlcoholConsump
Plotting correlations for: AnyHealthcare
Plotting correlations for: NoDocbcCost
Plotting correlations for: GenHlth
Plotting correlations for: MentHlth
Plotting correlations for: PhysHlth
Plotting correlations for: DiffWalk
Plotting correlations for: Sex
Plotting correlations for: Age
Plotting correlations for: Education

Plotting correlations for: Income
```

In [ ]:
```
plot_correlation(df, "Diabetes_012")
```

Out[ ]:
Pearson Spearman KendallTau

In [ ]:
```
plot_correlation(df, "HighBP")
```

Out[ ]:
Pearson Spearman KendallTau

In [ ]:
```
plot_correlation(df, "HighChol")
```

Out[ ]:
Pearson Spearman KendallTau

In [ ]:
```
plot_correlation(df, "CholCheck")
```

Out[ ]:
Pearson Spearman KendallTau

In [ ]:
```
plot_correlation(df, "BMI")
```

Out[ ]:
Pearson Spearman KendallTau

In [ ]:
```
plot_correlation(df, "Smoker")
```

Out[ ]:
Pearson Spearman KendallTau

In [ ]:
```
plot_correlation(df, "Stroke")
```

Out[ ]:
Pearson Spearman KendallTau

In [ ]:
```
plot_correlation(df, "HeartDiseaseorAttack")
```

Out[ ]:
Pearson Spearman KendallTau

In [ ]:
```
plot_correlation(df, "PhysActivity")
```

Out[ ]:
Pearson Spearman KendallTau

Data Preparation and Identifying and printing the numerical, categorical, and binary/flag features in the DataFrame for further EDA.

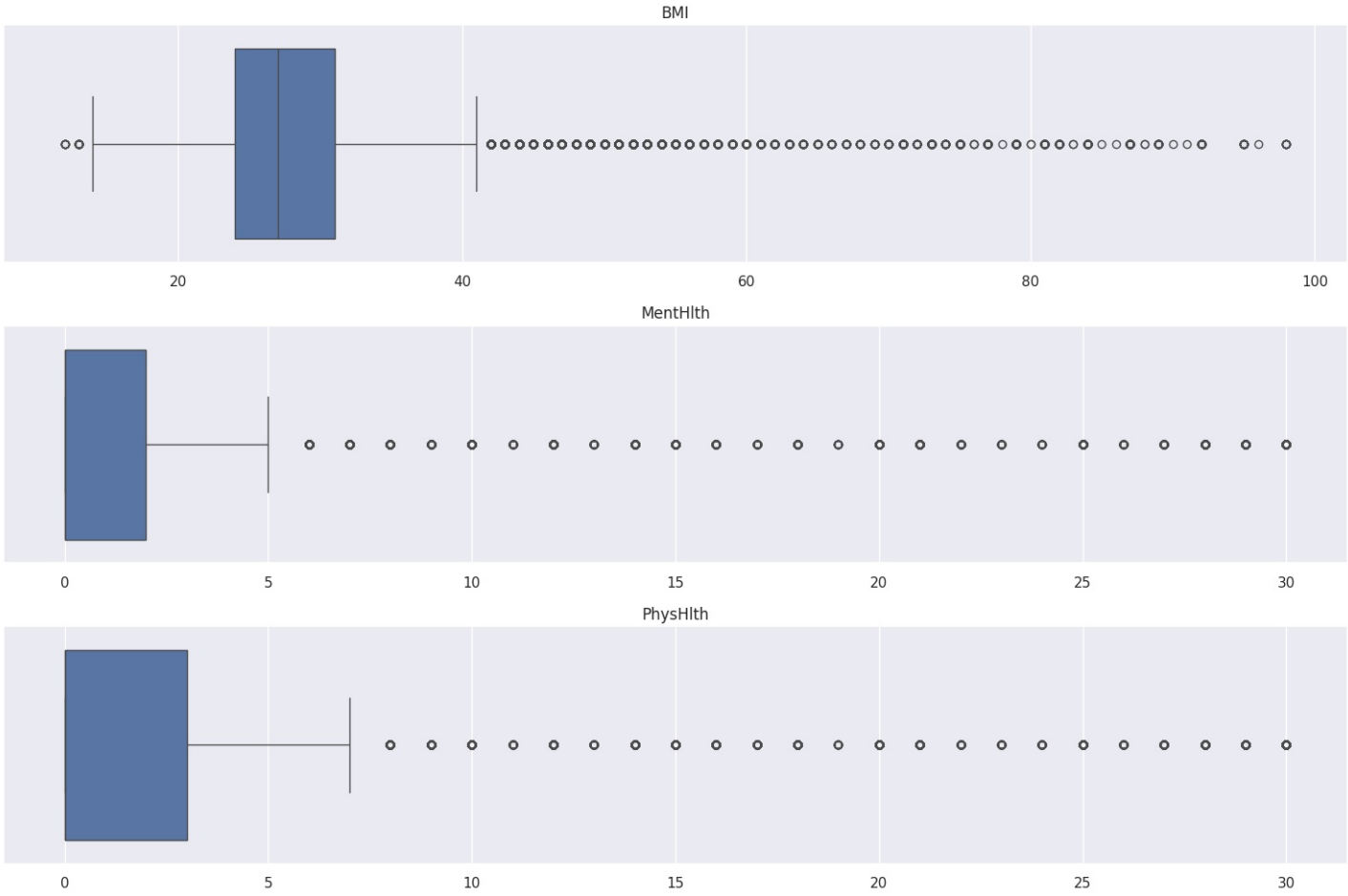
In [13]:
```
# Classify variables
def classify_variables():
    numerical = ['BMI', 'MentHlth', 'PhysHlth']
    categorical = ['Diabetes_012', 'Age']
    binary = ['HighBP', 'HighChol', 'CholCheck', 'Smoker', 'Stroke', 'HeartDiseaseorAttack',
              'PhysActivity', 'Fruits', 'Veggies', 'HvyAlcoholConsump', 'AnyHealthcare',
              'NoDocbcCost', 'DiffWalk', 'Sex']
    ordinal = ['GenHlth', 'Education', 'Income']
    return numerical, categorical, binary, ordinal
```

```
numerical, categorical, binary, ordinal = classify_variables()

non_numerical = categorical + binary + ordinal  # All non-numerical variables

print("Numerical Variables:", numerical)
print("Non Numerical Variables:", non_numerical)
print("Categorical Variables:", categorical)
print("Binary Variables:", binary)
print("Ordinal Variables:", ordinal)
```

```
Numerical Variables: ['BMI', 'MentHlth', 'PhysHlth']
Non Numerical Variables: ['Diabetes_012', 'Age', 'HighBP', 'HighChol', 'CholCheck', 'Smoker', 'Stroke', 'HeartDiseaseorAttack', 'PhysActivity', 'Fruits', 'Veggies', 'HvyAlcoholConsump', 'AnyHealthcare', 'NoDocbcCost', 'DiffWalk', 'Sex', 'GenHlth', 'Education', 'Income
Categorical Variables: ['Diabetes_012', 'Age']
Binary Variables: ['HighBP', 'HighChol', 'CholCheck', 'Smoker', 'Stroke', 'HeartDiseaseorAttack', 'PhysActivity', 'Fruits', 'Veggies', 'HvyAlcoholConsump', 'AnyHealthcare', 'NoDocbcCost', 'DiffWalk', 'Sex']
Ordinal Variables: ['GenHlth', 'Education', 'Income']
```

Univariate Analysis

In [ ]:
```
# Set up the matplotlib figure and size
plt.figure(figsize=(15, 10))

# Iterate over each numerical feature to create a boxplot
for index, feature in enumerate(numerical):
    plt.subplot(len(numerical), 1, index + 1)
    sns.boxplot(x=df[feature])
    plt.title(feature)
    plt.xlabel('')  # Remove x-labels as they are redundant with titles

plt.tight_layout()
plt.show()
```



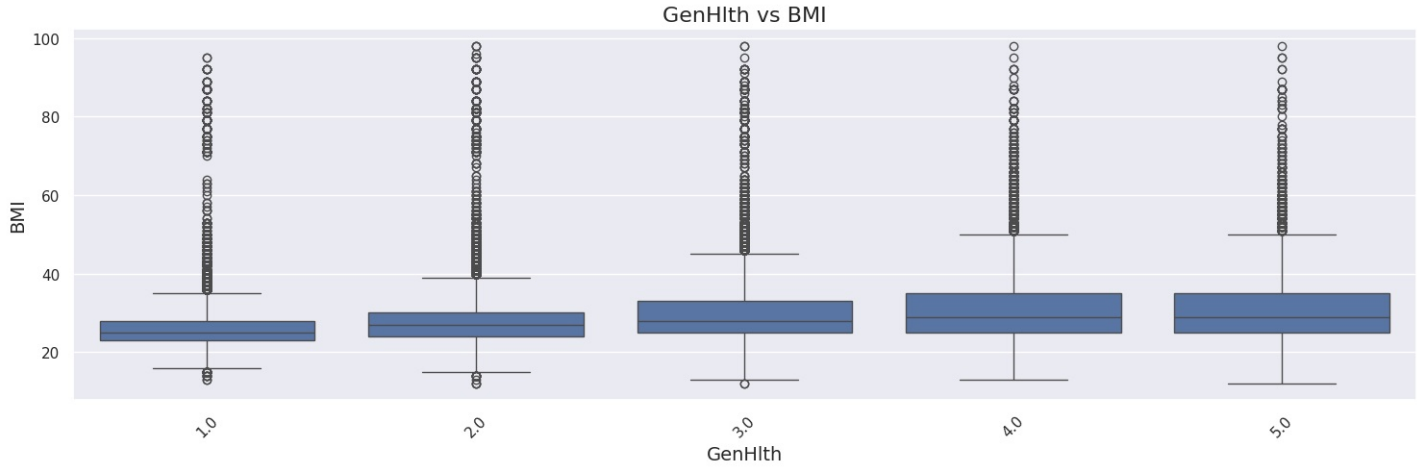
Skewness: All three variables (BMI, MentHlth, PhysHlth) show skewness towards lower values, with the median close to the lower quartile.

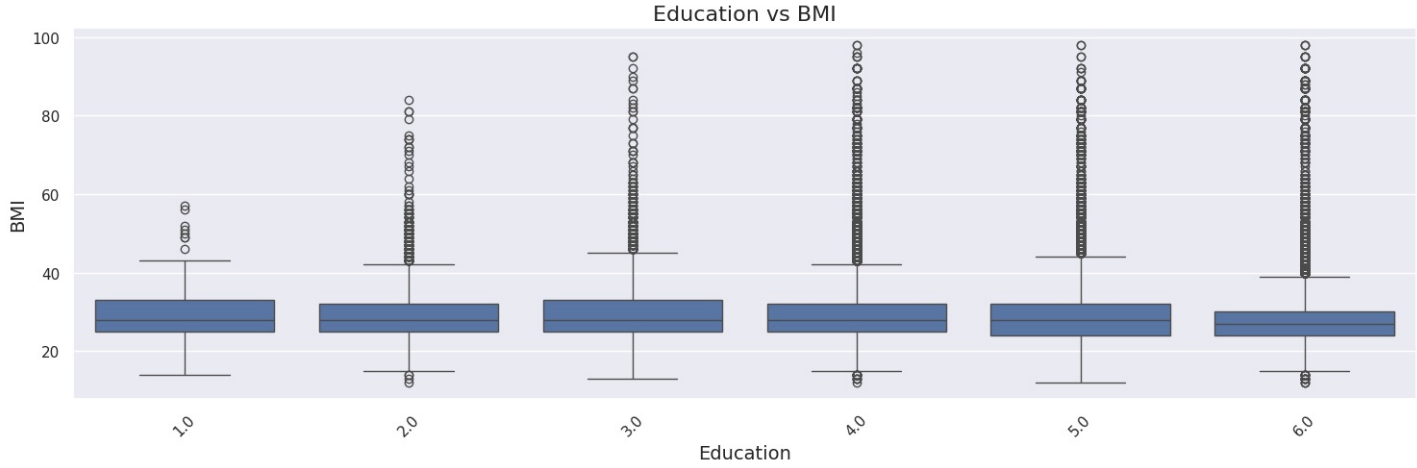
Outliers: Each variable has significant outliers on the higher end, which could be important data points representing individuals with severe conditions.

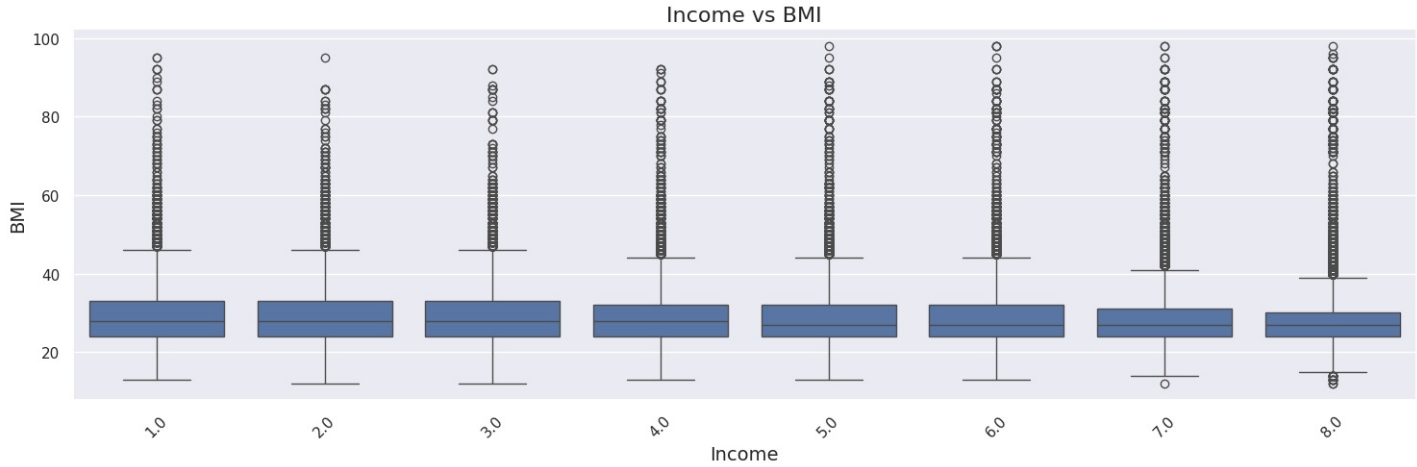
Central Tendency and Spread: The central tendency of all three variables is skewed towards lower values, and the IQR is relatively small, indicating that most data points are close to the median. However, the presence of outliers significantly a

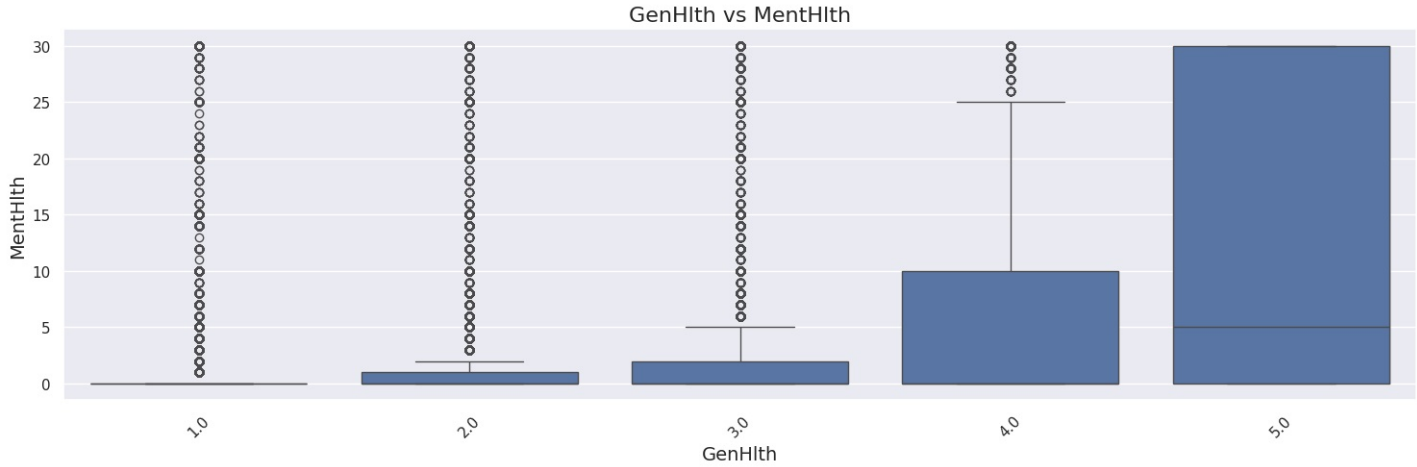
Univariate Analysis for Numerical vs Ordinal Variables

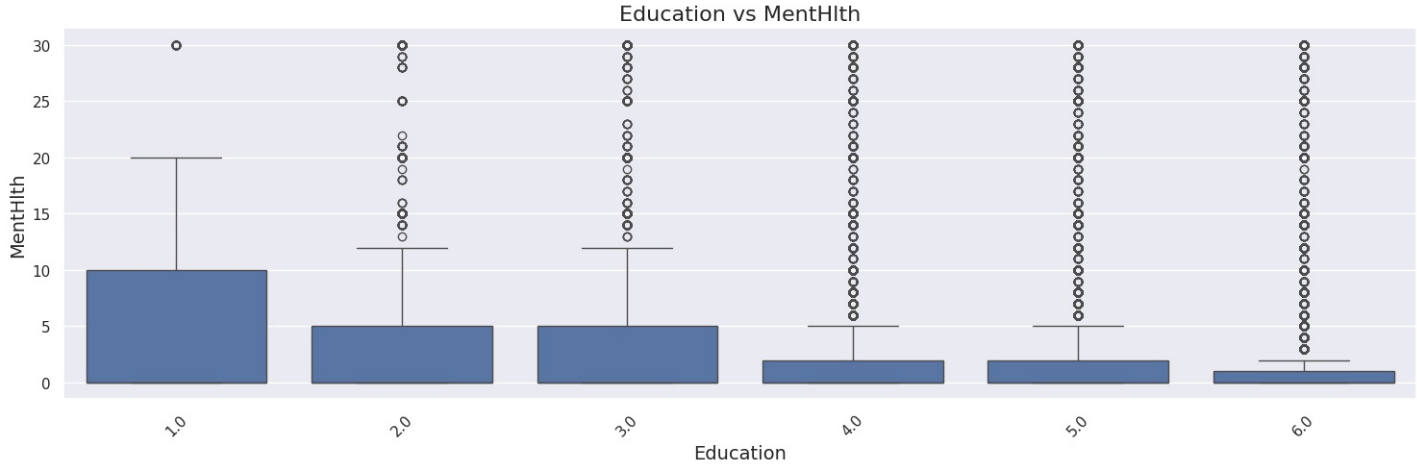
In [ ]:
```
# Iterate over each numerical feature
for num_feature in numerical:
    # Set up the matplotlib figure and size
    plt.figure(figsize=(15, len(ordinal) * 5))

    # Iterate over each ordinal feature to create a box plot
    for index, ord_feature in enumerate(ordinal):
        plt.subplot(len(ordinal), 1, index + 1)
        sns.boxplot(data=df, x=ord_feature, y=num_feature)
        plt.title(f'{ord_feature} vs {num_feature}', fontsize=16)
        plt.xlabel(ord_feature, fontsize=14)
        plt.ylabel(num_feature, fontsize=14)
        plt.xticks(rotation=45)  # Rotate x-axis labels by 45 degrees for readability

    plt.tight_layout()
    plt.show()
```

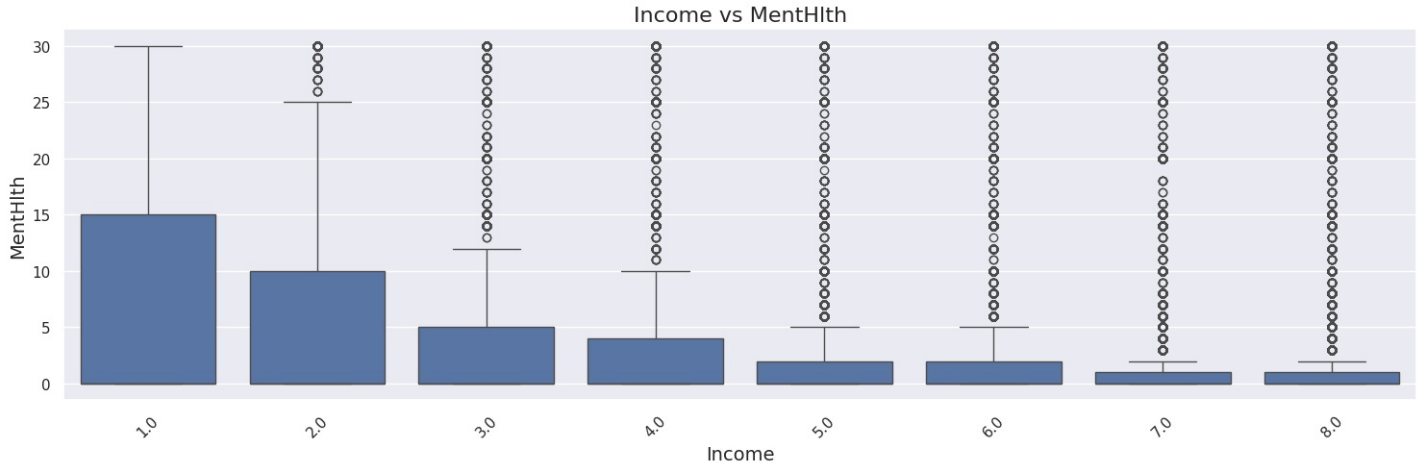

GenHlth vs BMI
BMI
100
80
60
40
20
1.0
2.0
3.0
4.0
5.0
GenHlth

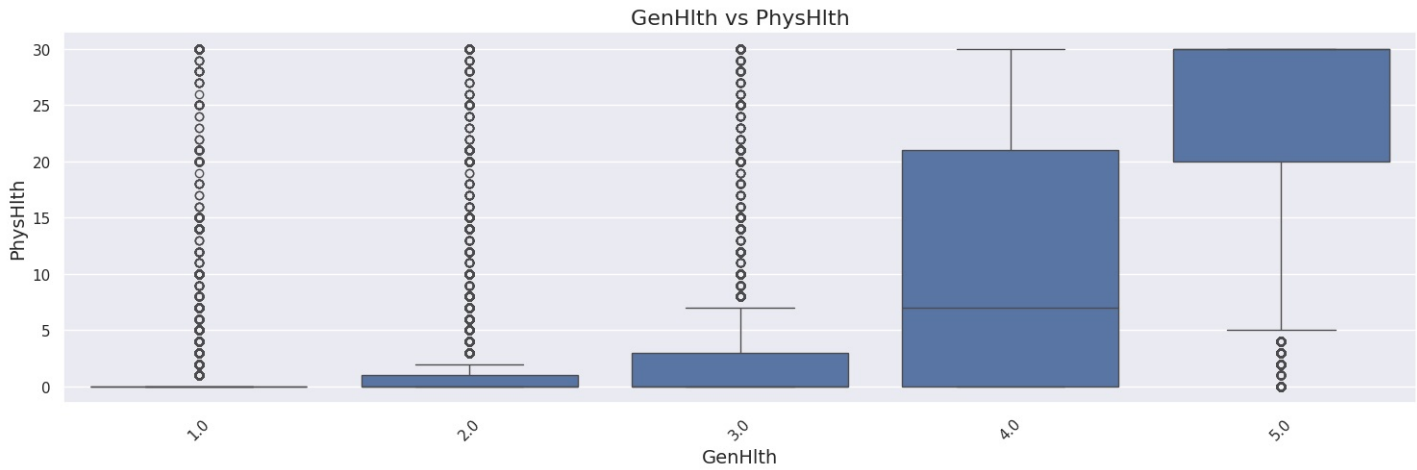

Education vs BMI
BMI
100
80
60
40
20
1.0
2.0
3.0
4.0
5.0
6.0
Education

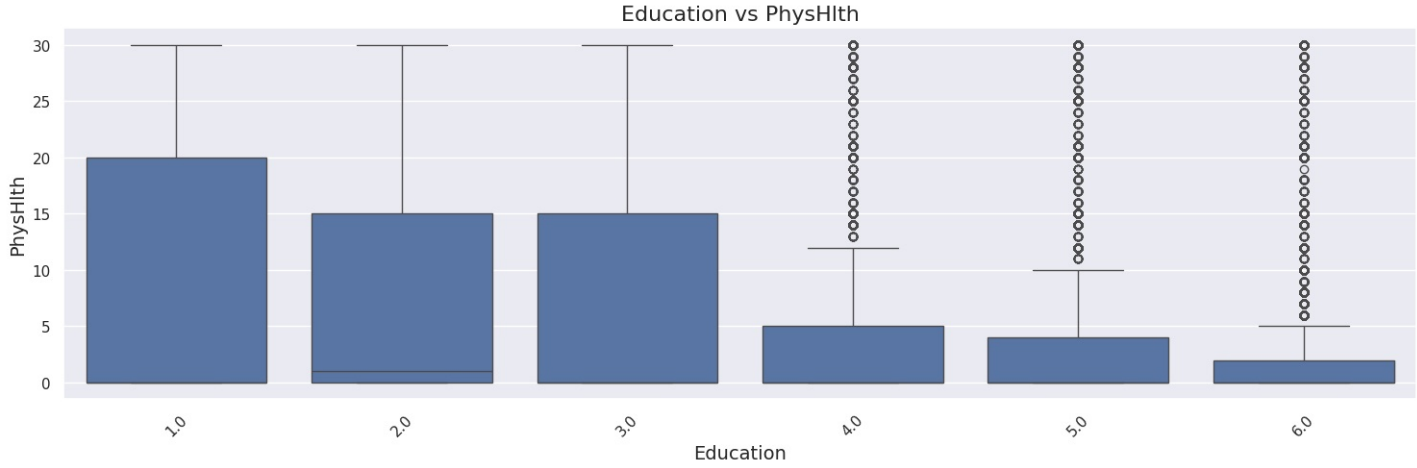

Income vs BMI
BMI
100
80
60
40
20
1.0
2.0
3.0
4.0
5.0
6.0
7.0
8.0
Income

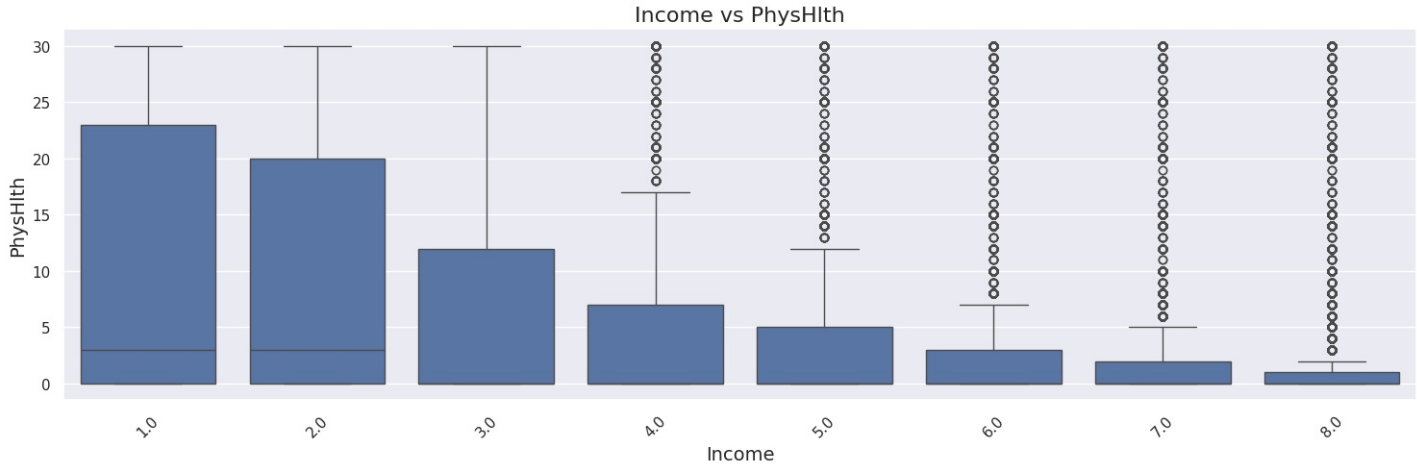

GenHlth vs MentHlth
MentHlth
GenHlth
1.0
2.0
3.0
4.0
5.0


Education vs MentHlth
MentHlth
Education
1.0
2.0
3.0
4.0
5.0
6.0


Income vs MentHlth
MentHlth
Income
1.0
2.0
3.0
4.0
5.0
6.0
7.0
8.0







BMI Analysis

1. **GenHlth vs BMI**:
   - This plot shows the relationship between general health (GenHlth) and Body Mass Index (BMI). There is a slight increase in BMI as general health worsens, but the median BMI values remain relatively consistent across different levels category.
2. **Education vs BMI**:
   - This plot illustrates the relationship between education level and BMI. Higher education levels (4, 5, 6) show a slightly lower median BMI compared to lower education levels (1, 2, 3), suggesting that higher education might be associate
3. **Income vs BMI**:
   - This plot examines the relationship between income and BMI. There is a slight decrease in median BMI as income increases, indicating that higher income levels might be associated with lower BMI, though the difference is not pronou

Mental Health Analysis

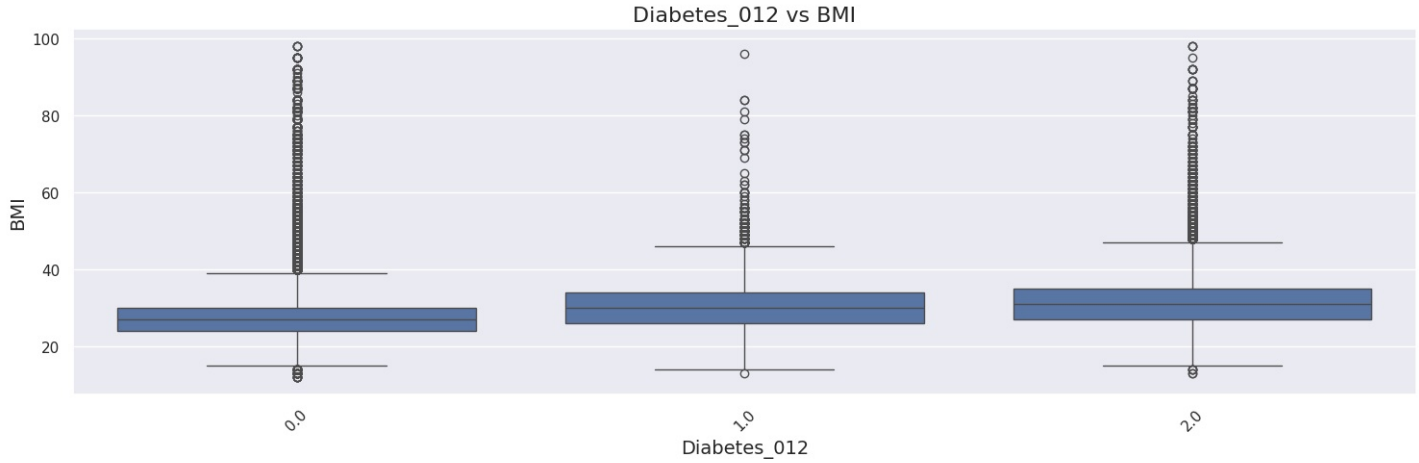
1. **GenHlth vs MentHlth**:
   - This plot shows the relationship between general health (GenHlth) and mental health (MentHlth). As general health worsens, the number of days with poor mental health increases significantly, especially for the poorest health category
2. **Education vs MentHlth**:
   - This plot illustrates the relationship between education level and mental health. Higher education levels (4, 5, 6) are associated with fewer days of poor mental health, indicating a possible link between higher education and better ment
3. **Income vs MentHlth**:
   - This plot examines the relationship between income and mental health. Higher income levels are associated with fewer days of poor mental health, suggesting that higher income might contribute to better mental health.

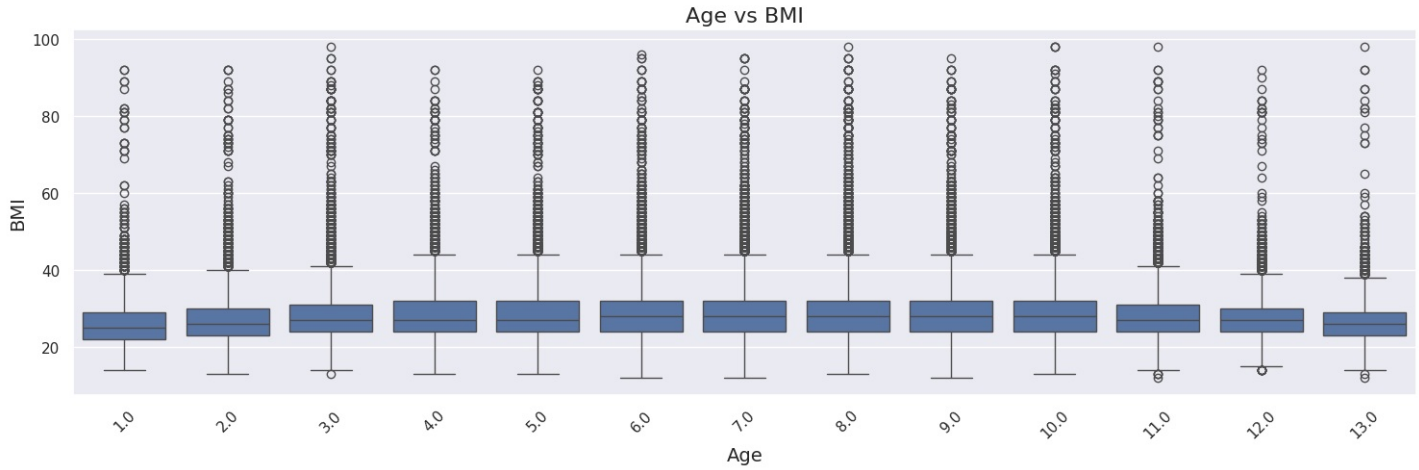
Physical Health Analysis

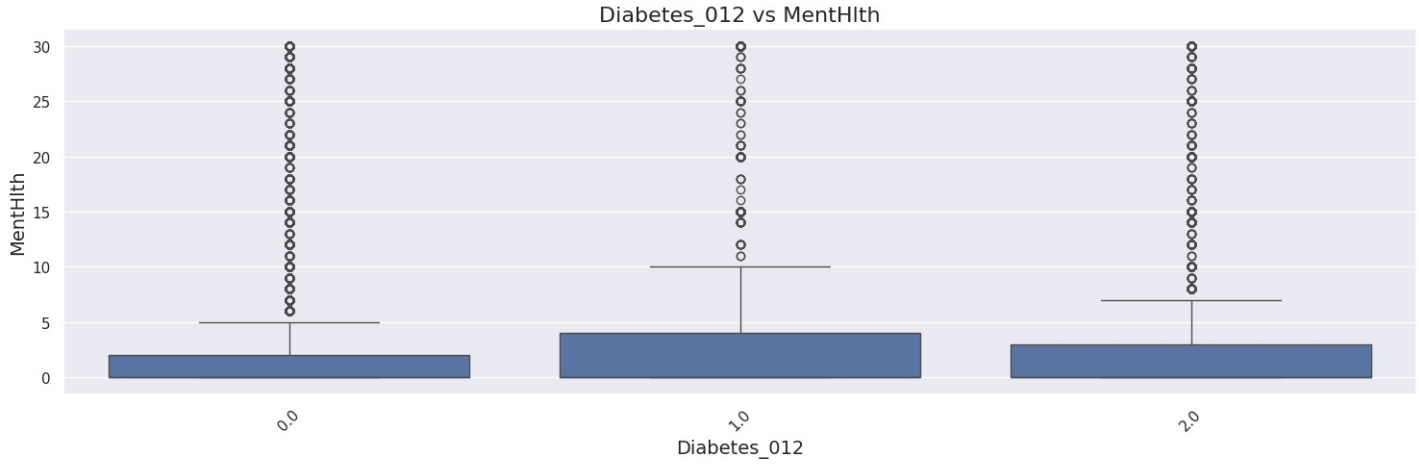
1. **GenHlth vs PhysHlth**:
   - This plot shows the relationship between general health (GenHlth) and physical health (PhysHlth). As general health worsens, the number of days with poor physical health increases dramatically, particularly in the poorest health categ
2. **Education vs PhysHlth**:
   - This plot illustrates the relationship between education level and physical health. Higher education levels (4, 5, 6) are associated with fewer days of poor physical health, indicating that higher education might be linked to better physical
3. **Income vs PhysHlth**:
   - This plot examines the relationship between income and physical health. Higher income levels are associated with fewer days of poor physical health, suggesting that higher income might contribute to better physical health.

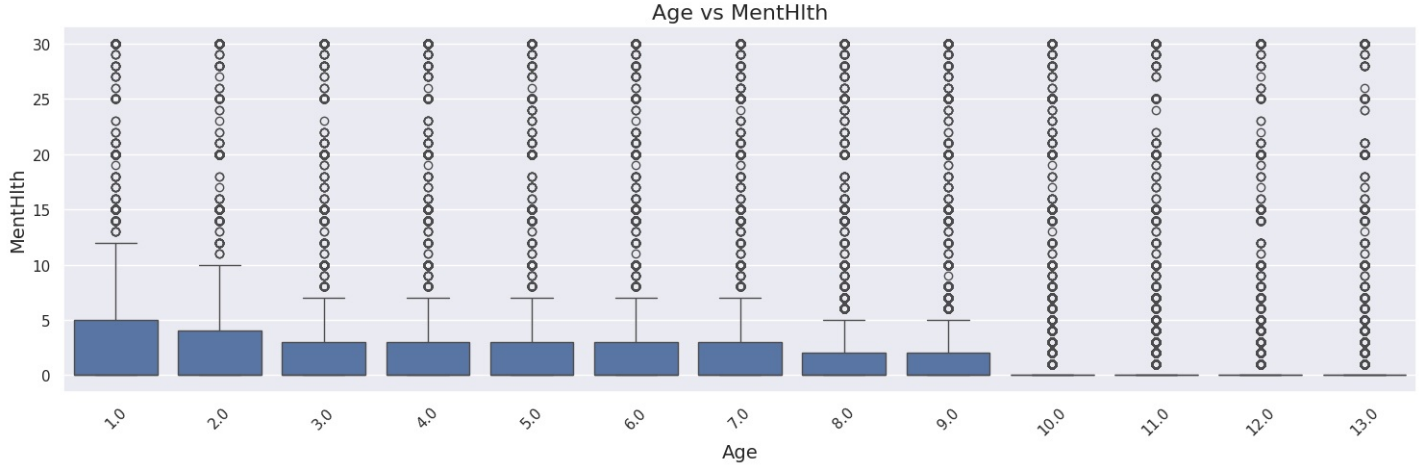
Univariate Analysis for Numerical vs Categorical Variables

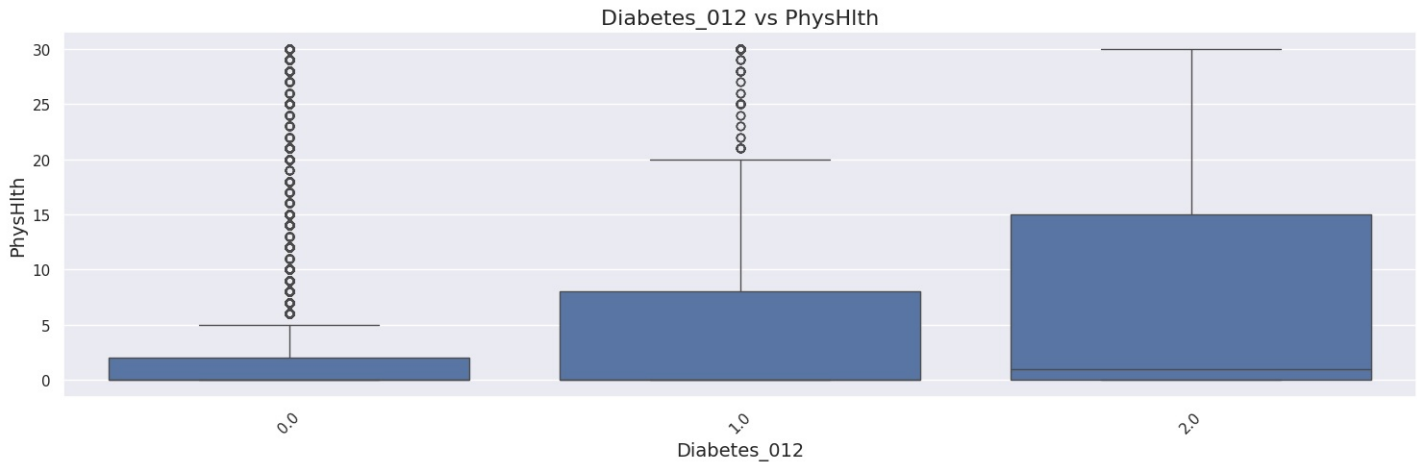
In [ ]:
```
# Iterate over each numerical feature
for num_feature in numerical:
    # Set up the matplotlib figure and size
    plt.figure(figsize=(15, len(categorical) * 5))

    # Iterate over each categorical feature to create a box plot
    for index, ord_feature in enumerate(categorical):
        plt.subplot(len(categorical), 1, index + 1)
        sns.boxplot(data=df, x=ord_feature, y=num_feature)
        plt.title(f'{ord_feature} vs {num_feature}', fontsize=16)
        plt.xlabel(ord_feature, fontsize=14)
        plt.ylabel(num_feature, fontsize=14)
        plt.xticks(rotation=45)  # Rotate x-axis labels by 45 degrees for readability

    plt.tight_layout()
    plt.show()
```

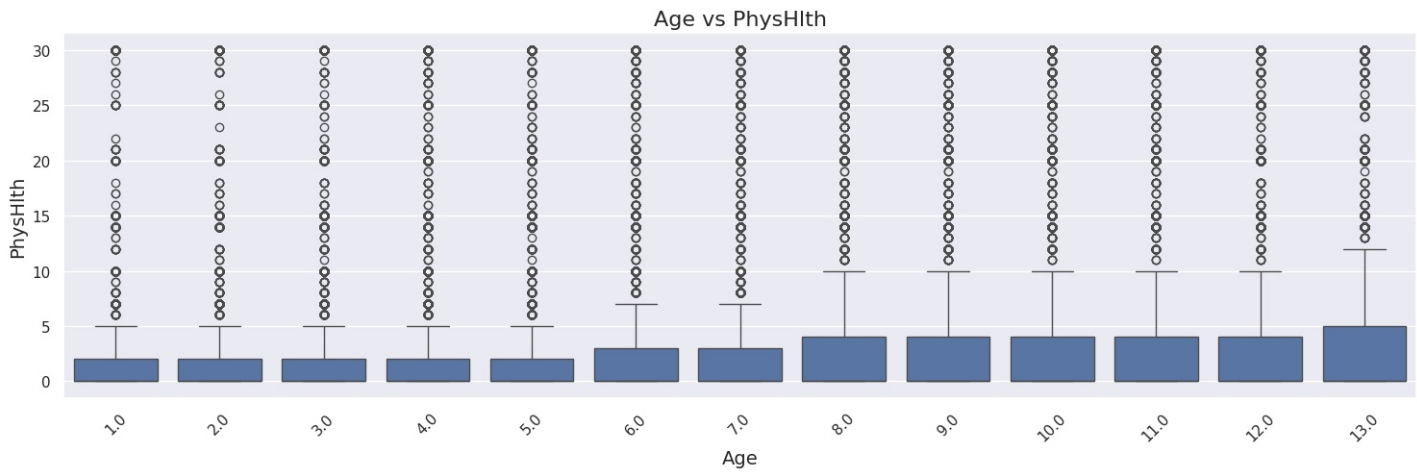












BMI Analysis

1. **Diabetes_012 vs BMI**:
   - This plot shows the relationship between diabetes status (Diabetes_012) and Body Mass Index (BMI). There is an increasing trend in median BMI from those without diabetes (0) to prediabetes (1) and diabetes (2). Individuals with diab the increase in median and upper quartile values.
2. **Age vs BMI**:
   - This plot illustrates the relationship between age groups and BMI. BMI appears relatively stable across different age groups, with a slight decrease in the upper quartile for older age groups (10-13). There are numerous outliers in each within each group.

Mental Health Analysis

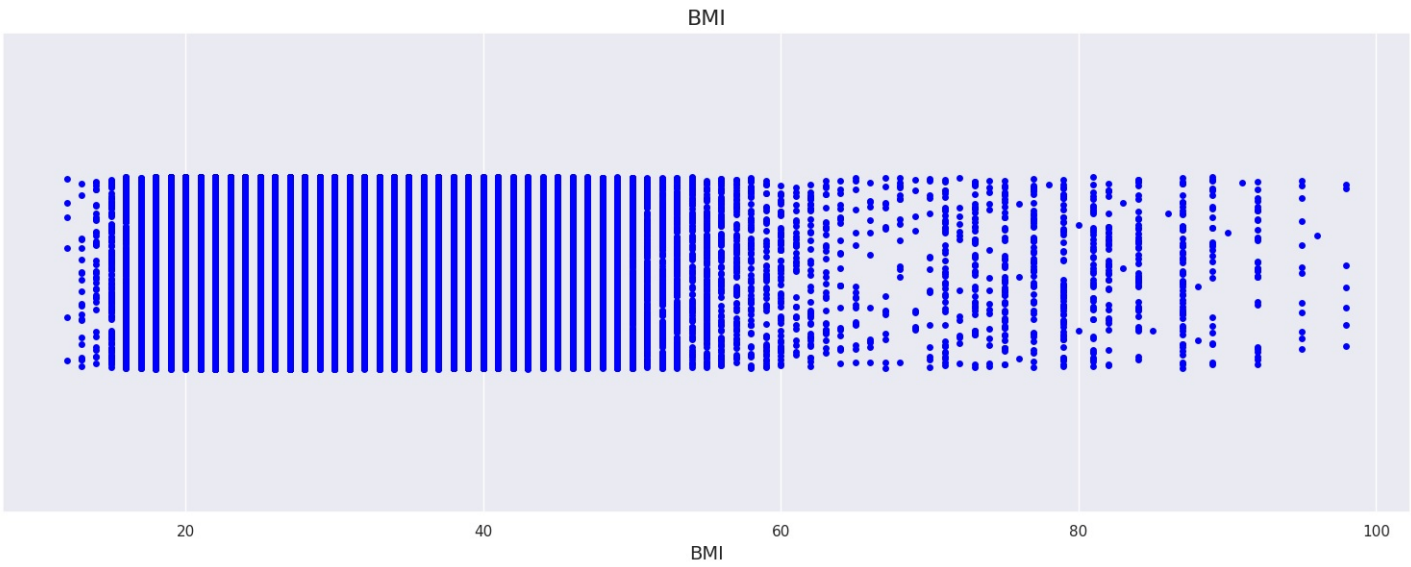
1. **Diabetes_012 vs MentHlth**:
   - This plot shows the relationship between diabetes status and mental health (MentHlth). Individuals with diabetes (2) have a higher median number of poor mental health days compared to those without diabetes (0) and prediabetes (1) worse mental health.
2. **Age vs MentHlth**:
   - This plot examines the relationship between age groups and mental health. The median number of poor mental health days is relatively consistent across age groups, with a slight decrease in older age groups (10-13). Outliers are pres health days.

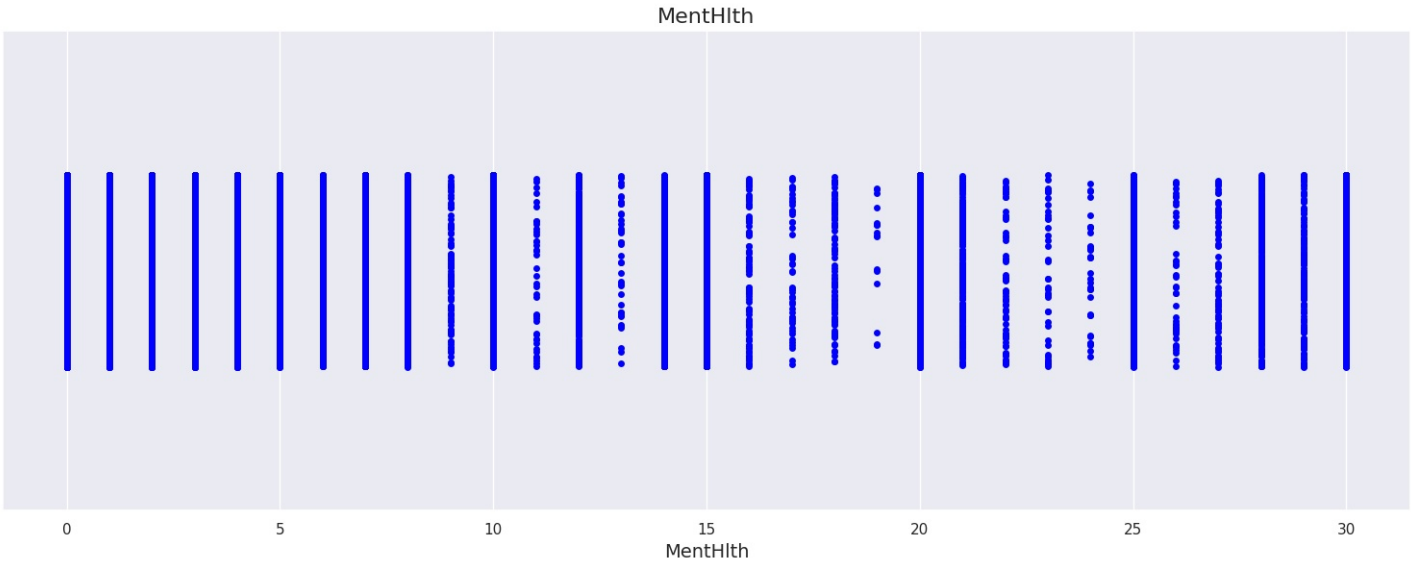
Physical Health Analysis

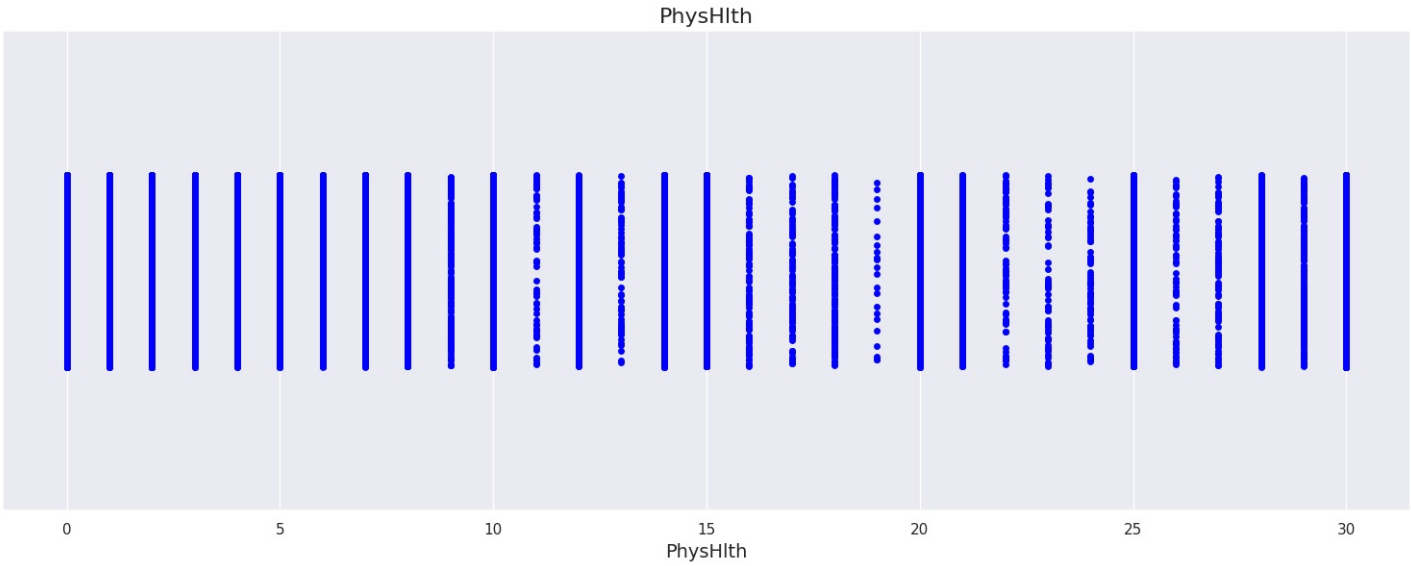
1. **Diabetes_012 vs PhysHlth**:
   - This plot shows the relationship between diabetes status and physical health (PhysHlth). Individuals with diabetes (2) have a higher median number of poor physical health days compared to those without diabetes (0) and prediabetes worse physical health.
2. **Age vs PhysHlth**:
   - This plot examines the relationship between age groups and physical health. The median number of poor physical health days is consistent across age groups, with a slight decrease in older age groups (10-13). Outliers are present in days.

Strip Plot

In [ ]:
```
# Set up the matplotlib figure
plt.figure(figsize=(15, 6 * len(numerical)))

# Iterate over each numerical feature to create a strip plot
for index, feature in enumerate(numerical):
    plt.subplot(len(numerical), 1, index + 1)  # Creating a subplot for each feature
    sns.stripplot(x=df[feature], color='blue', jitter=0.2)  # Adding jitter for better visibility of points
    plt.title(feature, fontsize=16)  # title
    plt.xlabel(feature, fontsize=14)  # x-label

plt.tight_layout()
plt.show()
```







General Observations:

Skewness: Both MentHlth and PhysHlth variables show a left-skewed distribution, with a high concentration of data points at lower values (fewer days of poor health) and a long tail towards higher values.

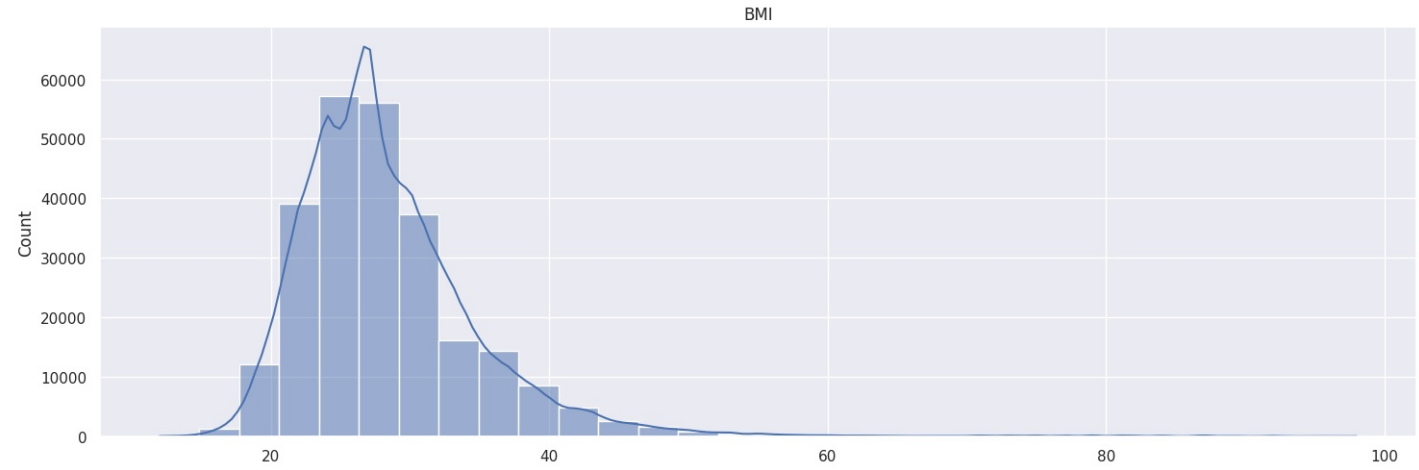
Outliers and Extremes: All three variables display outliers or extreme values. For BMI, outliers are seen at the very low and very high ends. For MentHlth and PhysHlth, outliers are more evenly distributed but still visible at higher values.

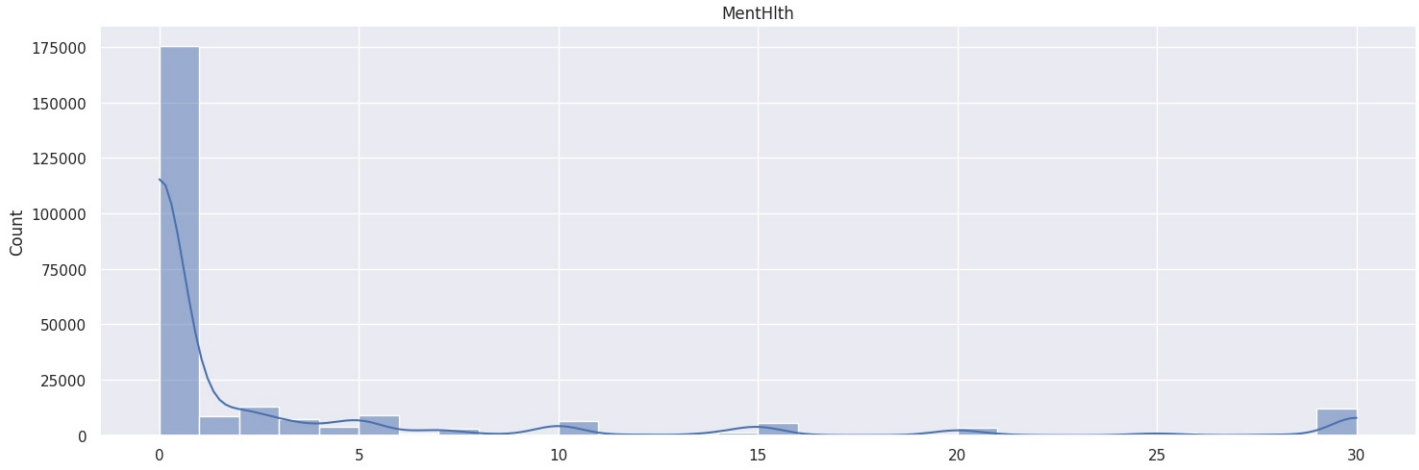
Data Distribution: The strip plots indicate a varied distribution across different ranges for each variable, providing a clear visual of individual data points' spread and density.

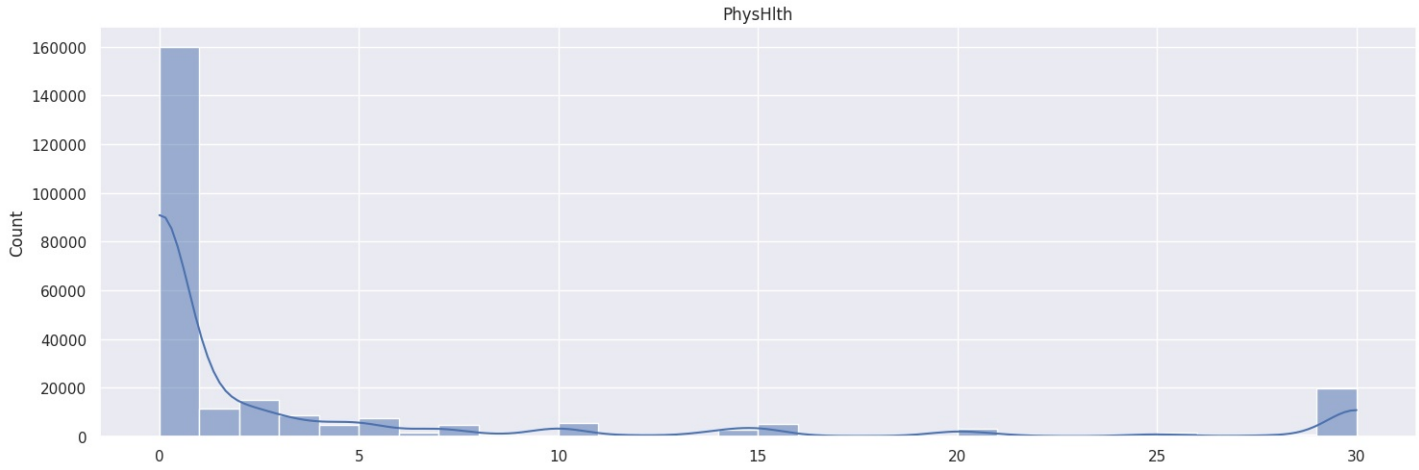
Histogram

Numerical

In [ ]:
```
# Set up the matplotlib figure and size
plt.figure(figsize=(15, 5 * len(numerical)))

# Iterate over each numerical feature to create a histogram
for index, feature in enumerate(numerical):
    plt.subplot(len(numerical), 1, index + 1)
    sns.histplot(data=df, x=feature, kde=True, bins=30)  # Added KDE plot and adjusted bin count
    plt.title(feature)
    plt.xlabel('')  # Remove x-labels as they are redundant with titles
    plt.ylabel('Count')  # Ensure y-label is consistently set to 'Count'

plt.tight_layout()
plt.show()
```







BMI:

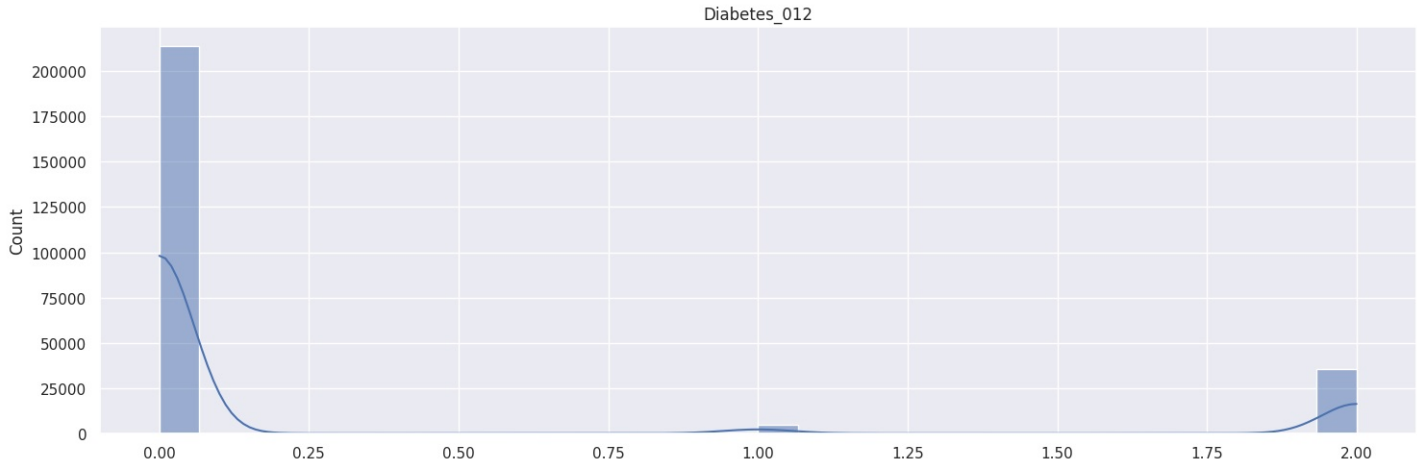
Shows a typical right-skewed distribution with most values in the normal to overweight range. There are fewer extremely high BMI values, which could be clinically significant.

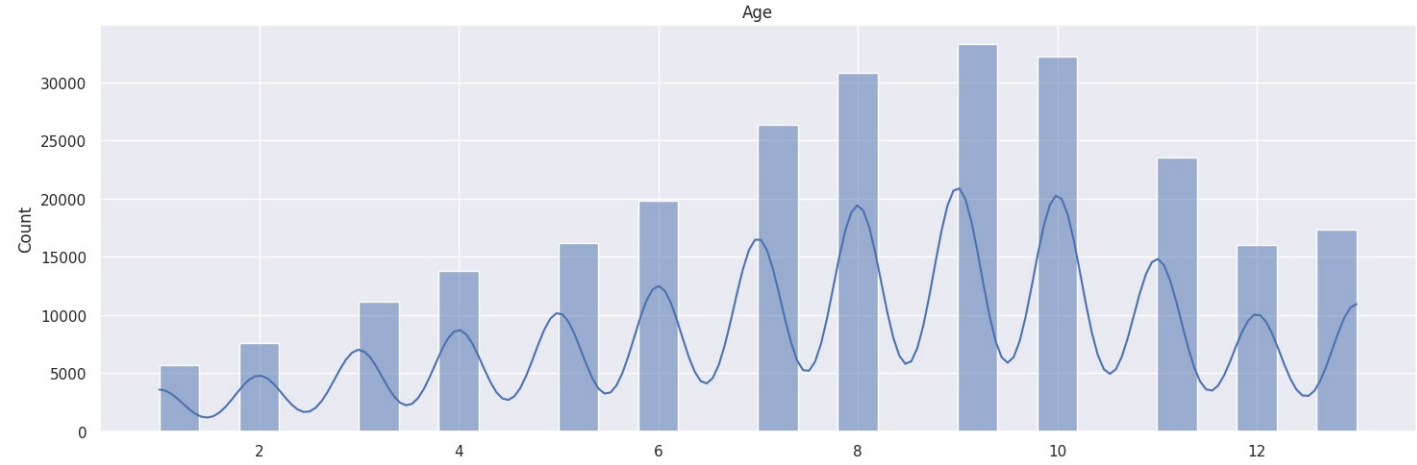
MentHlth and PhysHlth:

Both variables exhibit a highly right-skewed distribution with a majority of individuals reporting few or no days of poor health. The presence of outliers indicates that some individuals experience extended periods of poor mental and physical heal

Categorical

In [ ]:
```
# Set up the matplotlib figure and size
plt.figure(figsize=(15, 5 * len(categorical)))

# Iterate over each numerical feature to create a histogram
for index, feature in enumerate(categorical):
    plt.subplot(len(categorical), 1, index + 1)
    sns.histplot(data=df, x=feature, kde=True, bins=30)  # Added KDE plot and adjusted bin count
    plt.title(feature)
    plt.xlabel('')  # Remove x-labels as they are redundant with titles
    plt.ylabel('Count')  # Ensure y-label is consistently set to 'Count'

plt.tight_layout()
plt.show()
```

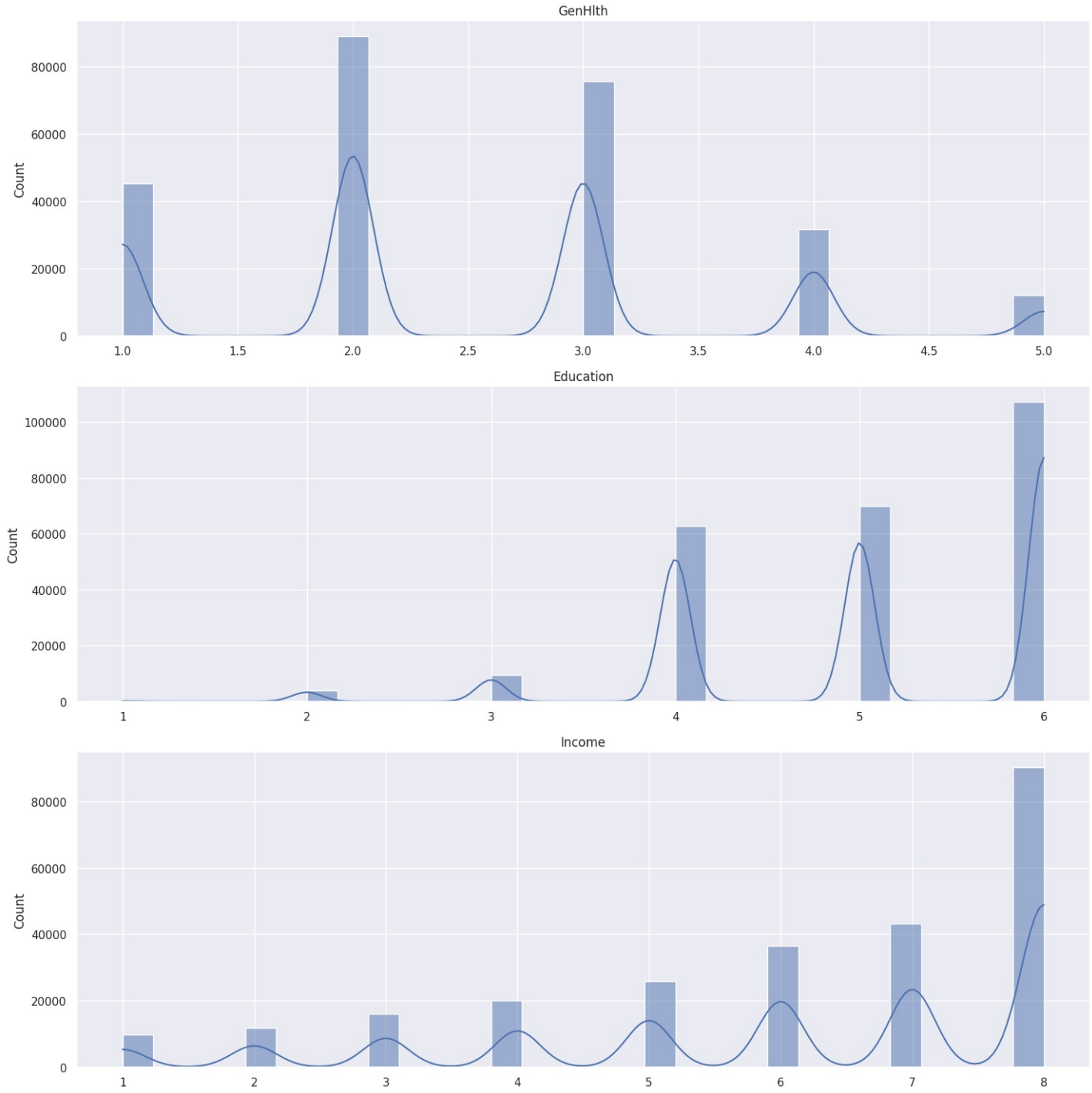




Ordinal

In [ ]:

```
# Set up the matplotlib figure and size
plt.figure(figsize=(15, 5 * len(ordinal)))

# Iterate over each numerical feature to create a histogram
for index, feature in enumerate(ordinal):
    plt.subplot(len(ordinal), 1, index + 1)
    sns.histplot(data=df, x=feature, kde=True, bins=30)  # Added KDE plot and adjusted bin count
    plt.title(feature)
    plt.xlabel('')  # Remove x-labels as they are redundant with titles
    plt.ylabel('Count')  # Ensure y-label is consistently set to 'Count'

plt.tight_layout()
plt.show()
```



GenHlth Distribution:

The plot shows the distribution of general health ratings (GenHlth), which are categorized from 1 (excellent) to 5 (poor). The most common ratings are 2 and 3, indicating that many individuals rate their health as "very good" or "good". There are fair (4), or poor (5).

Education Distribution:

The plot shows the distribution of education levels, which range from 1 to 6. The highest count is for education level 6, indicating that many individuals in the dataset have a higher education level. Other peaks are observed at levels 4 and 5, wh

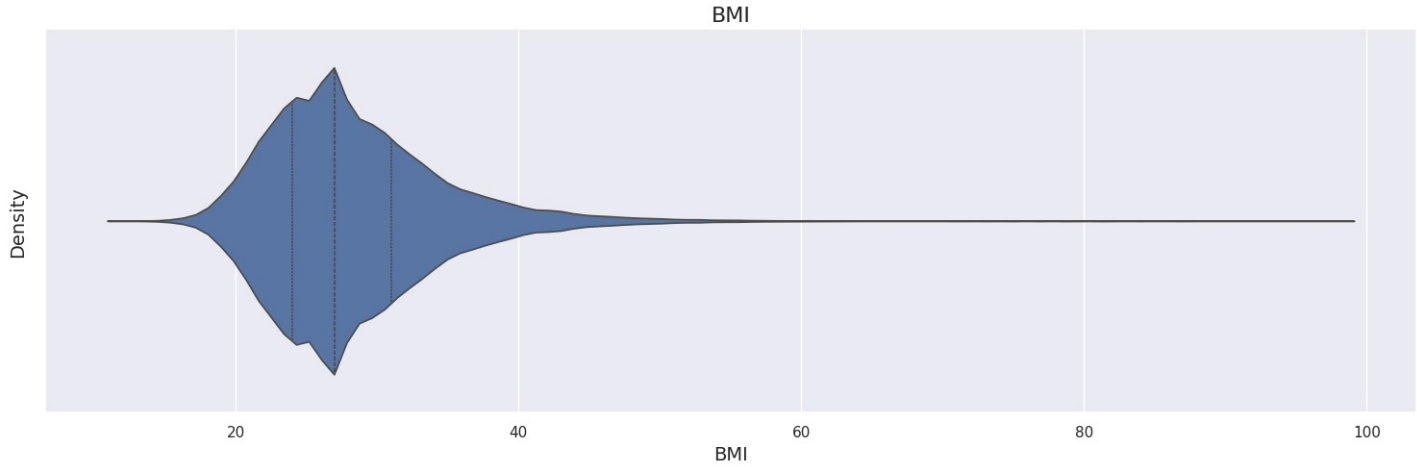
Income Distribution:

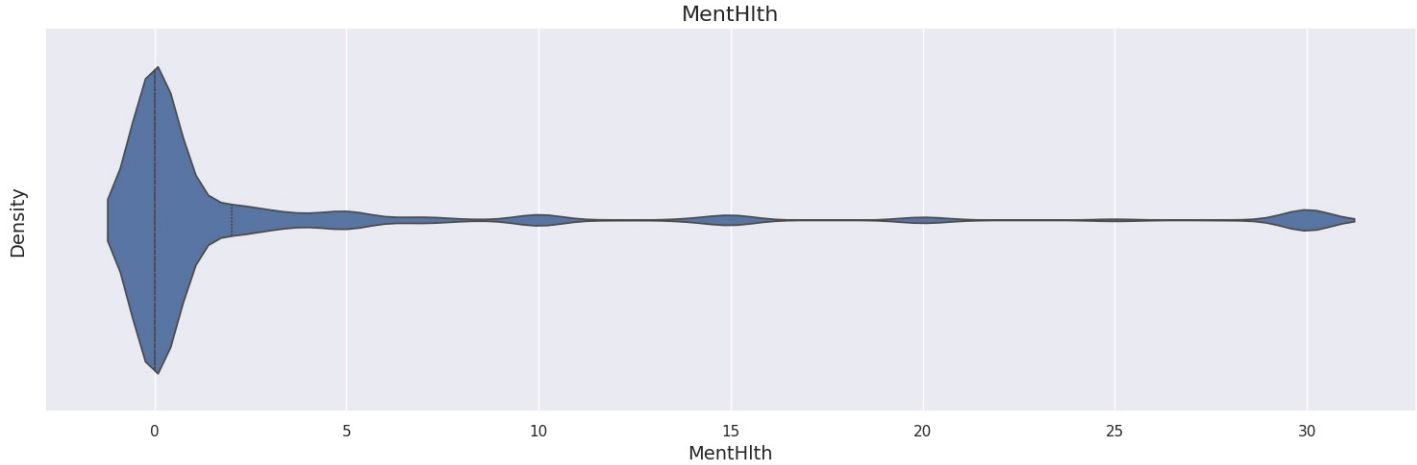
The plot shows the distribution of income levels, which range from 1 to 8. There are noticeable peaks at levels 4, 6, and 8, suggesting that these income levels are more common in the dataset. The distribution has smaller peaks at levels 1, 2, 3 levels among individuals.

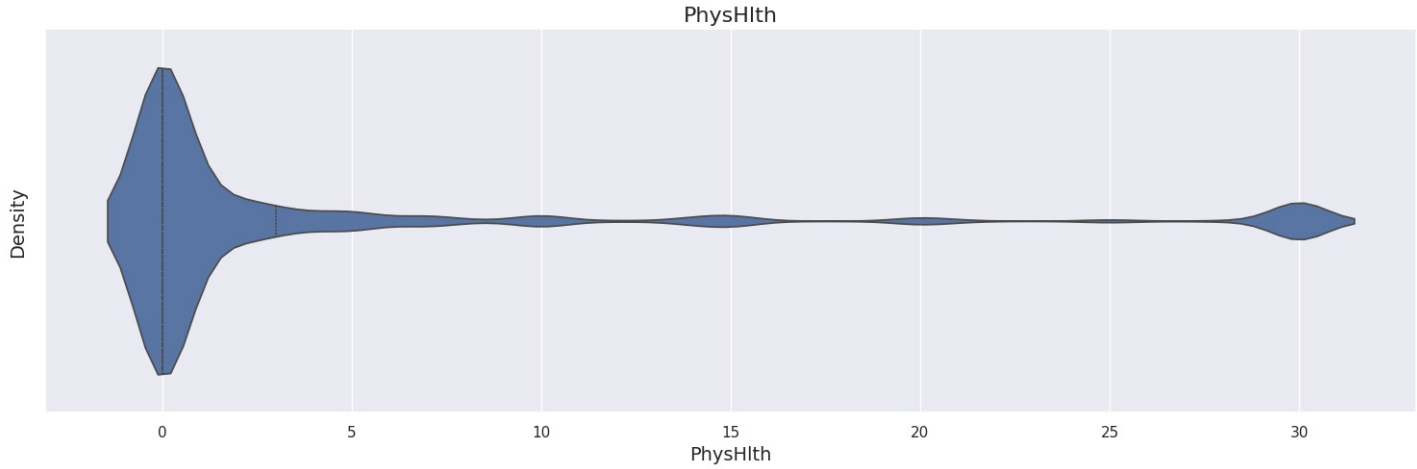
Violin Plots

Numerical

In [ ]:
```
# Set up the matplotlib figure and size
plt.figure(figsize=(15, 5 * len(numerical)))

# Iterate over each numerical feature to create a violin plot
for index, feature in enumerate(numerical):
    plt.subplot(len(numerical), 1, index + 1)  # Create a subplot for each feature
    sns.violinplot(data=df, x=feature, inner='quartile')  # inner='quartile' adds quartiles
    plt.title(feature, fontsize=16)  # Setting the title with a larger font size
    plt.xlabel(feature, fontsize=14)  # Setting the x-label with a readable font size
    plt.ylabel('Density', fontsize=14)  # Setting the y-label to 'Density'

plt.tight_layout()  # Adjusting subplots to fit into the figure area nicely
plt.show()  # Displaying the plots
```







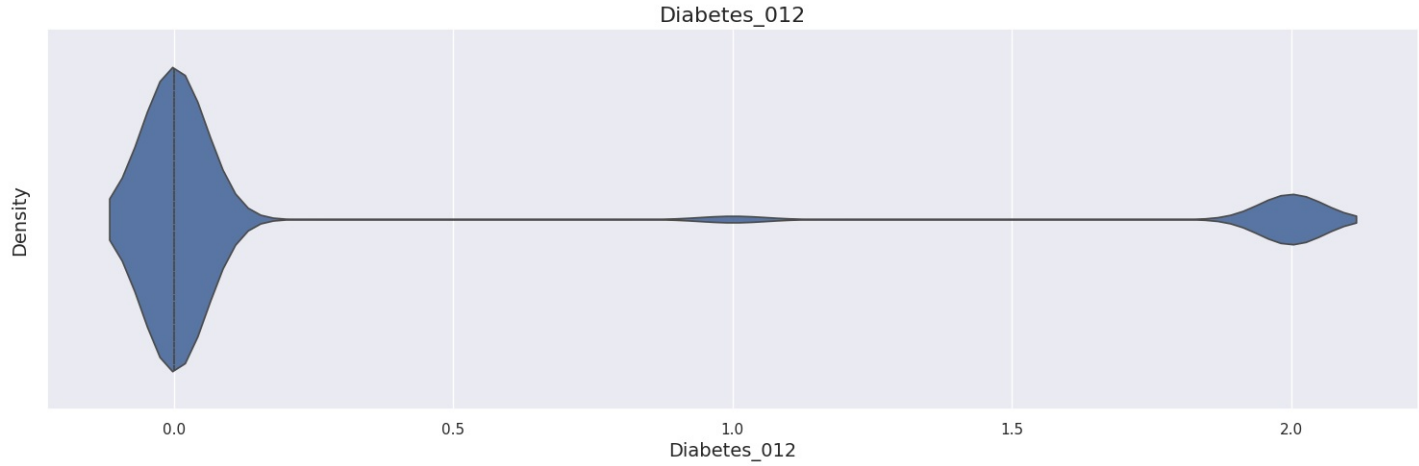
BMI: Most individuals have a BMI between 25-30, with density tapering off at higher and lower values.

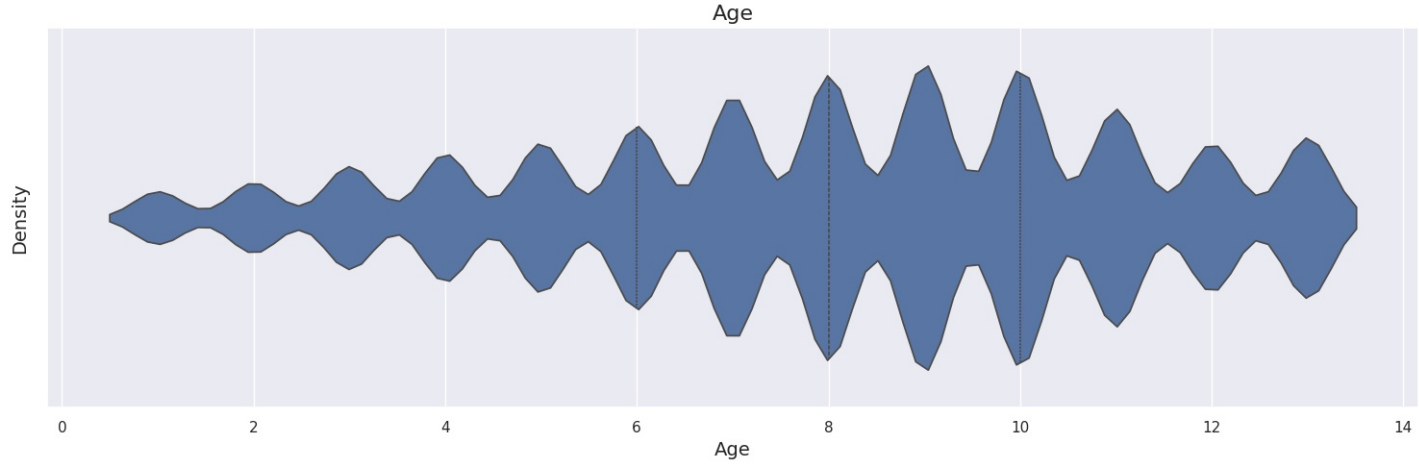
MentHlth: Most individuals report 0 poor mental health days, with decreasing density as the number of poor mental health days increases.

PhysHlth: Similar to MentHlth, most individuals report 0 poor physical health days, with density decreasing as the number of poor physical health days increases.

Categorical

In [ ]:
```
# Set up the matplotlib figure and size
plt.figure(figsize=(15, 5 * len(categorical)))

# Iterate over each numerical feature to create a violin plot
for index, feature in enumerate(categorical):
    plt.subplot(len(categorical), 1, index + 1)  # Create a subplot for each feature
    sns.violinplot(data=df, x=feature, inner='quartile')  # inner='quartile' adds quartiles
    plt.title(feature, fontsize=16)  # Setting the title with a larger font size
    plt.xlabel(feature, fontsize=14)  # Setting the x-label with a readable font size
    plt.ylabel('Density', fontsize=14)  # Setting the y-label to 'Density'

plt.tight_layout()  # Adjusting subplots to fit into the figure area nicely
plt.show()  # Displaying the plots
```



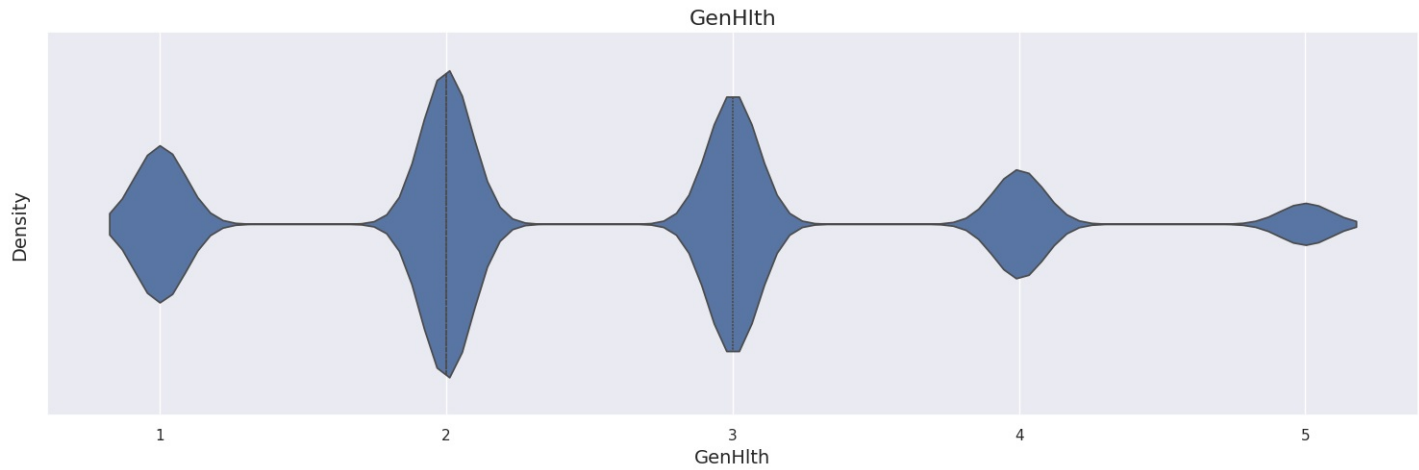


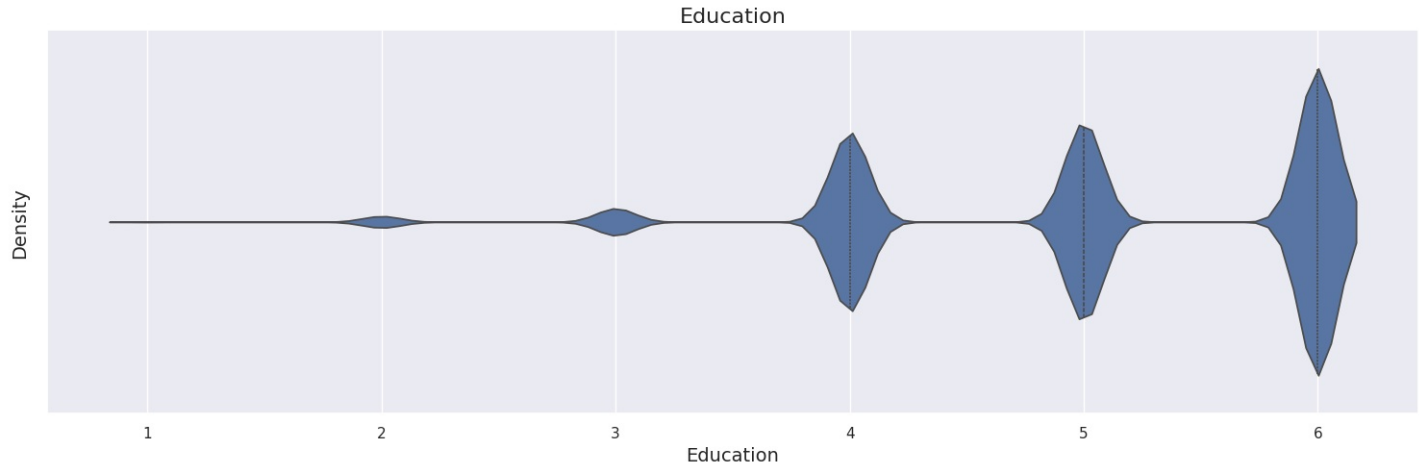
Diabetes_012: High density at 0 (no diabetes), with lower densities at 1 (prediabetes) and 2 (diabetes).

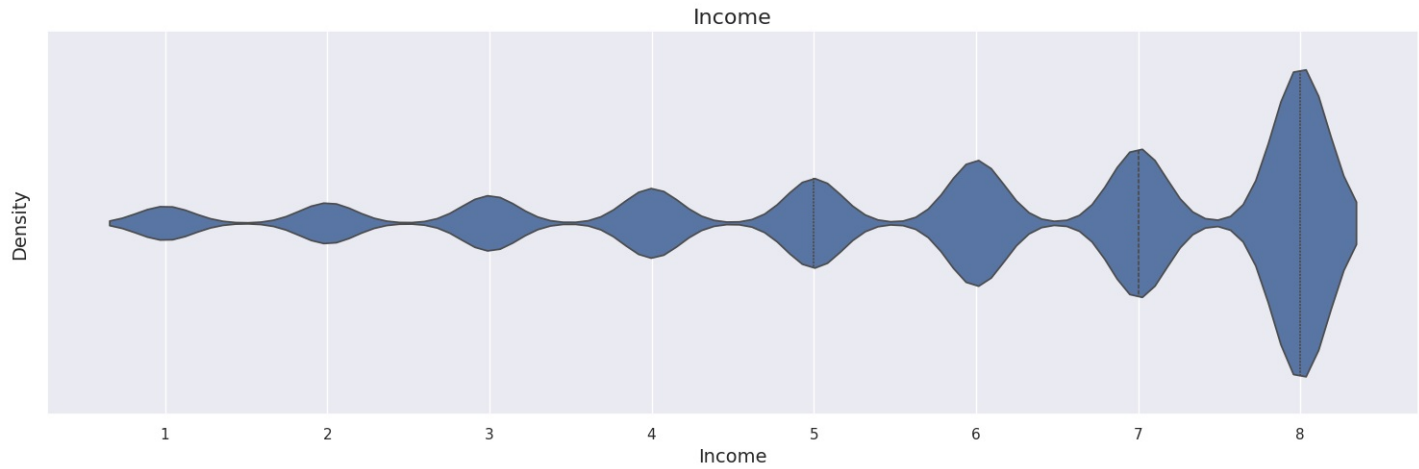
Age: Peaks at age groups 4, 8, and 10, indicating higher representation in these groups.

Ordinal

In [ ]:
```
# Set up the matplotlib figure and size
plt.figure(figsize=(15, 5 * len(ordinal)))

# Iterate over each numerical feature to create a violin plot
for index, feature in enumerate(ordinal):
    plt.subplot(len(ordinal), 1, index + 1)  # Create a subplot for each feature
    sns.violinplot(data=df, x=feature, inner='quartile')  # inner='quartile' adds quartiles
    plt.title(feature, fontsize=16)  # Setting the title with a larger font size
    plt.xlabel(feature, fontsize=14)  # Setting the x-label with a readable font size
    plt.ylabel('Density', fontsize=14)  # Setting the y-label to 'Density'

plt.tight_layout()  # Adjusting subplots to fit into the figure area nicely
plt.show()  # Displaying the plots
```







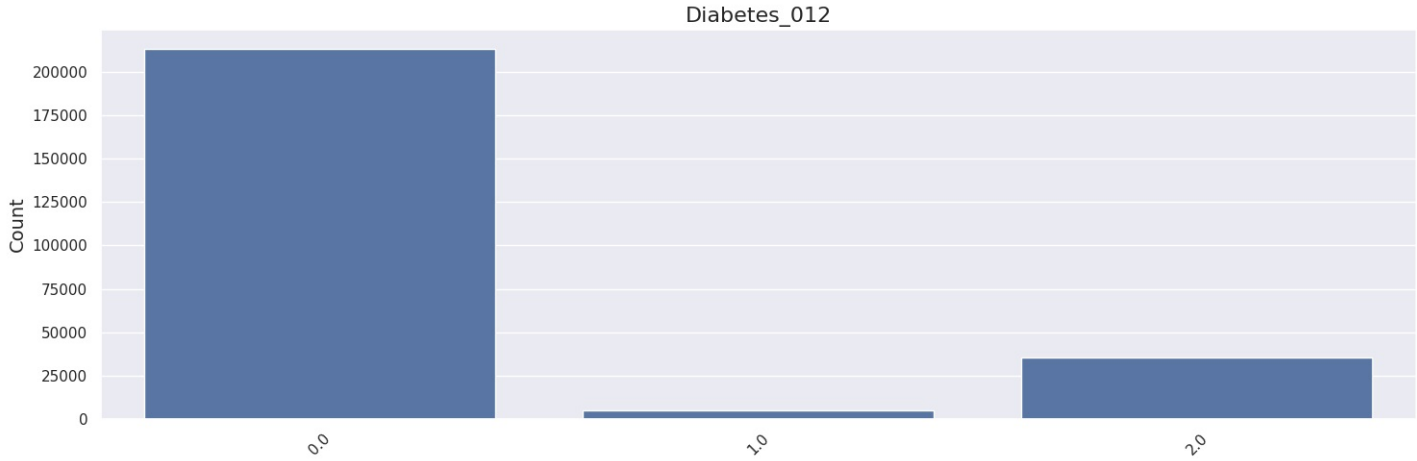
GenHlth: Peaks at 2 (very good) and 3 (good), with fewer individuals at 1 (excellent), 4 (fair), and 5 (poor).

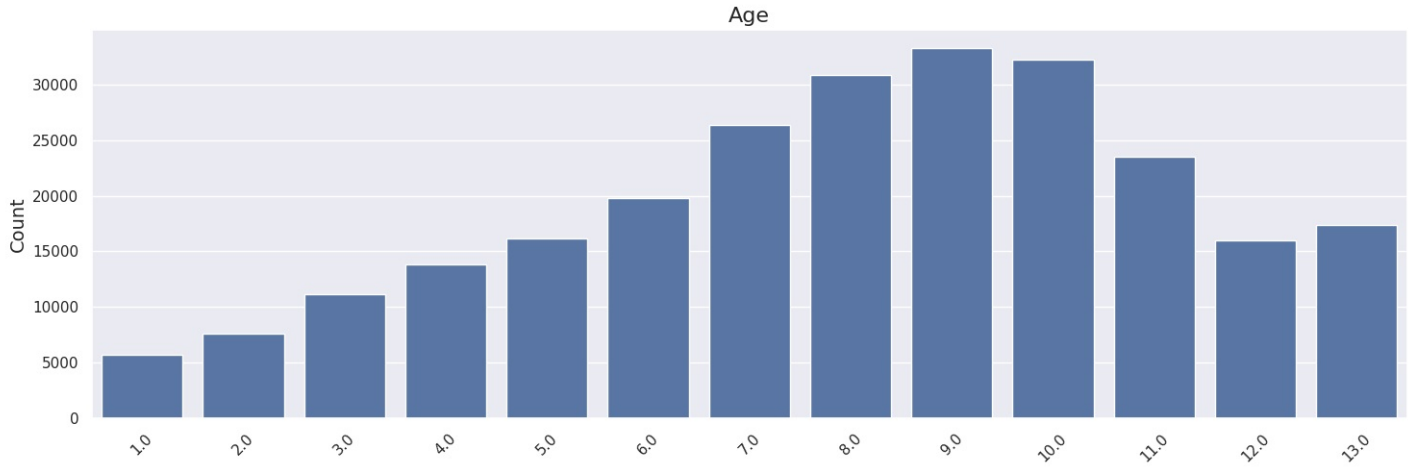
Education: Highest density at 6 (highest education level), with peaks at 4 and 5, and lower densities at 1, 2, and 3.

Income: Peaks at 4, 6, and 8, indicating these income levels are more common, with lower densities at other levels.

Categorical Variables - Countplot

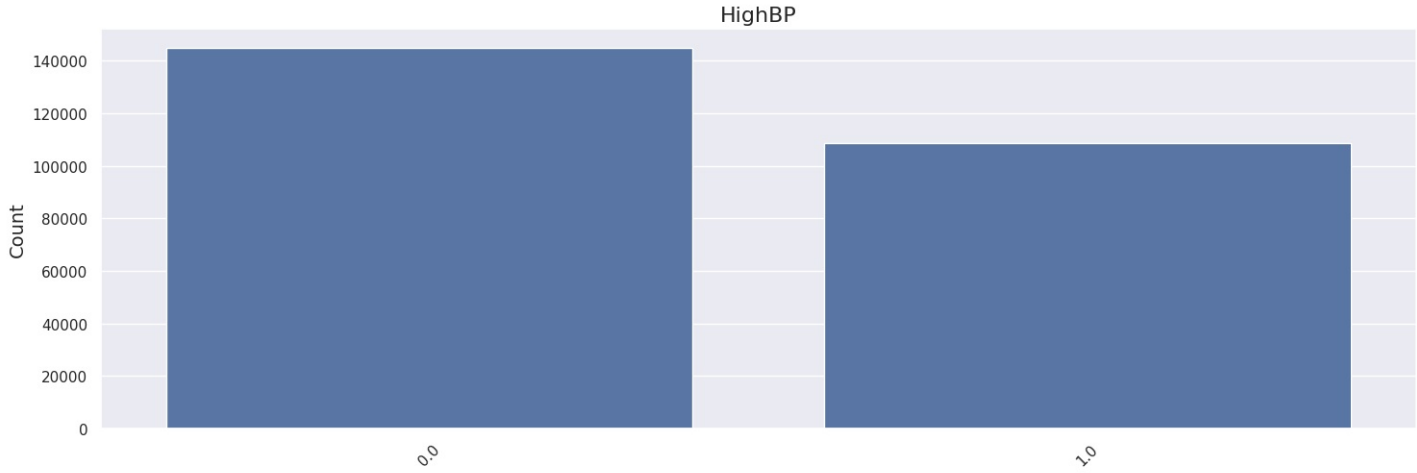
In [ ]:
```
# Set up the matplotlib figure and size
plt.figure(figsize=(15, 5 * len(categorical)))  # Adjust the figure size to fit all plots

# Iterate over each categorical feature to create a count plot
for index, feature in enumerate(categorical):
    plt.subplot(len(categorical), 1, index + 1)
    sns.countplot(data=df, x=feature)
    plt.title(feature, fontsize=16)
    plt.xlabel('')  # Remove x-labels as they are redundant with titles
    plt.ylabel('Count', fontsize=14)  # Ensure y-label is consistently set to 'Count'
    plt.xticks(rotation=45)  # Rotate x-axis labels by 45 degrees for readability

plt.tight_layout()
plt.show()
```

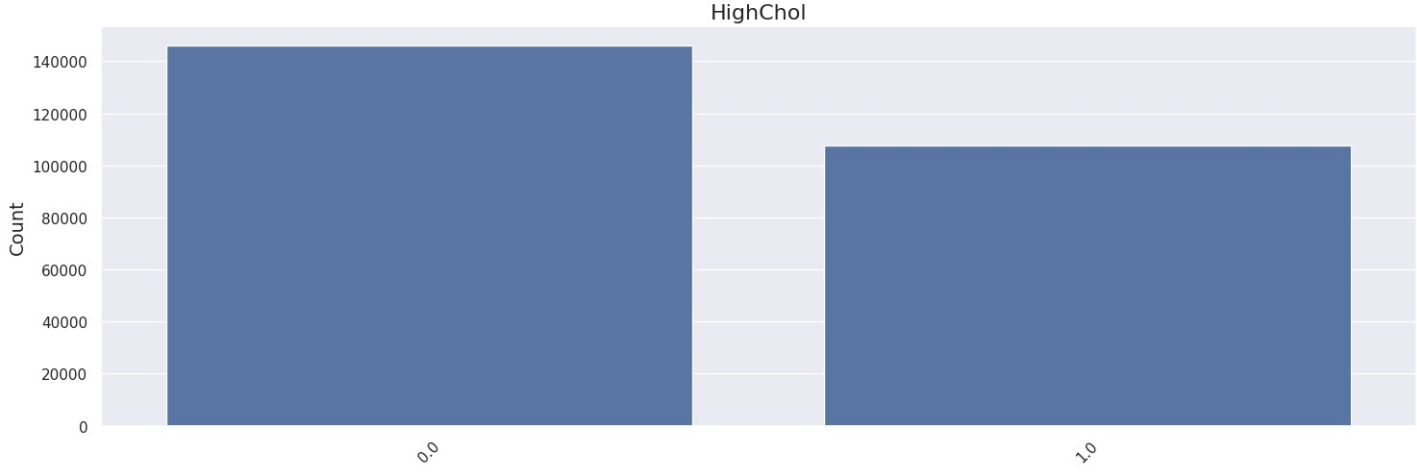


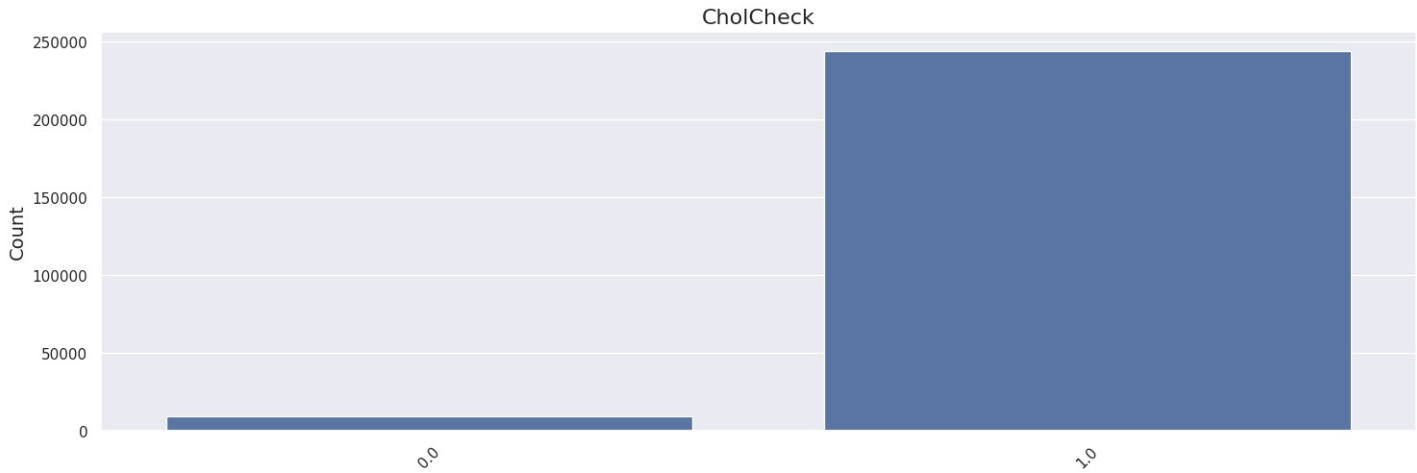


Binary Values - Countplot

In [ ]:
```
# Set up the matplotlib figure and size
plt.figure(figsize=(15, 5 * len(binary)))  # Adjust the figure size to fit all plots

# Iterate over each categorical feature to create a count plot
for index, feature in enumerate(binary):
    plt.subplot(len(binary), 1, index + 1)
    sns.countplot(data=df, x=feature)
    plt.title(feature, fontsize=16)
    plt.xlabel('')  # Remove x-labels as they are redundant with titles
    plt.ylabel('Count', fontsize=14)  # Ensure y-label is consistently set to 'Count'
    plt.xticks(rotation=45)  # Rotate x-axis labels by 45 degrees for readability

plt.tight_layout()
plt.show()
```






CholCheck
Count
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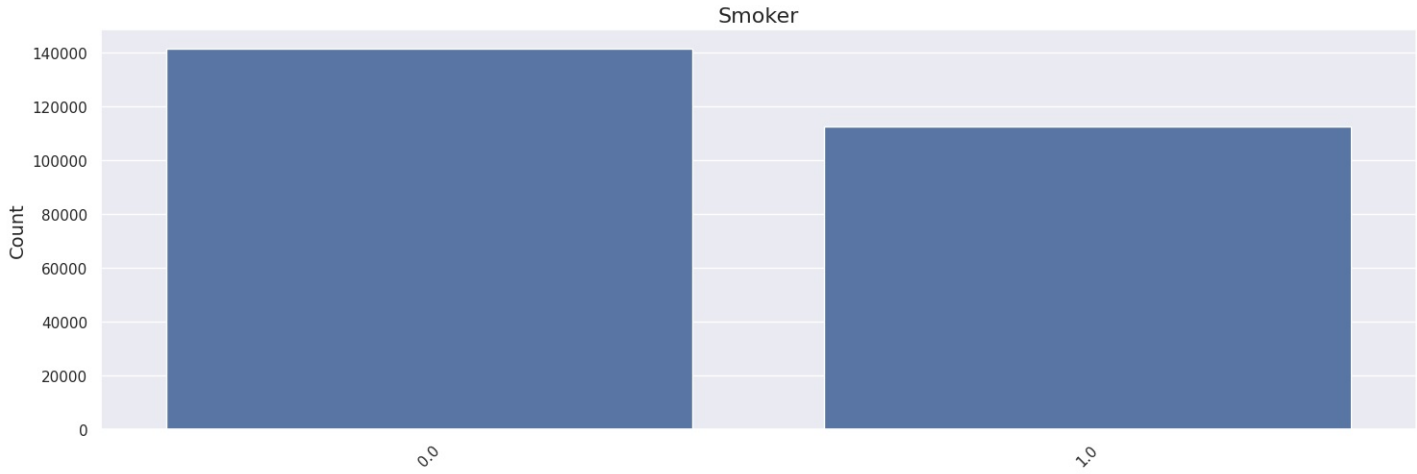
200000
150000
100000
50000
0
0.0
1.0


Smoker
Count
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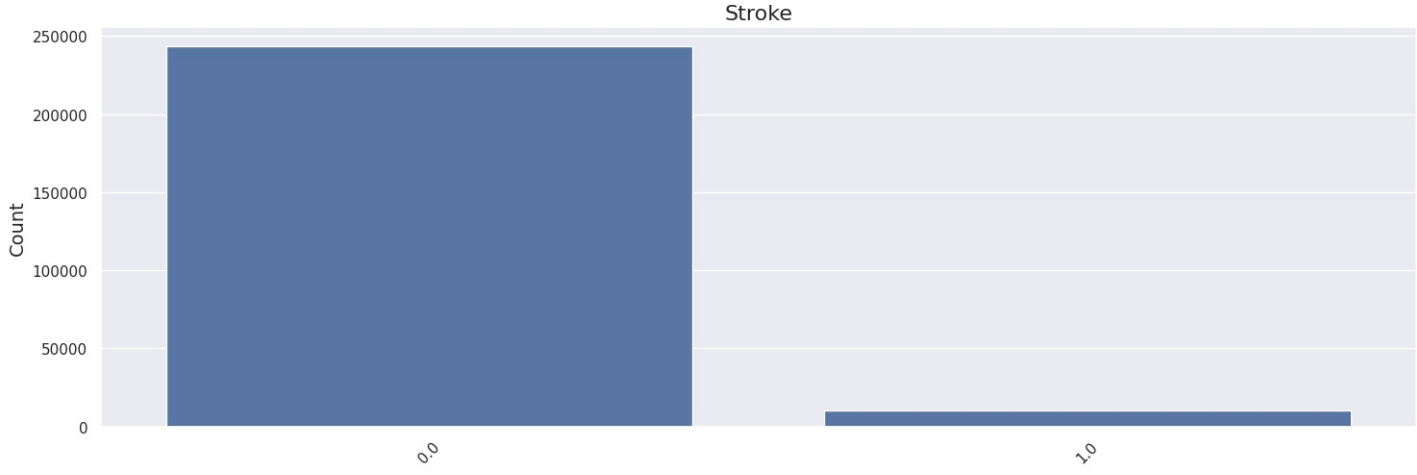
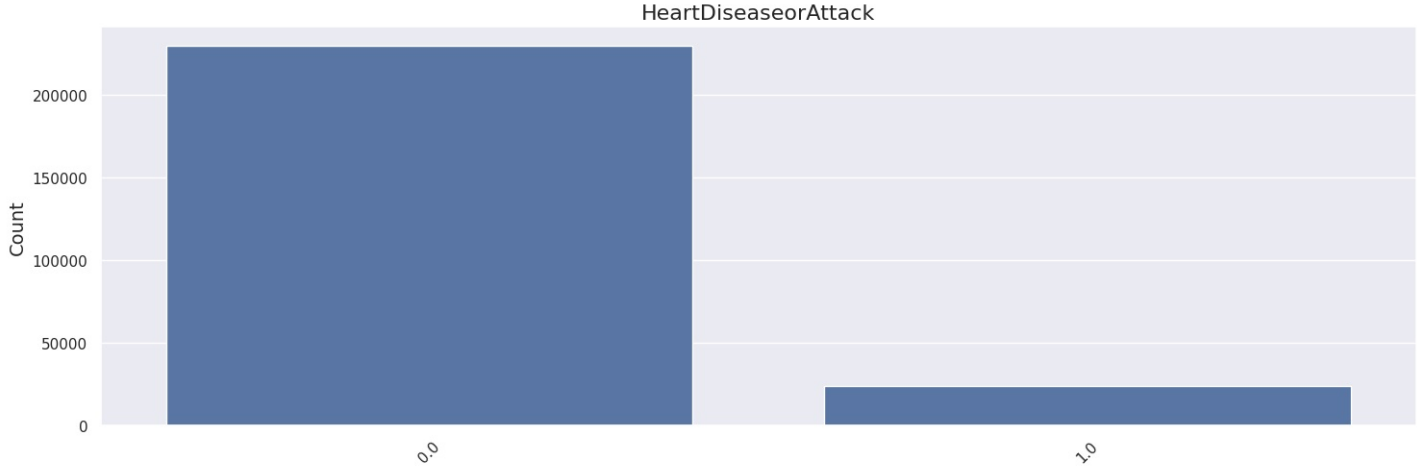
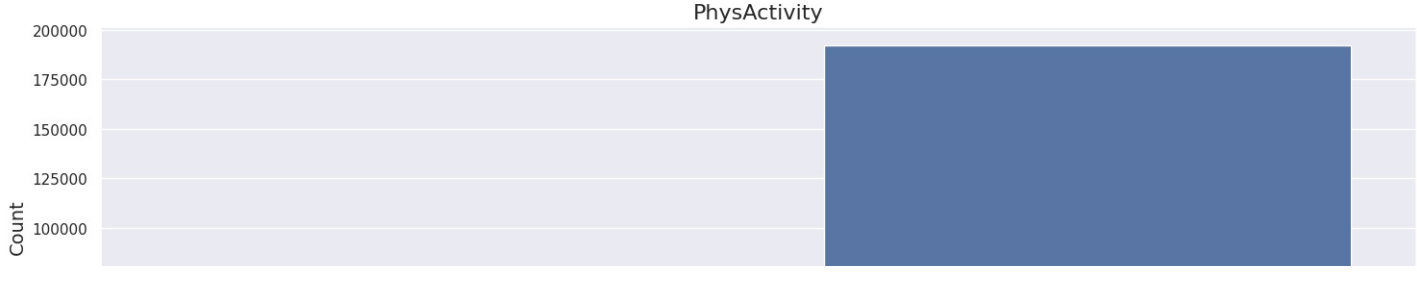
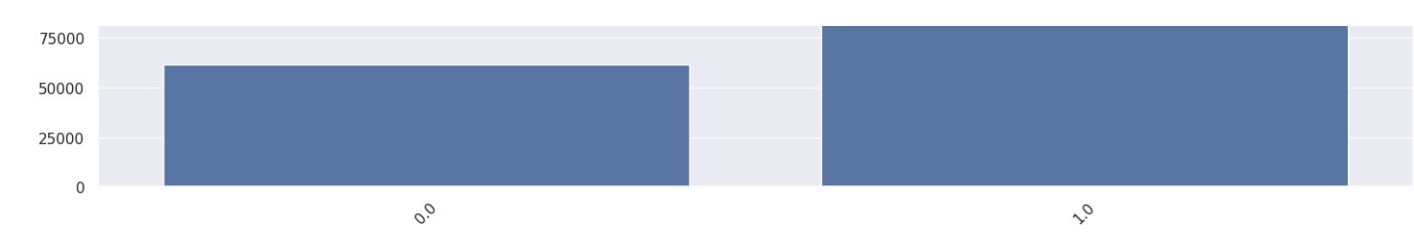
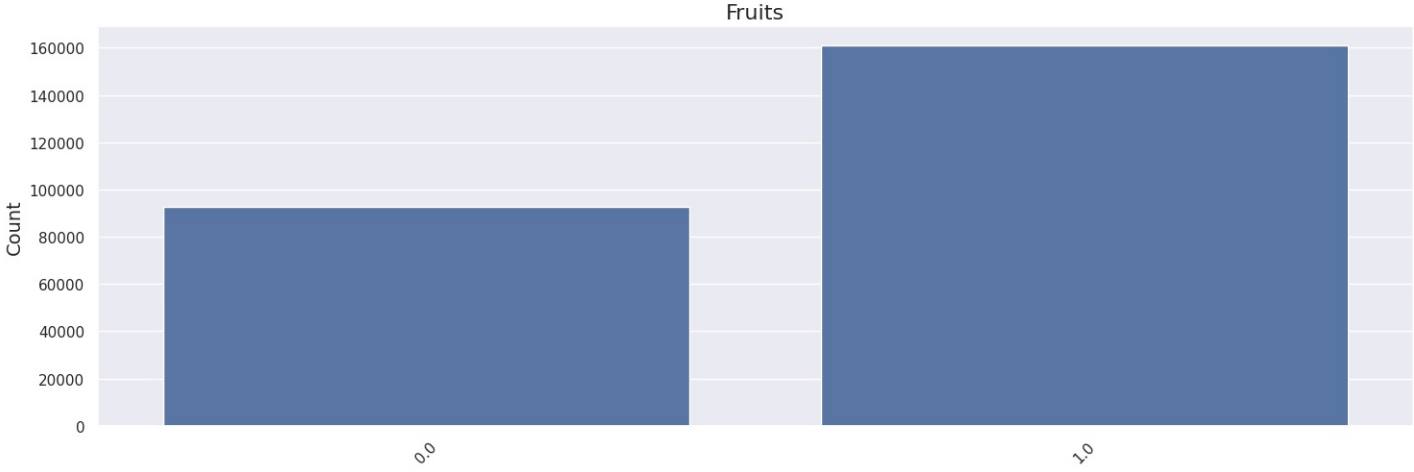
120000
100000
80000
60000
40000
20000
0
0.0
1.0

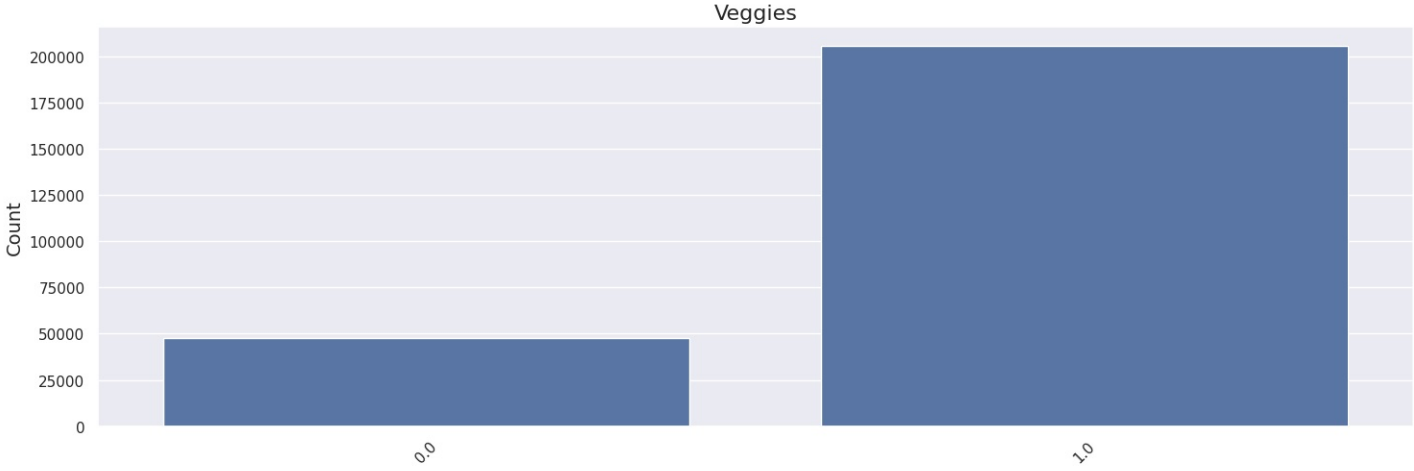

Stroke
Count
250000
200000
150000
100000
50000
0
0.0
1.0

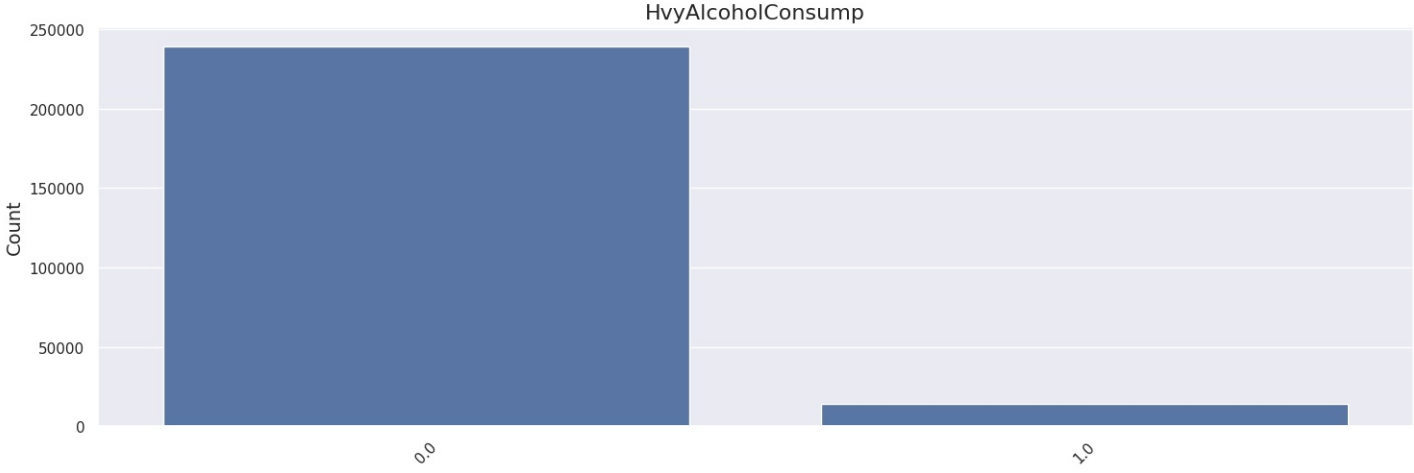

HeartDiseaseorAttack
Count
200000
150000
100000
50000
0
0.0
1.0


PhysActivity
Count
200000
175000
150000
125000
100000


75000
50000
25000
0
0.0
1.0


Fruits
160000
140000
120000
100000
80000
60000
40000
20000
0
Count
0.0
1.0


Veggies
200000
175000
150000
125000
100000
75000
50000
25000
0
Count
0.0
1.0


HvyAlcoholConsump
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200000
150000
100000
50000
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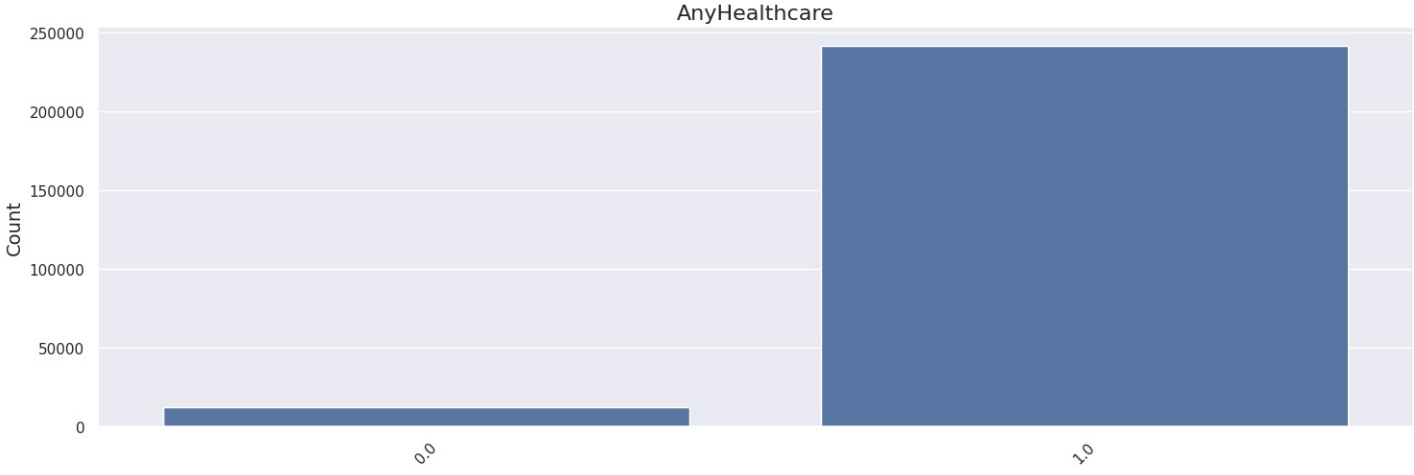
Count
0.0
1.0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100000
50000
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Count
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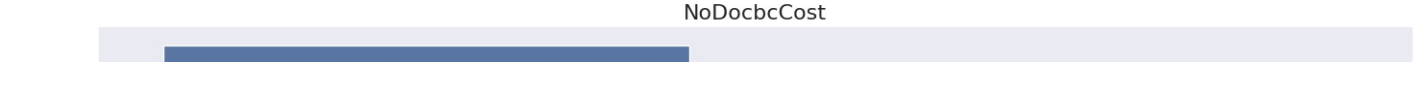
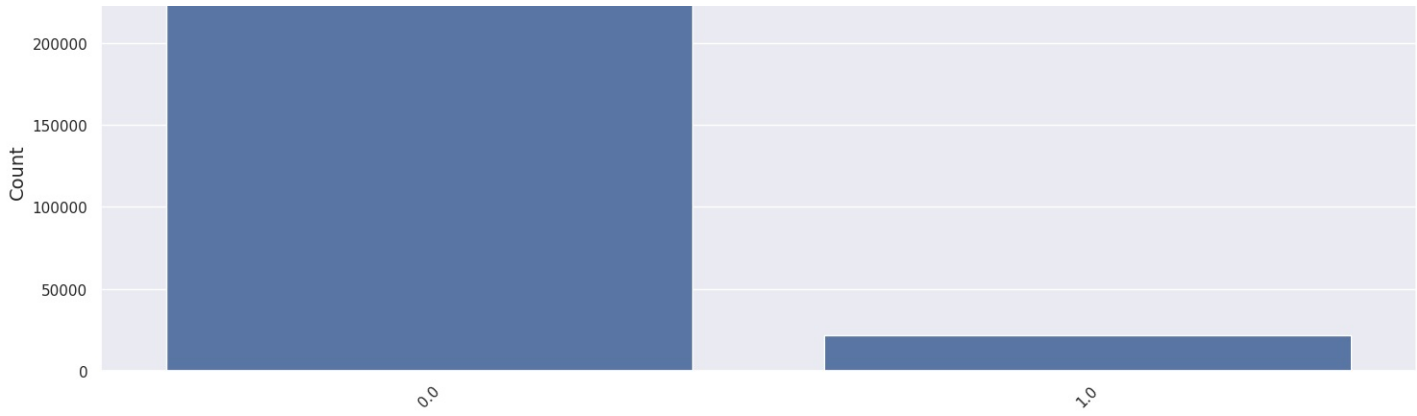
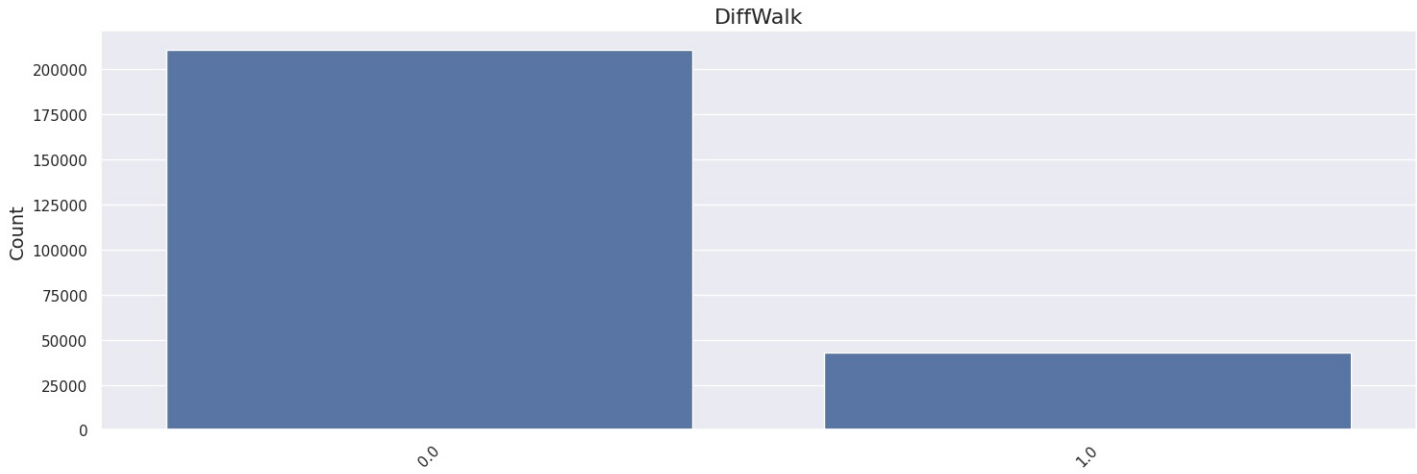
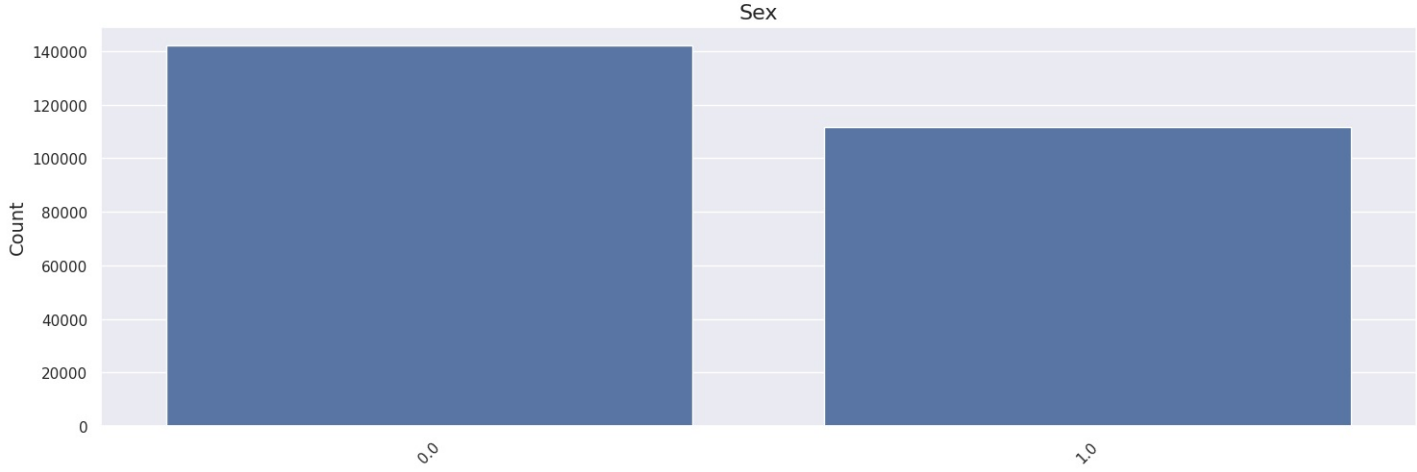
1.0


NoDocbcCost





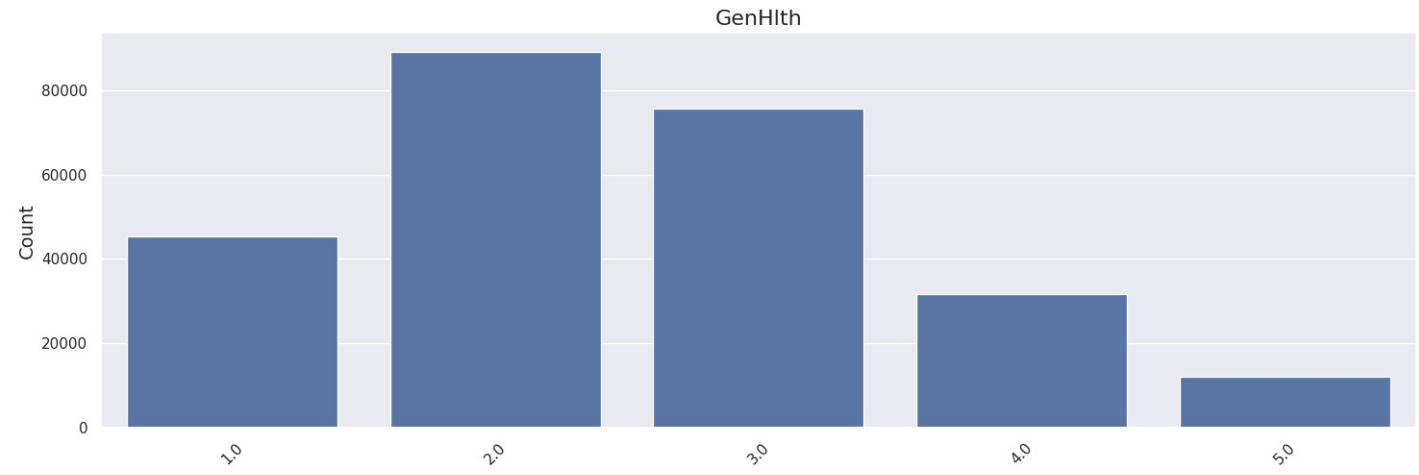


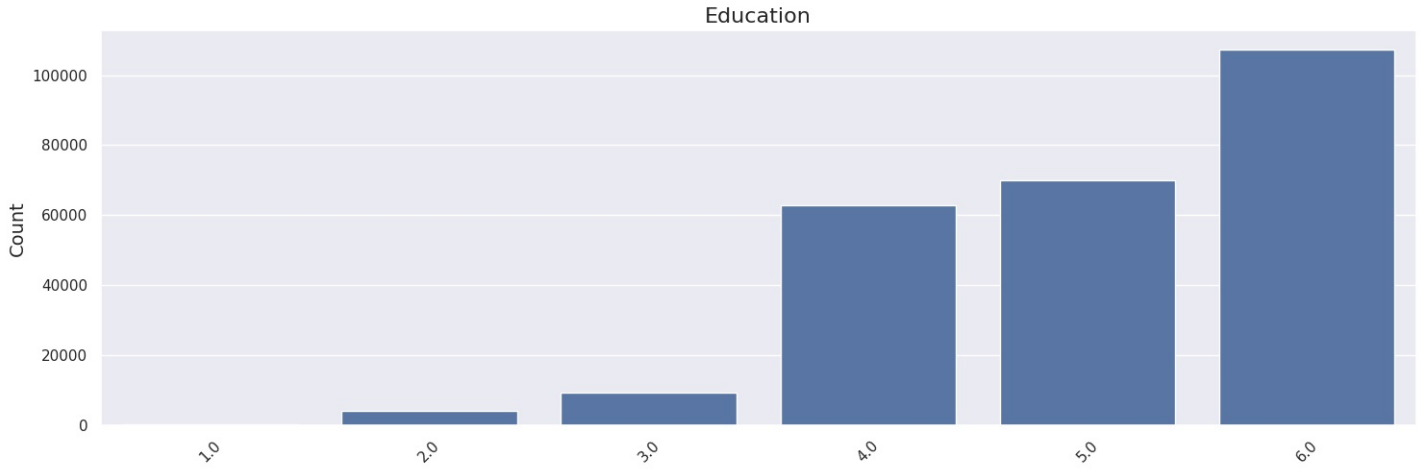
Ordinal Values - Countplot

In [ ]:
```
# Set up the matplotlib figure and size
plt.figure(figsize=(15, 5 * len(ordinal)))  # Adjust the figure size to fit all plots

# Iterate over each categorical feature to create a count plot
for index, feature in enumerate(ordinal):
    plt.subplot(len(ordinal), 1, index + 1)
    sns.countplot(data=df, x=feature)
    plt.title(feature, fontsize=16)
    plt.xlabel('')  # Remove x-labels as they are redundant with titles
    plt.ylabel('Count', fontsize=14)  # Ensure y-label is consistently set to 'Count'
    plt.xticks(rotation=45)  # Rotate x-axis labels by 45 degrees for readability

plt.tight_layout()
plt.show()
```





Histplot with hue

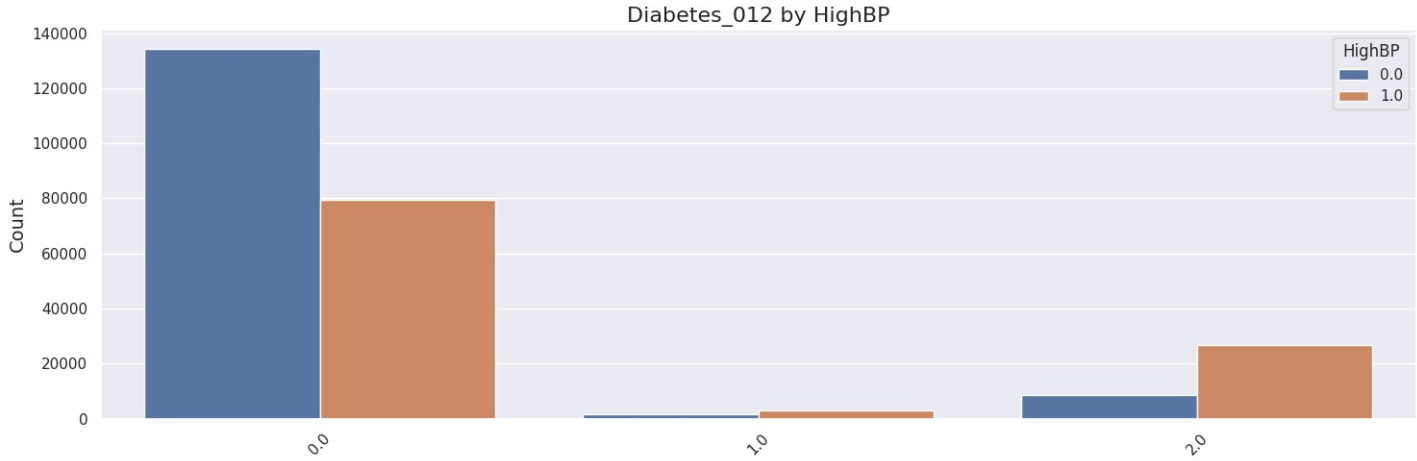
Categorical vs Binary

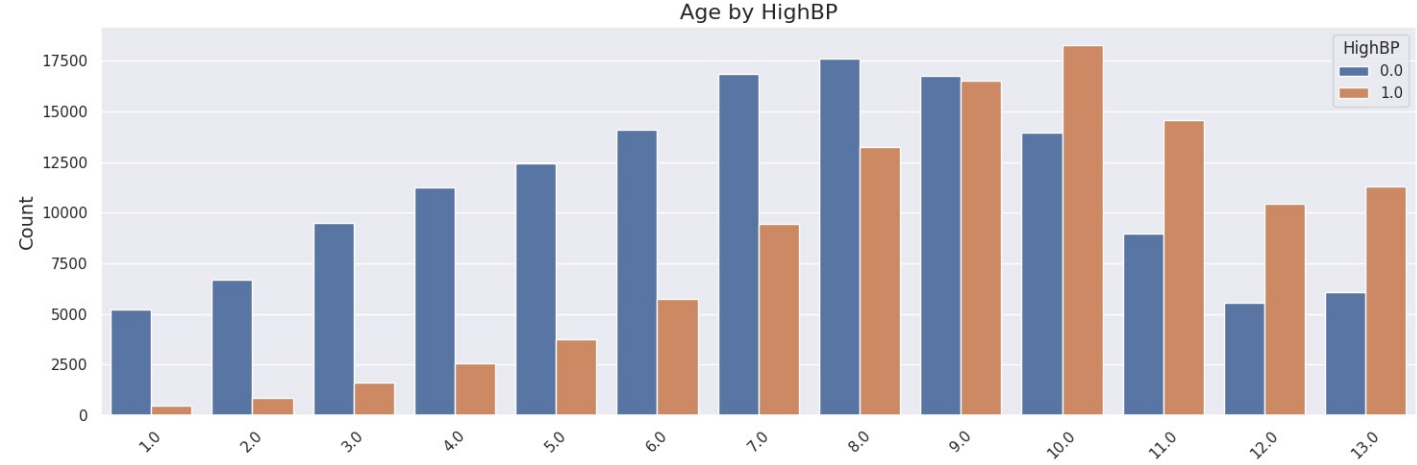
In [ ]:

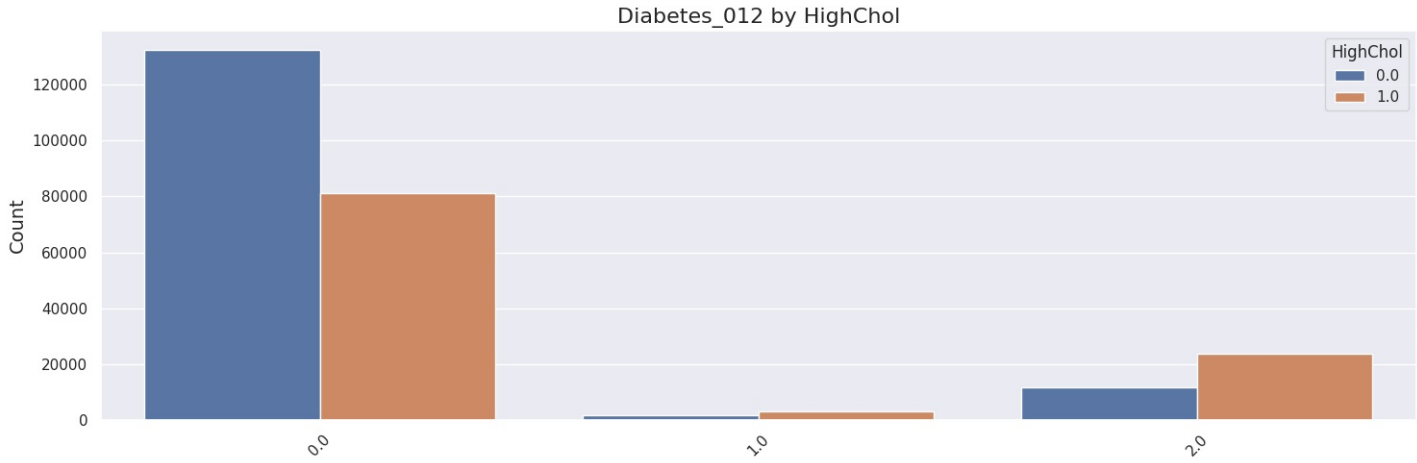
```
# Iterate over each binary feature as hue
for hue_feature in binary:
    # Set up the matplotlib figure and size
    plt.figure(figsize=(15, len(categorical) * 5))

    # Iterate over each categorical feature to create a count plot with hue
    for index, feature in enumerate(categorical):
        plt.subplot(len(categorical), 1, index + 1)
        sns.countplot(data=df, x=feature, hue=hue_feature)
        plt.title(f'{feature} by {hue_feature}', fontsize=16)
        plt.xlabel('')  # Remove x-labels as they are redundant with titles
        plt.ylabel('Count', fontsize=14)  # Ensure y-label is consistently set to 'Count'
        plt.xticks(rotation=45)  # Rotate x-axis labels by 45 degrees for readability
        plt.legend(title=hue_feature, loc='upper right')  # Add legend

    plt.tight_layout()
    plt.show()
```


Diabetes_012 by HighBP
Count
HighBP
0.0
1.0
0.0
1.0
2.0


Age by HighBP
Count
HighBP
0.0
1.0
1.0
2.0
3.0
4.0
5.0
6.0
7.0
8.0
9.0
10.0
11.0
12.0
13.0


Diabetes_012 by HighChol
Count
HighChol
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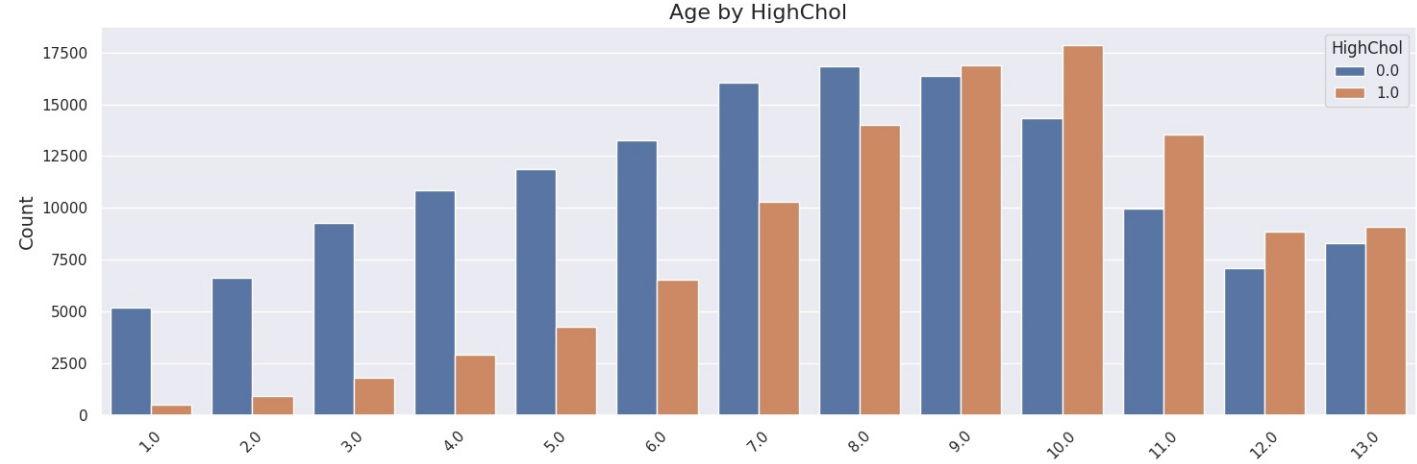
1.0
0.0
1.0
2.0


Age by HighChol
Count
HighChol
0.0
1.0
1.0
2.0
3.0
4.0
5.0
6.0
7.0
8.0
9.0
10.0
11.0
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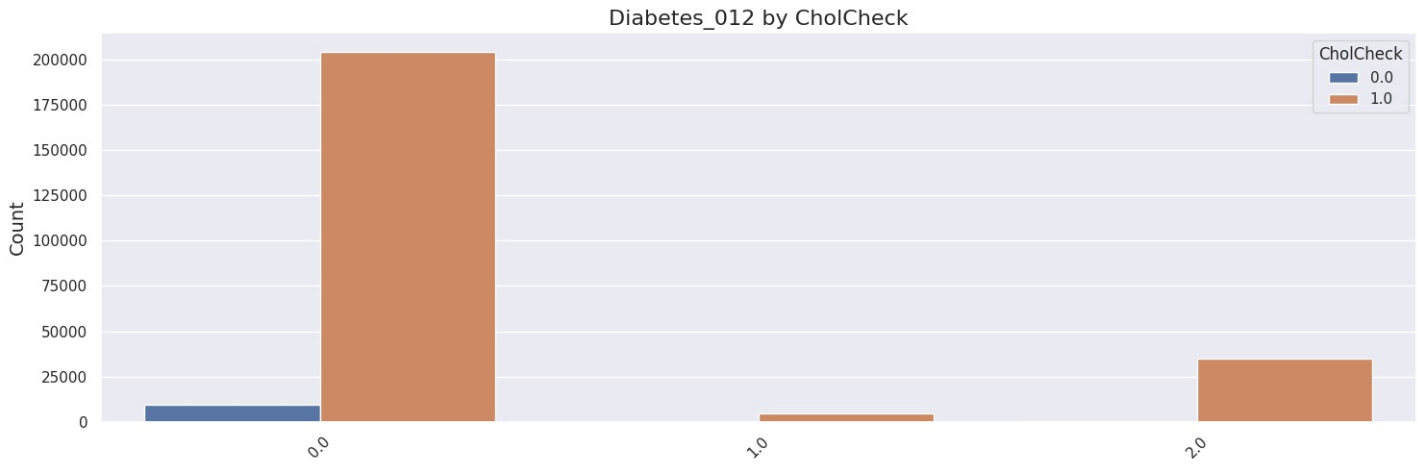
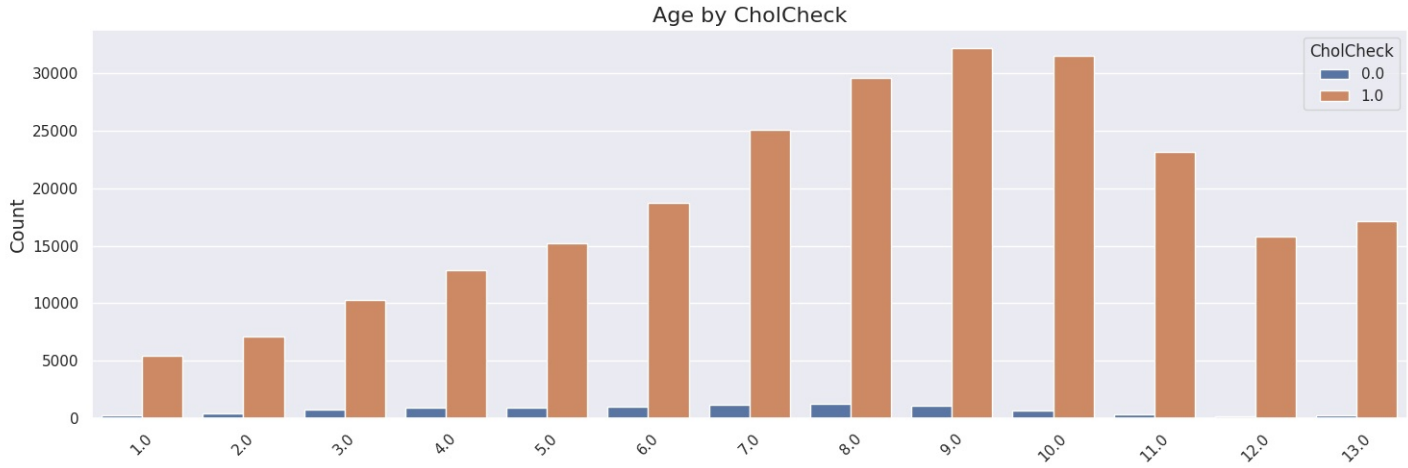
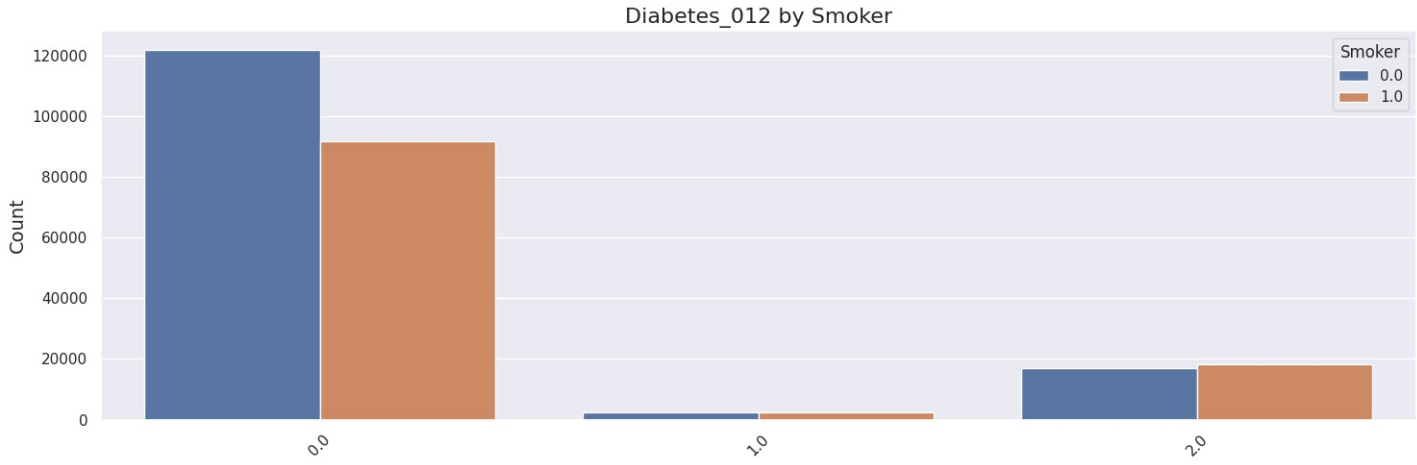
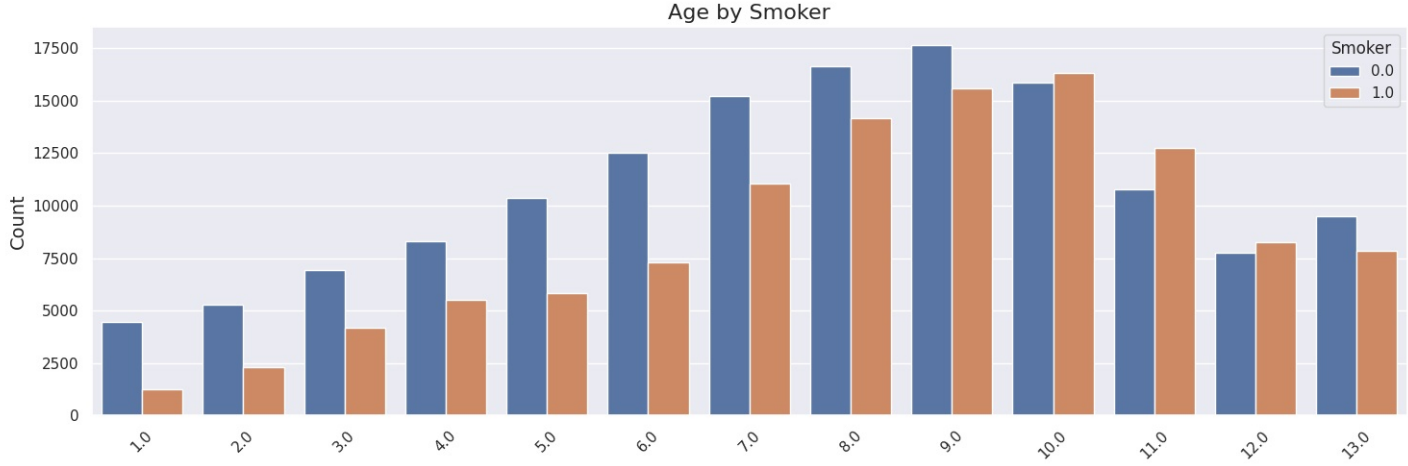
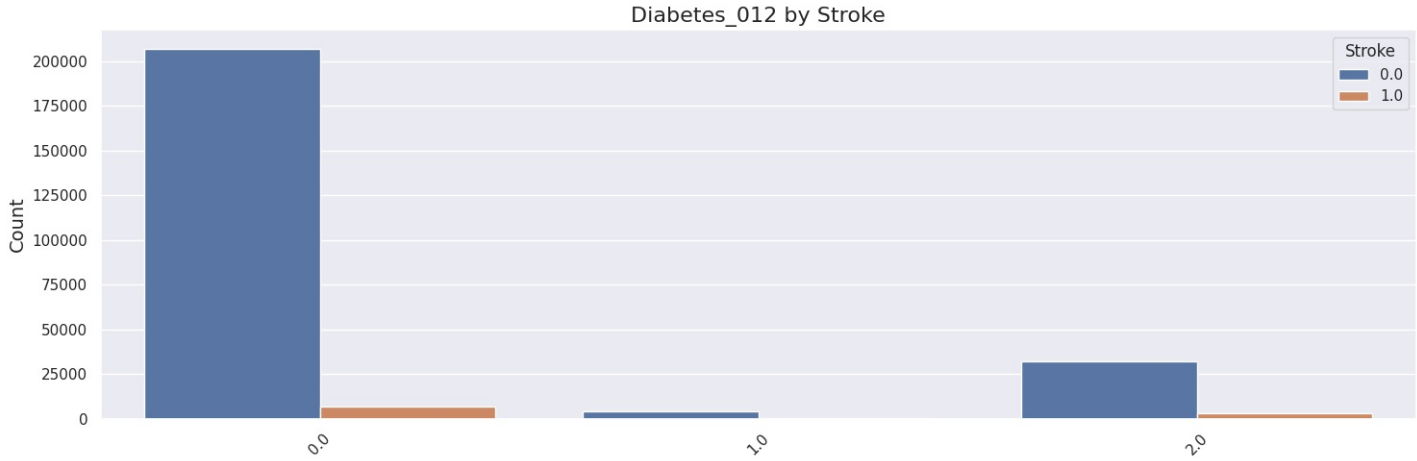
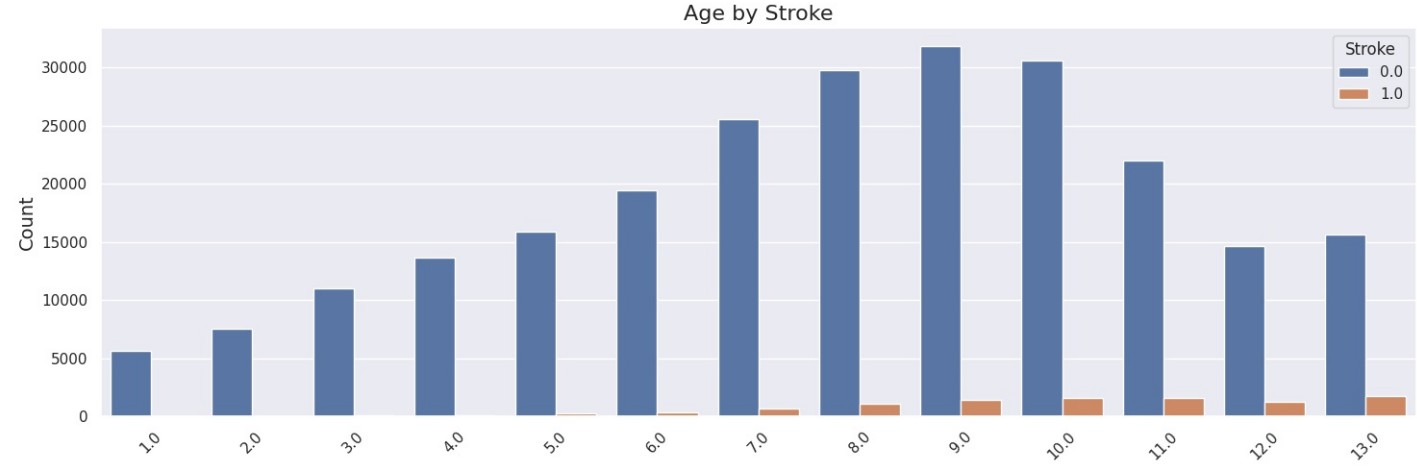

Diabetes_012 by CholCheck
Count
CholCheck
0.0
1.0
0.0
1.0
2.0

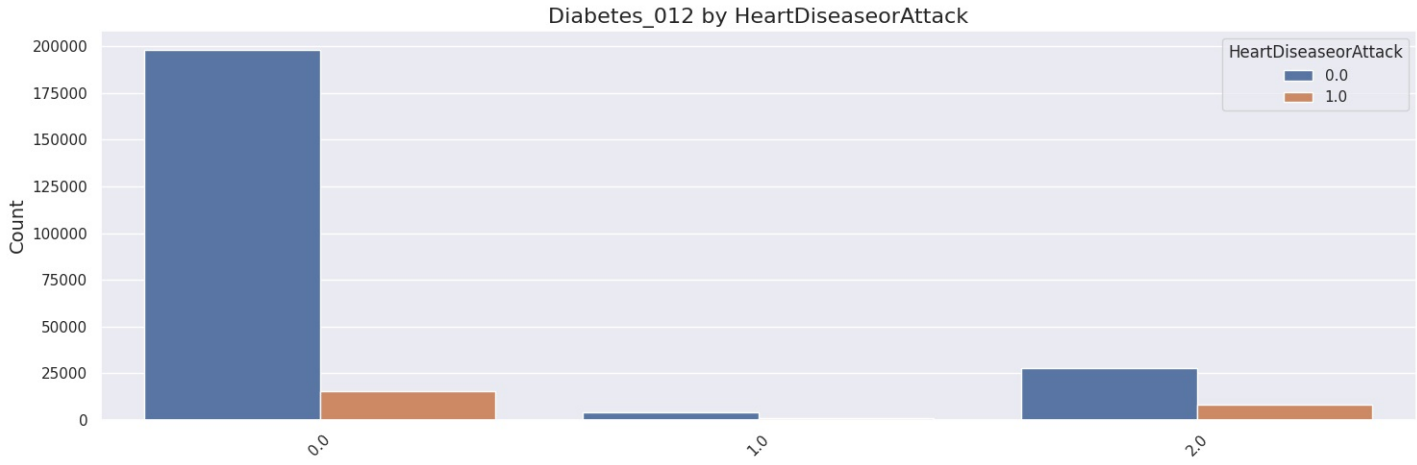

Age by CholCheck
Count
CholCheck
0.0
1.0
1.0
2.0
3.0
4.0
5.0
6.0
7.0
8.0
9.0
10.0
11.0
12.0
13.0

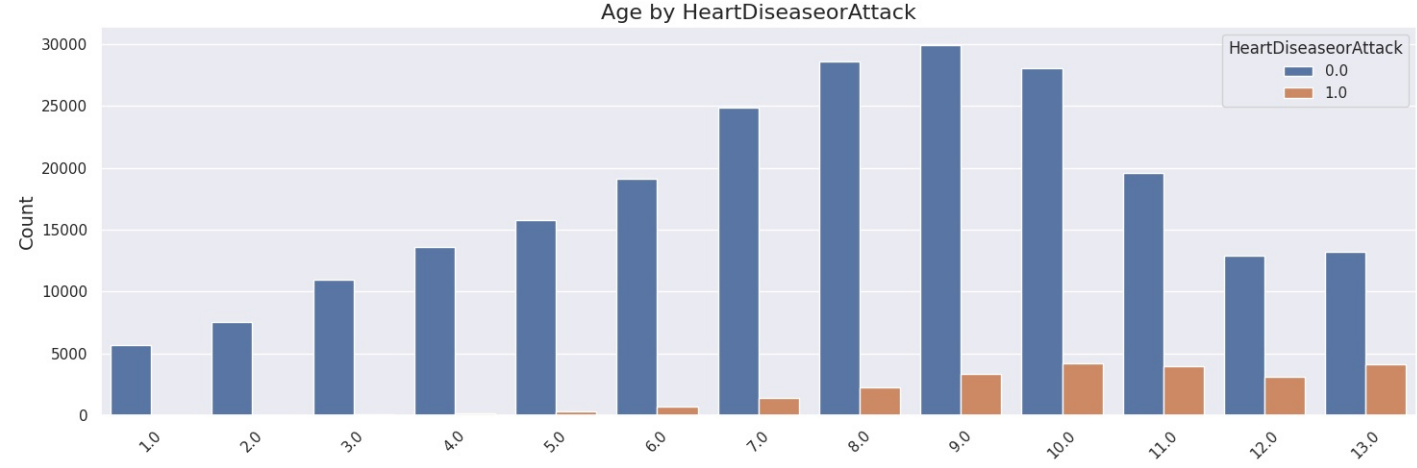

Diabetes_012 by Smoker
Count
Smoker
0.0
1.0
0.0
1.0
2.0


Age by Smoker
Count
Smoker
0.0
1.0
1.0
2.0
3.0
4.0
5.0
6.0
7.0
8.0
9.0
10.0
11.0
12.0
13.0


Diabetes_012 by Stroke
Stroke
0.0
1.0
Count
200000
175000
150000
125000
100000
75000
50000
25000
0
0.0
1.0
2.0


Age by Stroke
Stroke
0.0
1.0
Count
30000
25000
20000
15000
10000
5000
0
1.0
2.0
3.0
4.0
5.0
6.0
7.0
8.0
9.0
10.0
11.0
12.0
13.0


Diabetes_012 by HeartDiseaseorAttack
HeartDiseaseorAttack
0.0
1.0
Count
200000
175000
150000
125000
100000
75000
50000
25000
0
0.0
1.0
2.0


Age by HeartDiseaseorAttack
HeartDiseaseorAttack
0.0
1.0
Count
30000
25000
20000
15000
10000
5000
0
1.0
2.0
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5.0
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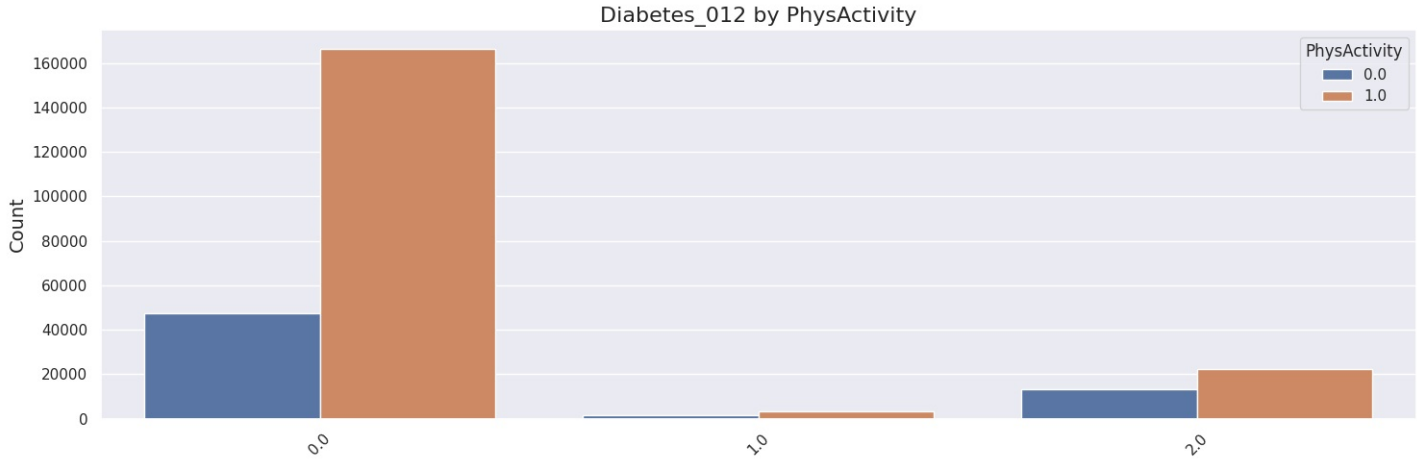
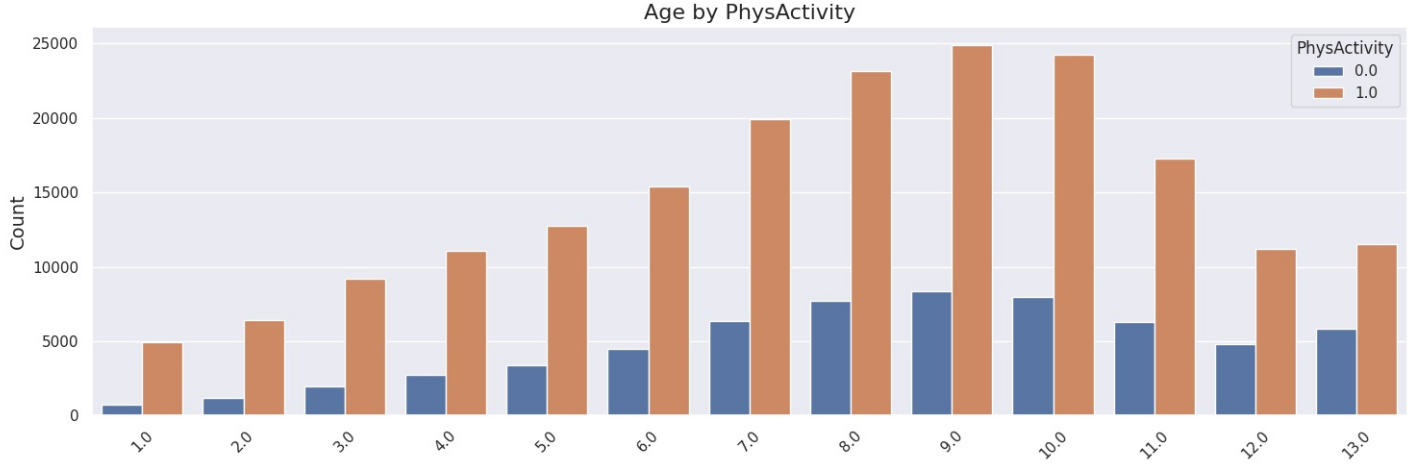
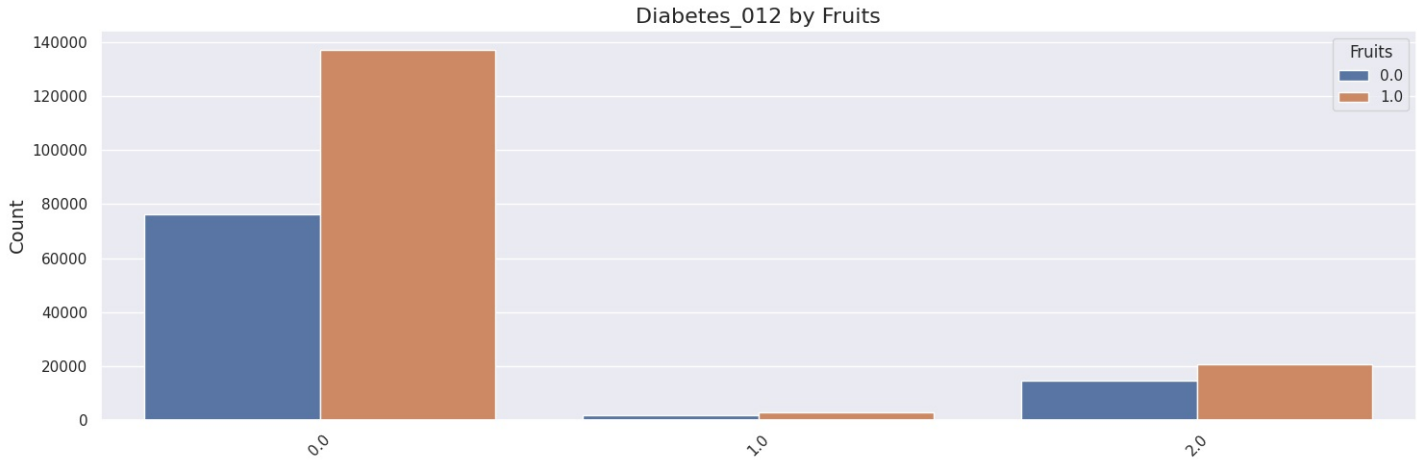
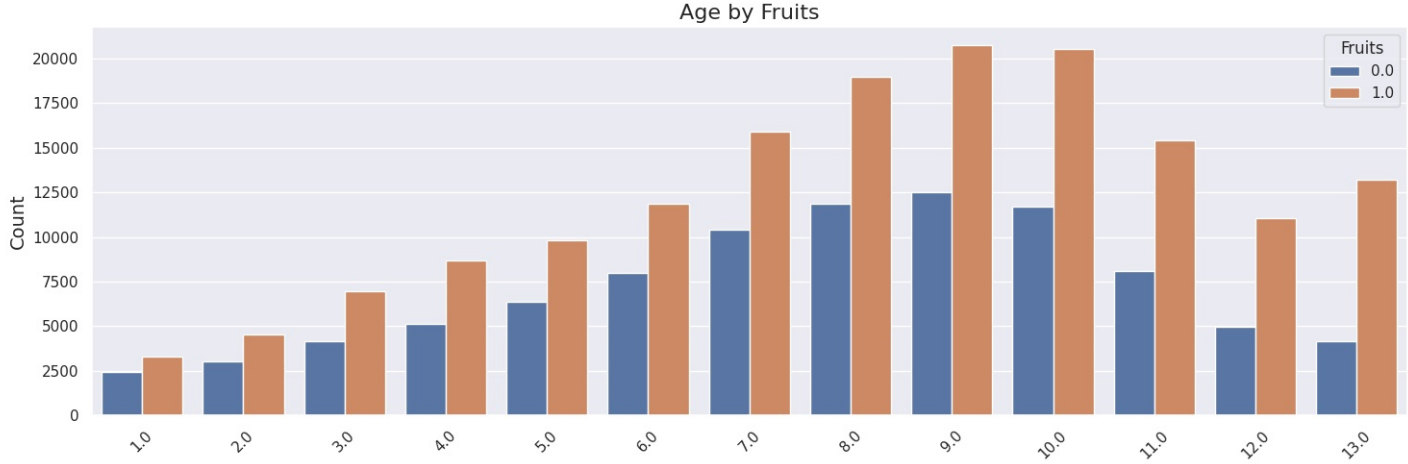
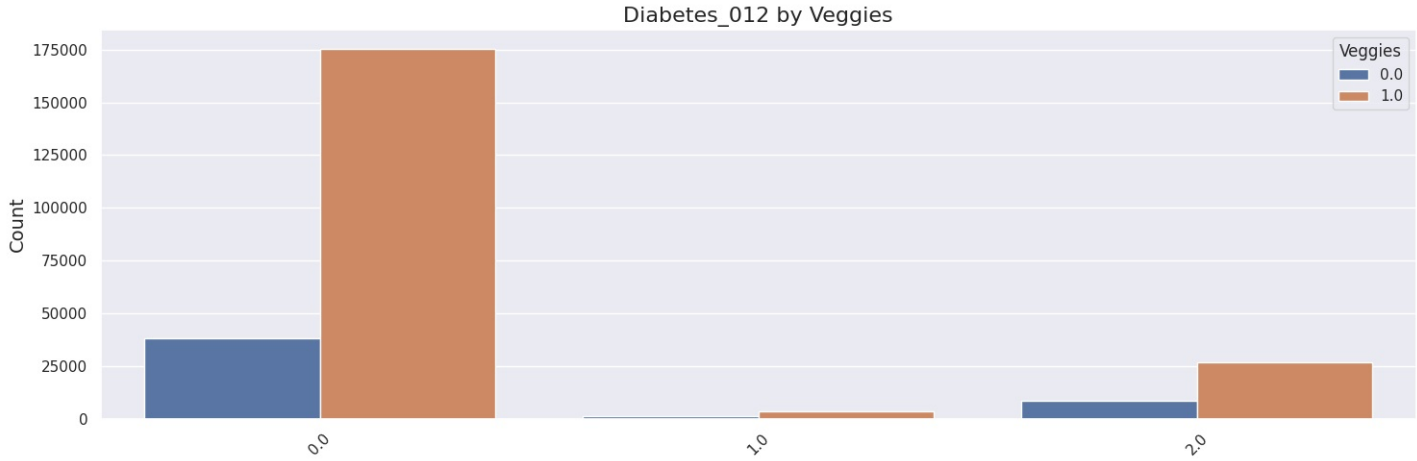
8.0
9.0
10.0
11.0
12.0
13.0

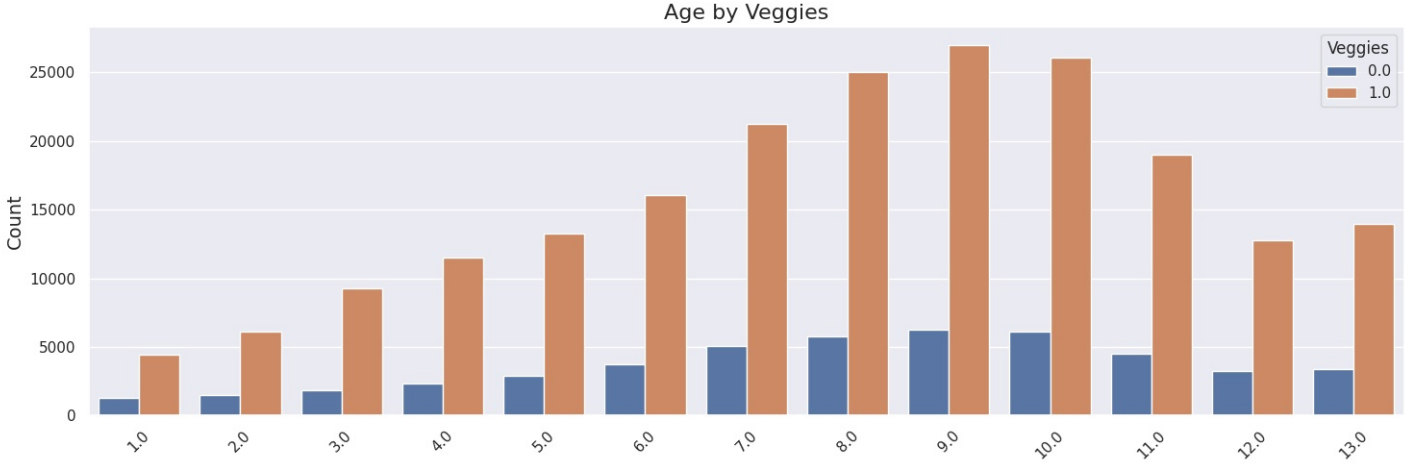

Diabetes_012 by PhysActivity
Count
PhysActivity
0.0
1.0
0.0
1.0
2.0

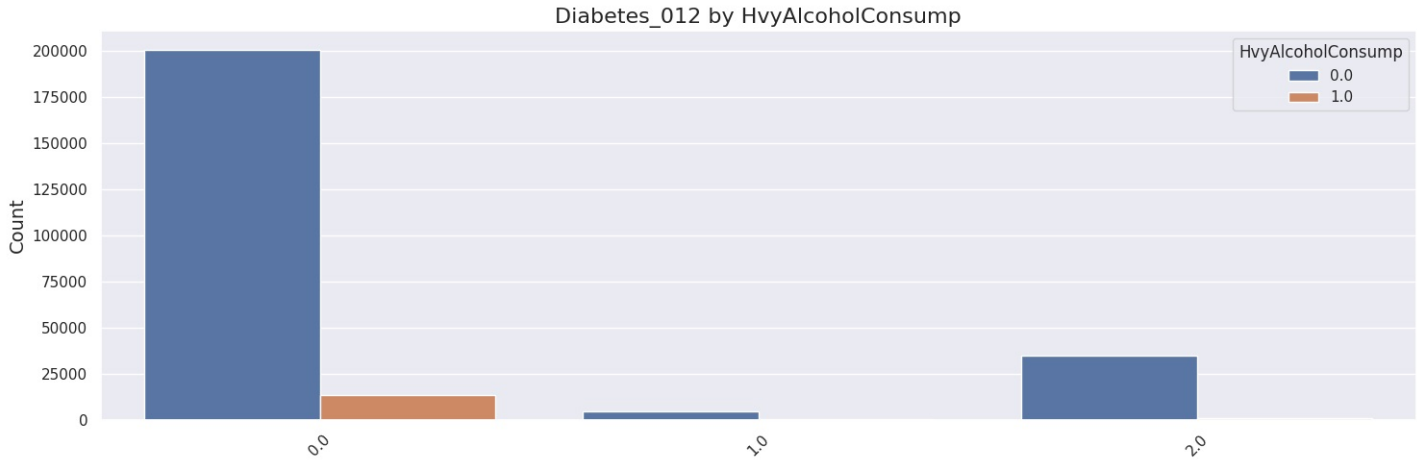

Age by PhysActivity
Count
PhysActivity
0.0
1.0
1.0
2.0
3.0
4.0
5.0
6.0
7.0
8.0
9.0
10.0
11.0
12.0
13.0

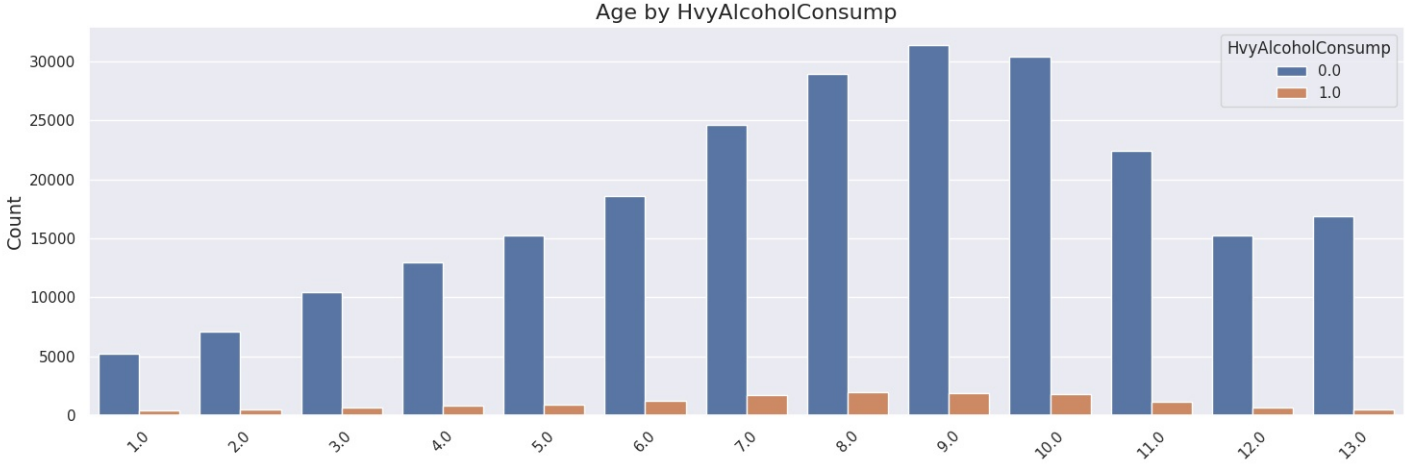

Diabetes_012 by Fruits
Count
Fruits
0.0
1.0
0.0
1.0
2.0

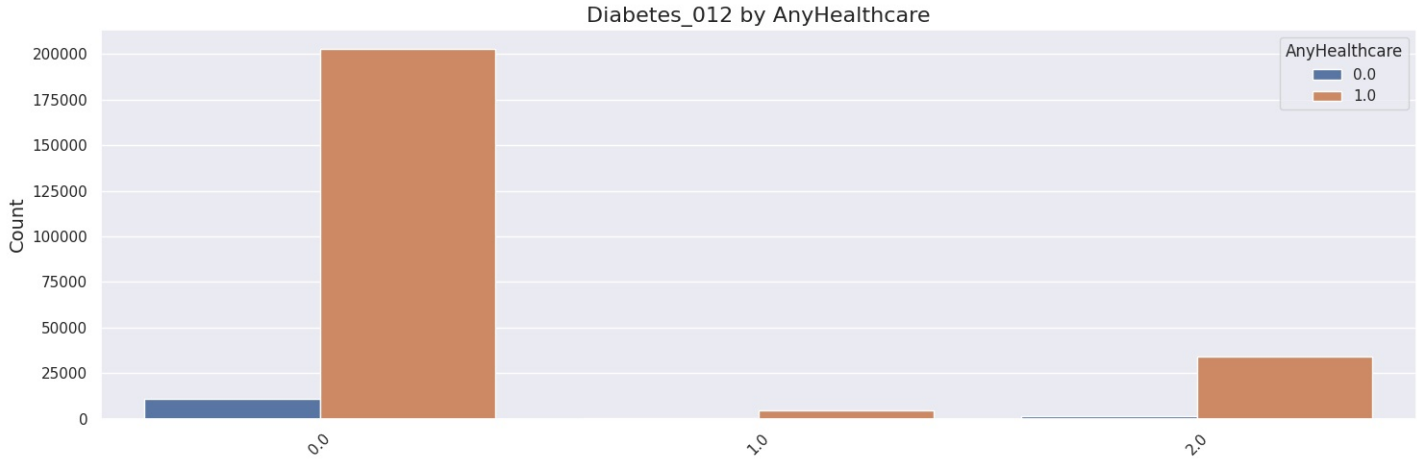

Age by Fruits
Count
Fruits
0.0
1.0
1.0
2.0
3.0
4.0
5.0
6.0
7.0
8.0
9.0
10.0
11.0
12.0
13.0

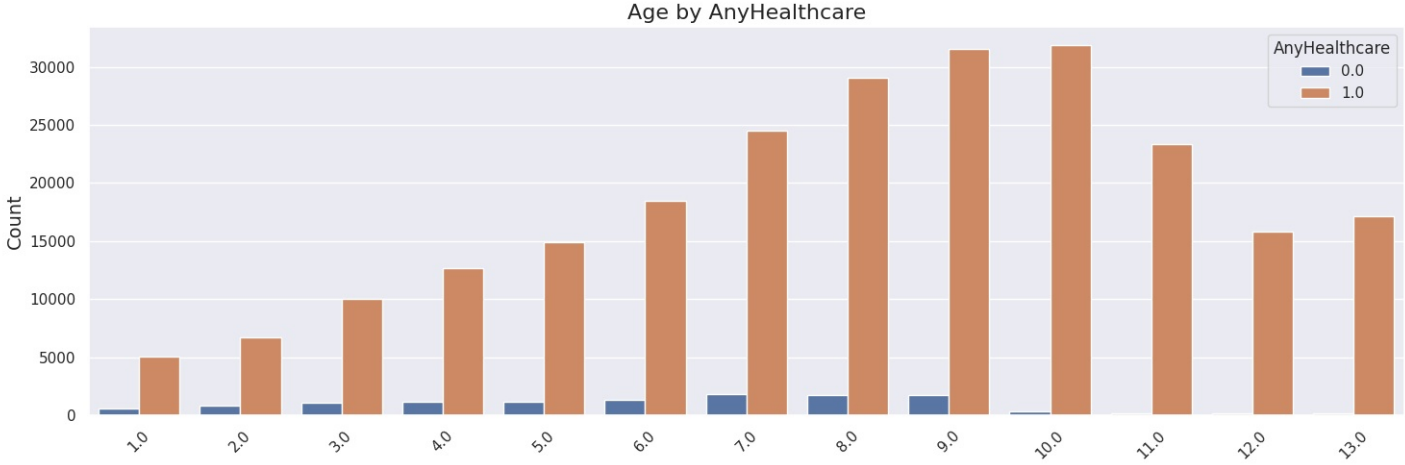

Diabetes_012 by Veggies
Count
Veggies
0.0
1.0
0.0
1.0
2.0

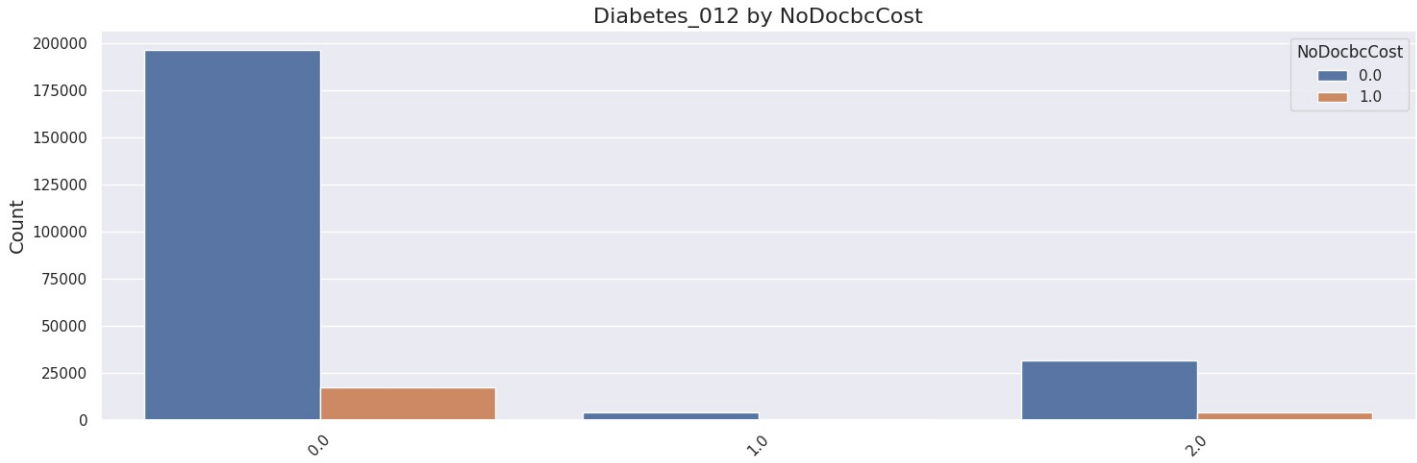

Age by Veggies
Count
Veggies
0.0
1.0
1.0
2.0
3.0
4.0
5.0
6.0
7.0
8.0
9.0
10.0
11.0
12.0
13.0

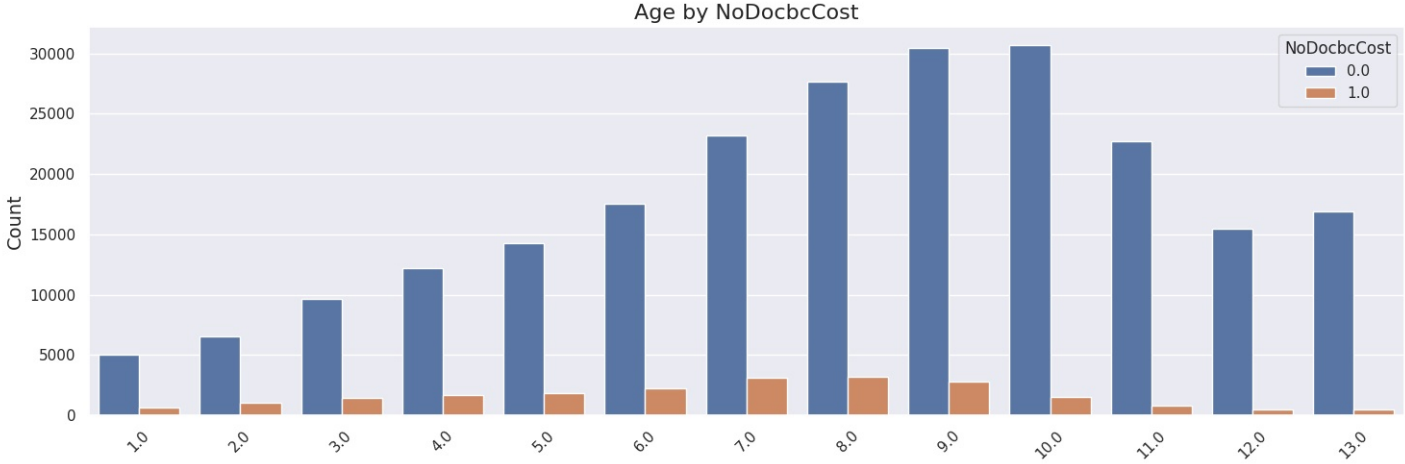

Diabetes_012 by HvyAlcoholConsump
Count
HvyAlcoholConsump
0.0
1.0
0.0
1.0
2.0

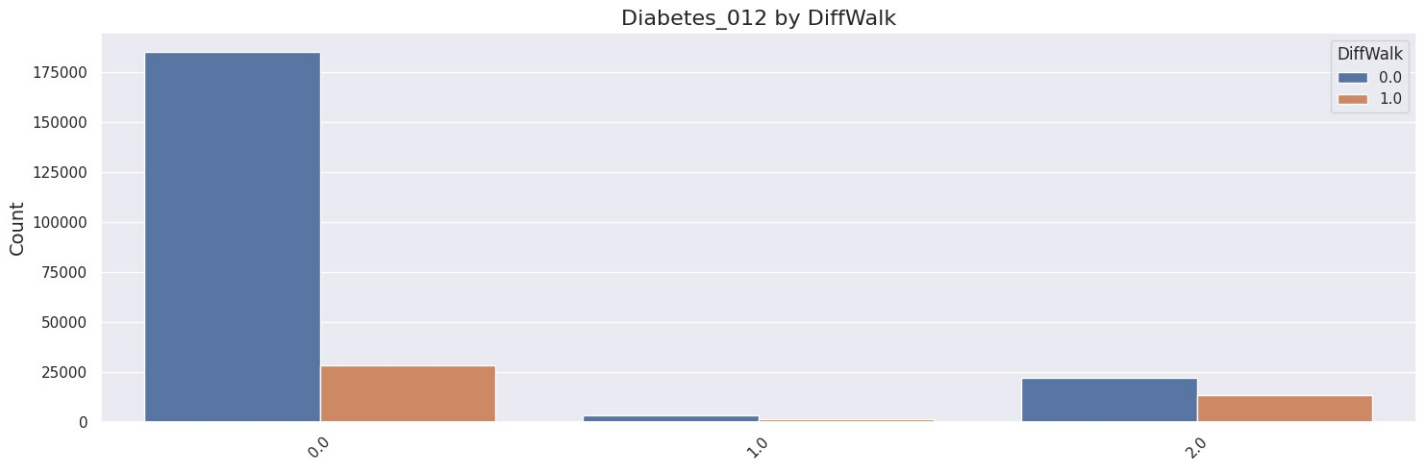

Age by HvyAlcoholConsump
Count
HvyAlcoholConsump
0.0
1.0
1.0
2.0
3.0
4.0
5.0
6.0
7.0
8.0
9.0
10.0
11.0
12.0
13.0

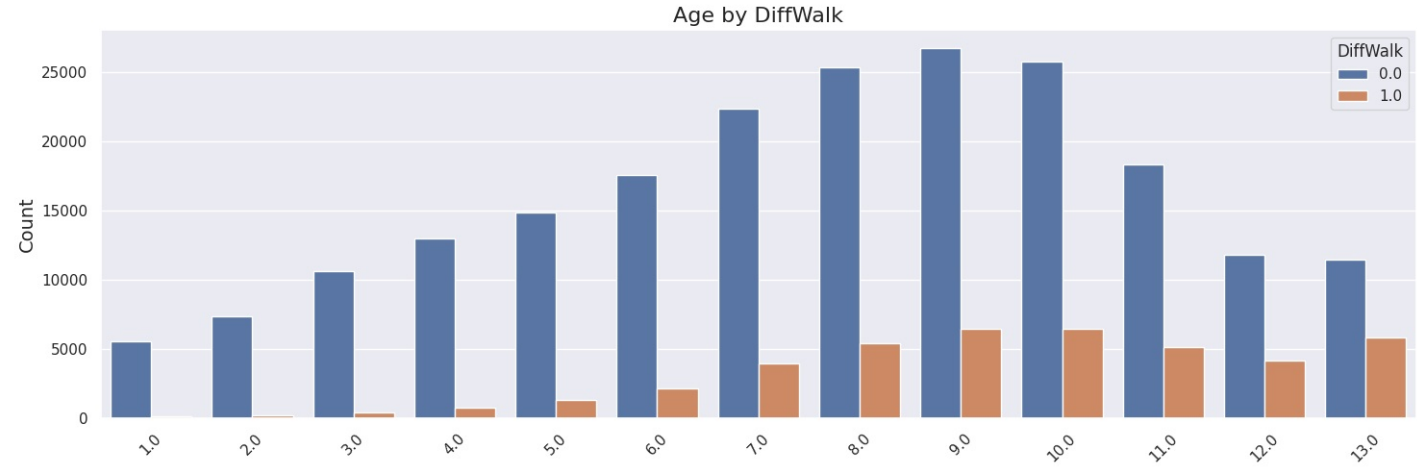

Diabetes_012 by AnyHealthcare
Count
AnyHealthcare
0.0
1.0
0.0
1.0
2.0

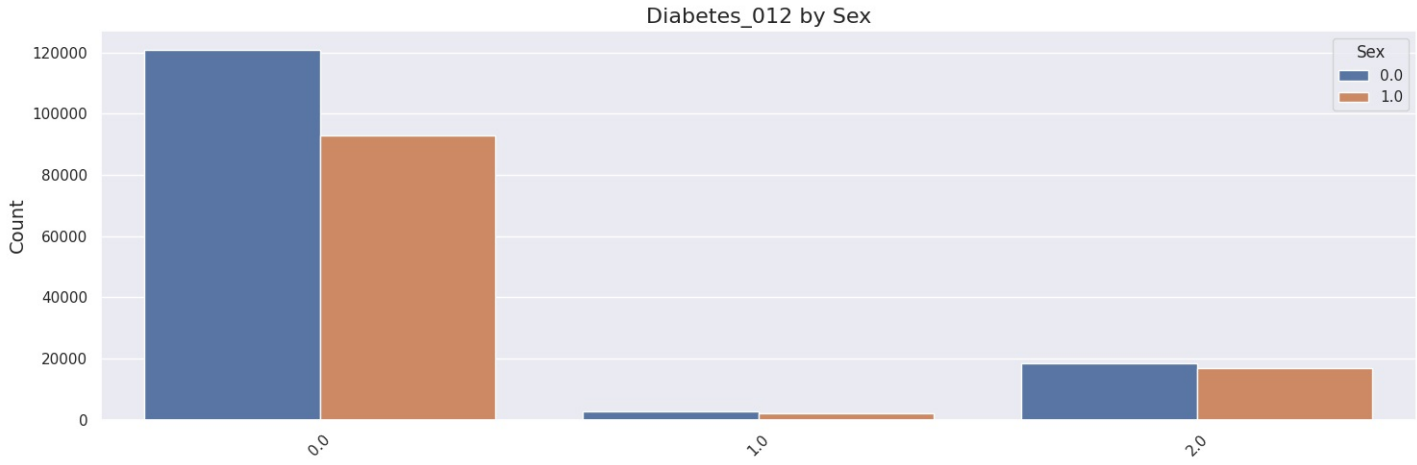

Age by AnyHealthcare
Count
AnyHealthcare
0.0
1.0
1.0
2.0
3.0
4.0
5.0
6.0
7.0
8.0
9.0
10.0
11.0
12.0
13.0

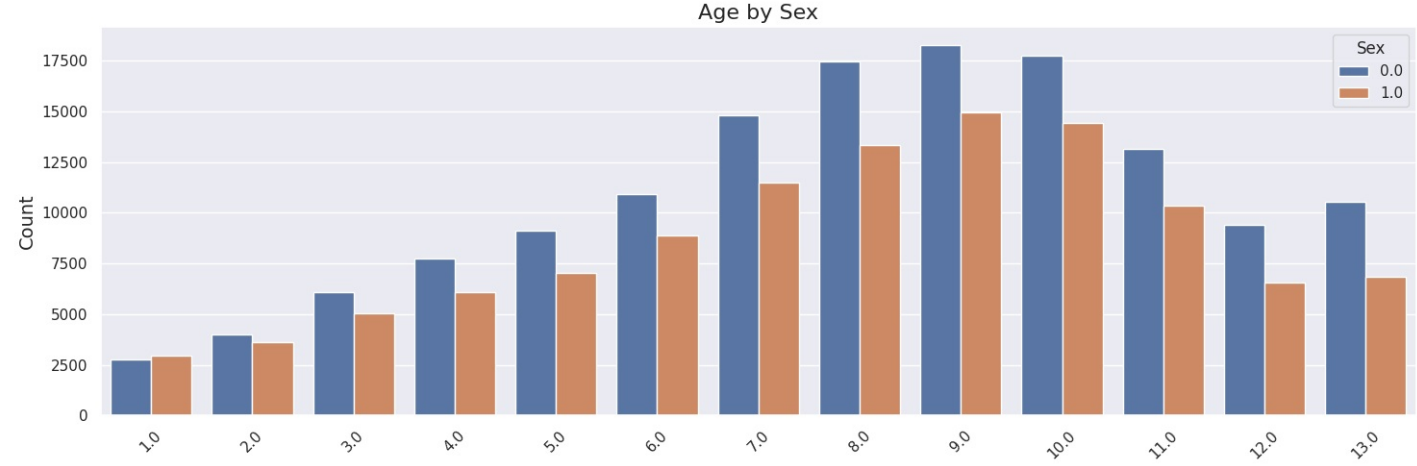

Diabetes_012 by NoDocbcCost
Count
NoDocbcCost
0.0
1.0
0.0
1.0
2.0


Age by NoDocbcCost
Count
NoDocbcCost
0.0
1.0
1.0
2.0
3.0
4.0
5.0
6.0
7.0
8.0
9.0
10.0
11.0
12.0
13.0









Diabetes_012 Distribution:

The majority of individuals have no diabetes (0), with a very small proportion of the population in the prediabetes (1) and diabetes (2) categories. This indicates that most of the dataset's individuals do not have diabetes.

Age Distribution:

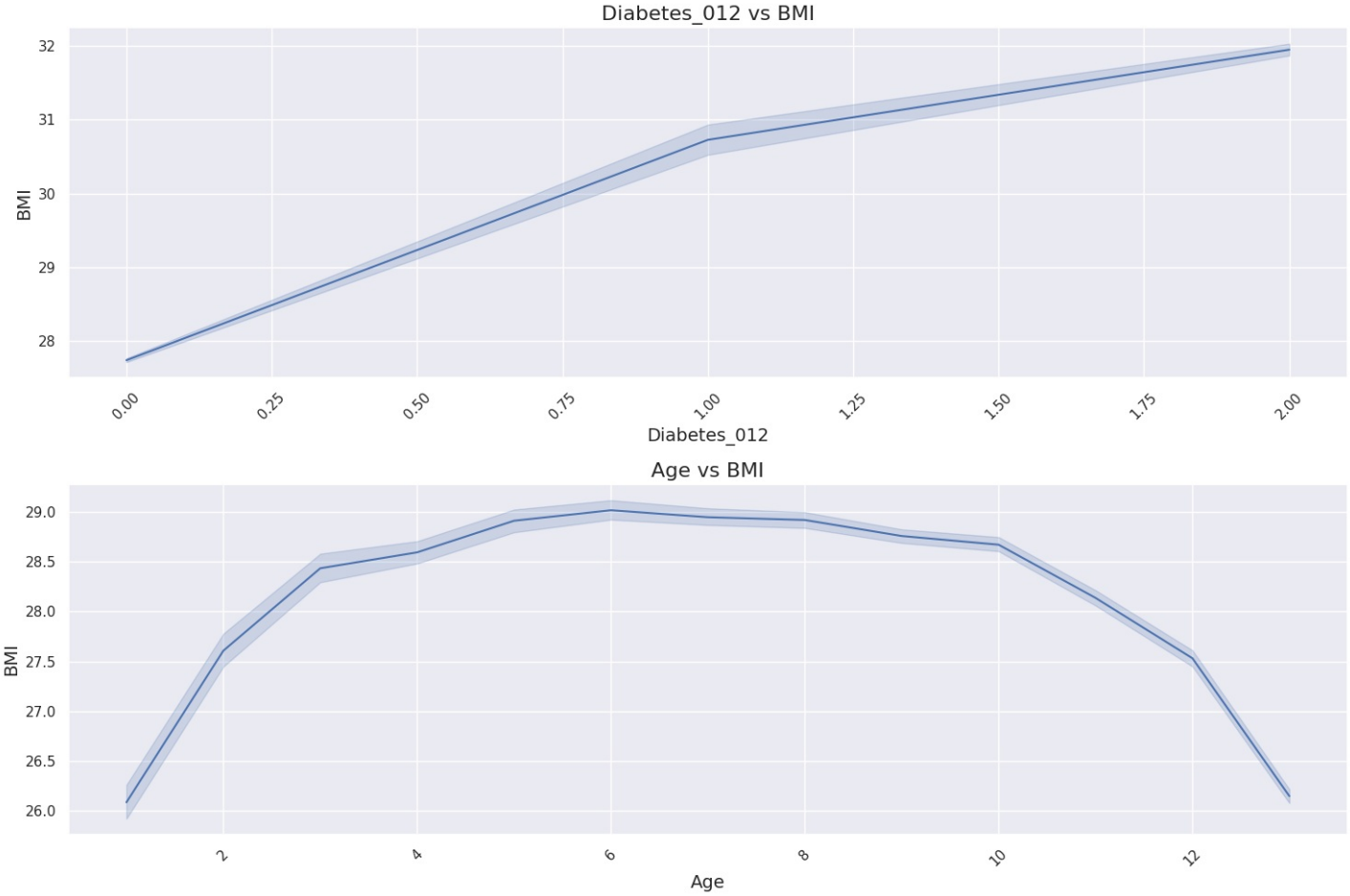
The age groups are coded numerically from 1 to 13, with each group representing different age ranges. The counts fluctuate across these age groups, with peaks observed in groups 4, 8, and 10, indicating that these age ranges have higher re

Line Plot

BMI

In [ ]:
```
# Define the numerical feature for the y axis for BMI
numerical_feature = 'BMI'
```

```
# Set up the matplotlib figure and size
plt.figure(figsize=(15, len(categorical) * 5))

# Iterate over each categorical feature to create a line plot
for index, feature in enumerate(categorical):
    plt.subplot(len(categorical), 1, index + 1)
    sns.lineplot(data=df, x=feature, y=numerical_feature)
    plt.title(f'{feature} vs {numerical_feature}', fontsize=16)
    plt.xlabel(feature, fontsize=14)
    plt.ylabel(numerical_feature, fontsize=14)
    plt.xticks(rotation=45)  # Rotate x-axis labels by 45 degrees for readability

plt.tight_layout()
plt.show()
```



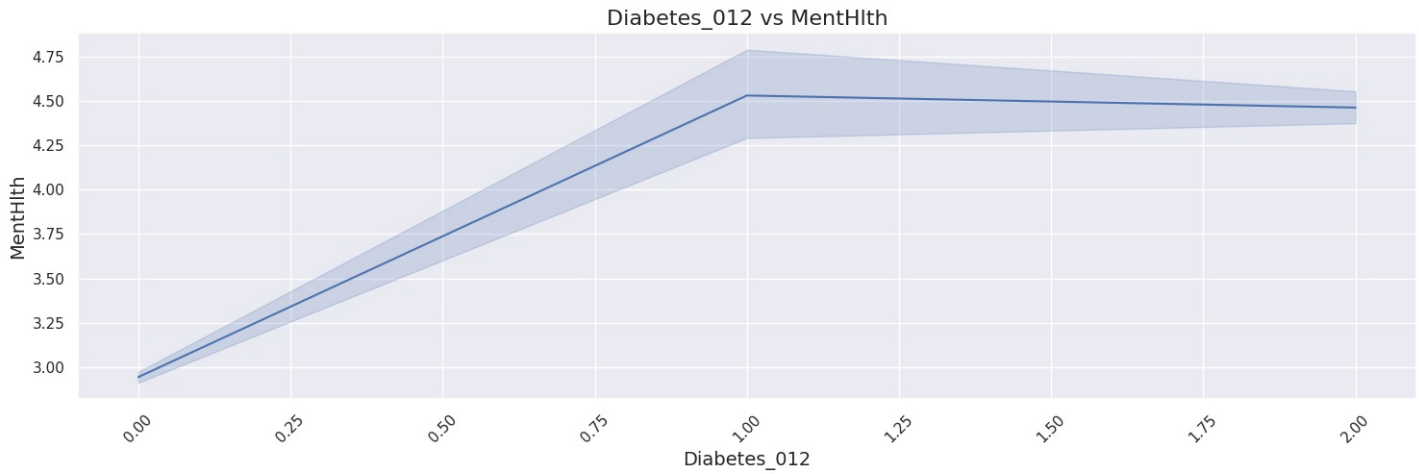
Diabetes_012 vs BMI: BMI increases with higher diabetes status, from 28 (no diabetes) to 32 (diabetes).

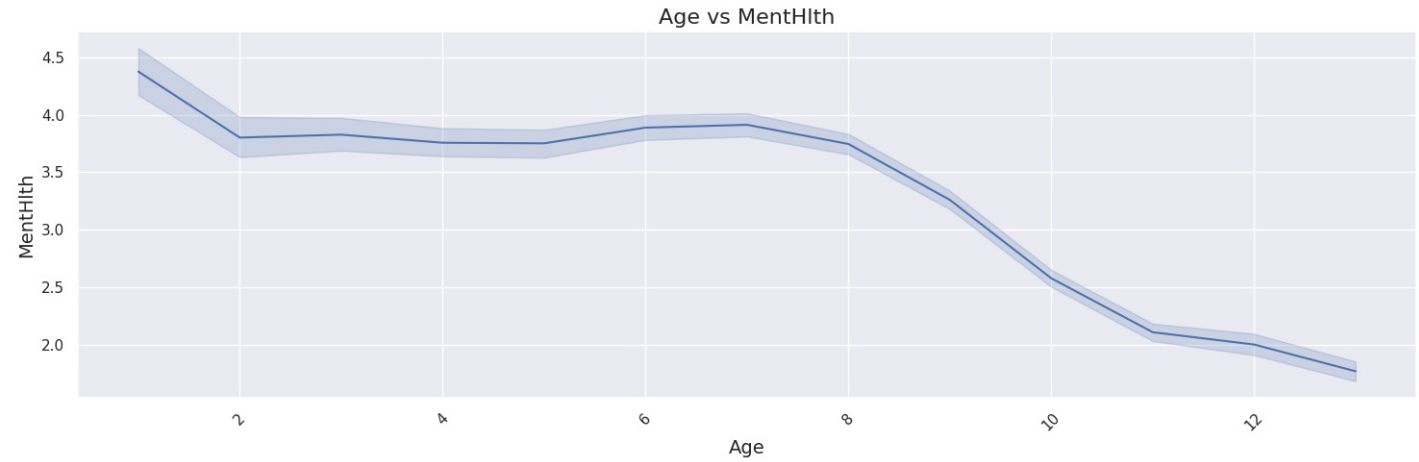
Age vs BMI: BMI peaks in middle age (around age group 6) and decreases in older age groups.

Mental Health

In [ ]:

```
# Define the numerical feature for the y axis for BMI
numerical_feature = 'MentHlth'
# Set up the matplotlib figure and size
plt.figure(figsize=(15, len(categorical) * 5))

# Iterate over each categorical feature to create a line plot
for index, feature in enumerate(categorical):
    plt.subplot(len(categorical), 1, index + 1)
    sns.lineplot(data=df, x=feature, y=numerical_feature)
    plt.title(f'{feature} vs {numerical_feature}', fontsize=16)
    plt.xlabel(feature, fontsize=14)
    plt.ylabel(numerical_feature, fontsize=14)
    plt.xticks(rotation=45)  # Rotate x-axis labels by 45 degrees for readability

plt.tight_layout()
plt.show()
```



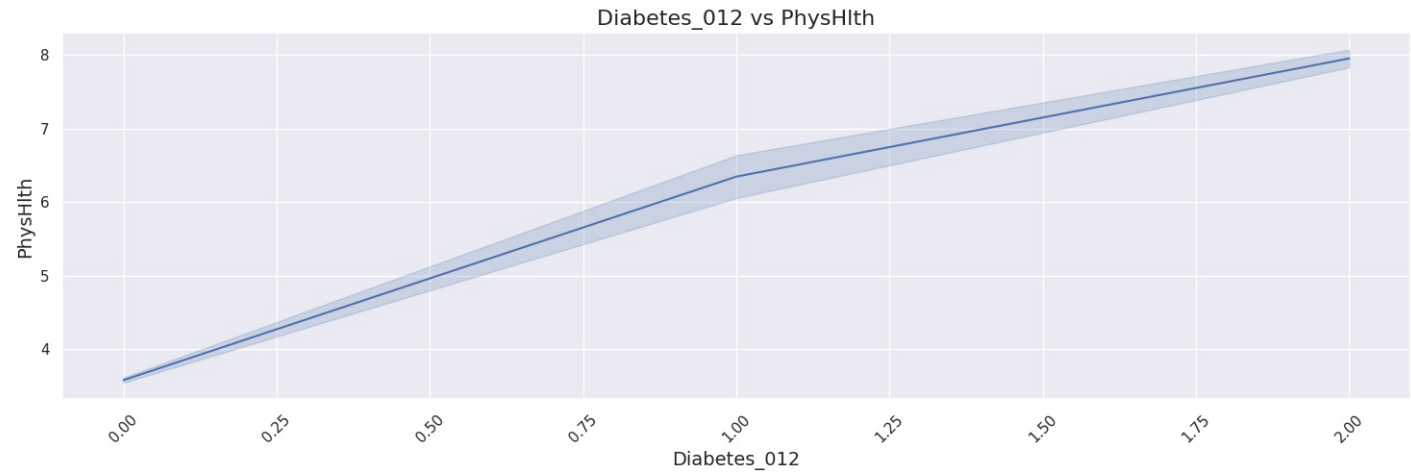


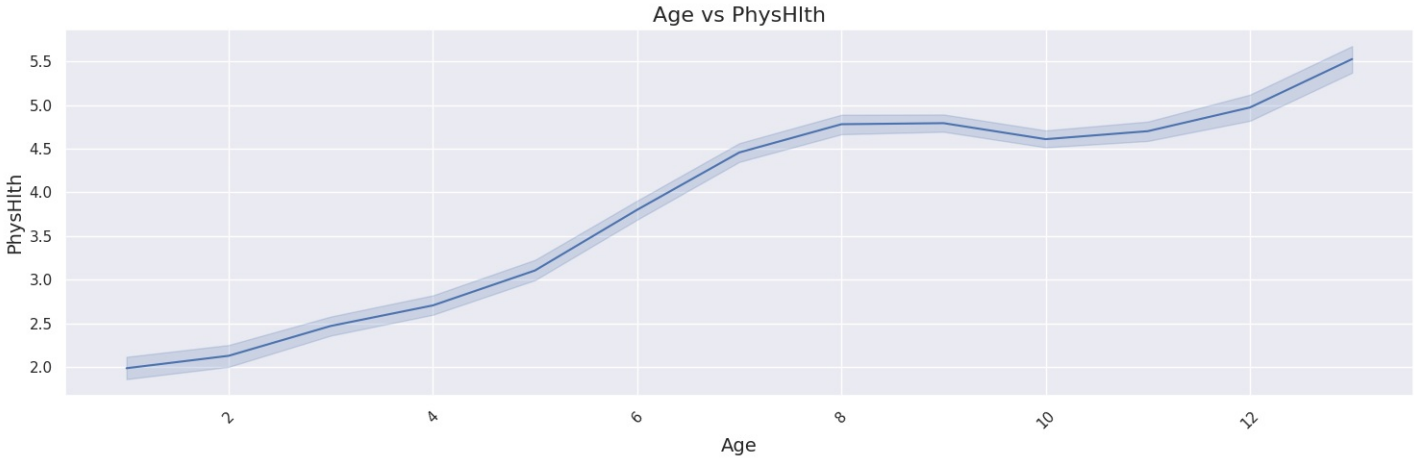
Diabetes_012 vs MentHlth: MentHlth (poor mental health days) increases with higher diabetes status, peaking at prediabetes (1) and slightly decreasing at diabetes (2).

Age vs MentHlth: MentHlth decreases with age, peaking in younger age groups and gradually declining in older age groups.

Physical Health

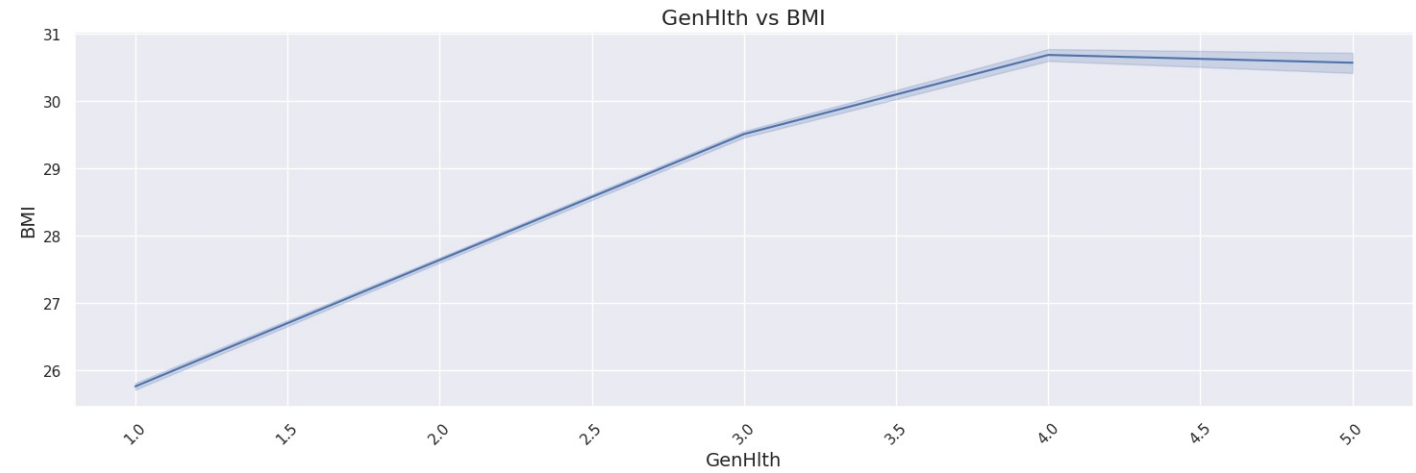
In [ ]:
```
# Define the numerical feature for the y axis for BMI
numerical_feature = 'PhysHlth'
# Set up the matplotlib figure and size
plt.figure(figsize=(15, len(categorical) * 5))

# Iterate over each categorical feature to create a line plot
for index, feature in enumerate(categorical):
    plt.subplot(len(categorical), 1, index + 1)
    sns.lineplot(data=df, x=feature, y=numerical_feature)
    plt.title(f'{feature} vs {numerical_feature}', fontsize=16)
    plt.xlabel(feature, fontsize=14)
    plt.ylabel(numerical_feature, fontsize=14)
    plt.xticks(rotation=45)  # Rotate x-axis labels by 45 degrees for readability

plt.tight_layout()
plt.show()
```

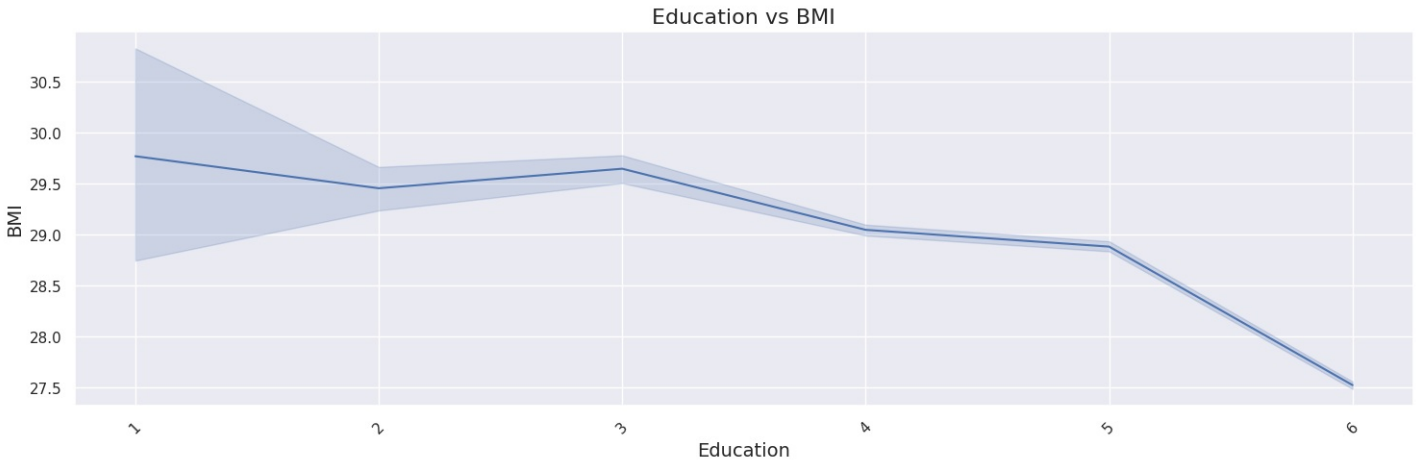


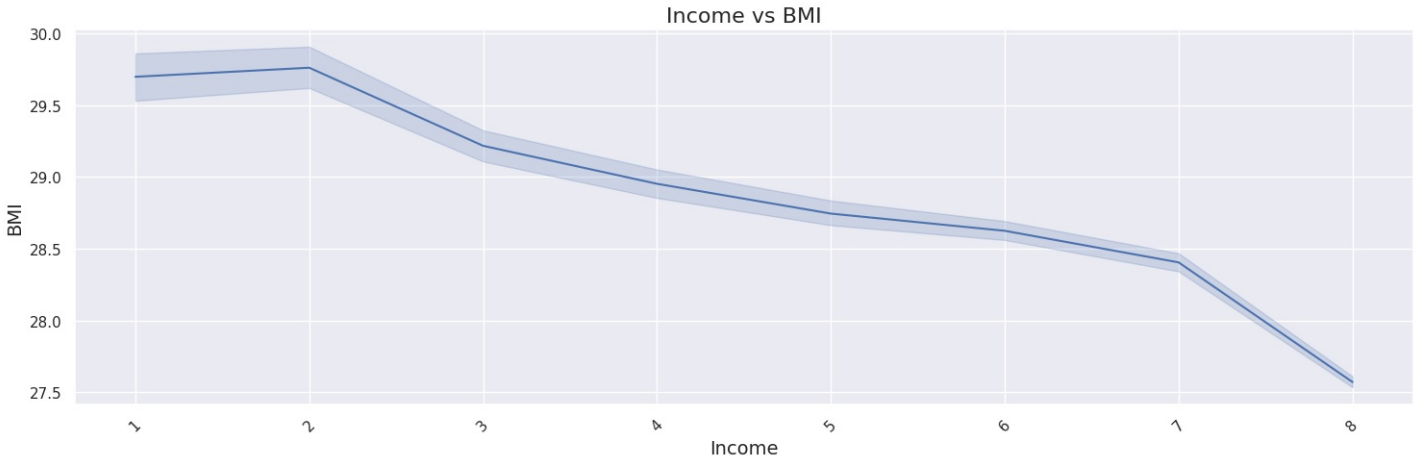


BMI vs Ordinal

In [ ]:
```
# Define the numerical feature for the y axis for BMI
numerical_feature = 'BMI'
# Set up the matplotlib figure and size
plt.figure(figsize=(15, len(ordinal) * 5))

# Iterate over each categorical feature to create a line plot
for index, feature in enumerate(ordinal):
    plt.subplot(len(ordinal), 1, index + 1)
    sns.lineplot(data=df, x=feature, y=numerical_feature)
    plt.title(f'{feature} vs {numerical_feature}', fontsize=16)
    plt.xlabel(feature, fontsize=14)
    plt.ylabel(numerical_feature, fontsize=14)
    plt.xticks(rotation=45)  # Rotate x-axis labels by 45 degrees for readability

plt.tight_layout()
plt.show()
```







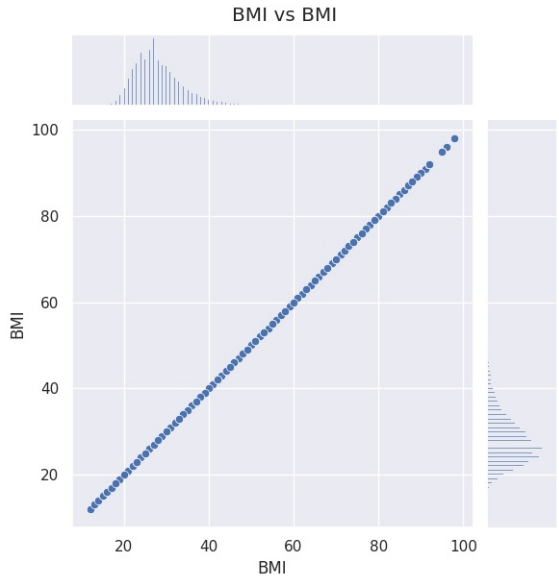
GenHlth vs BMI: BMI increases as general health worsens, from about 26 (excellent health) to 31 (poor health).

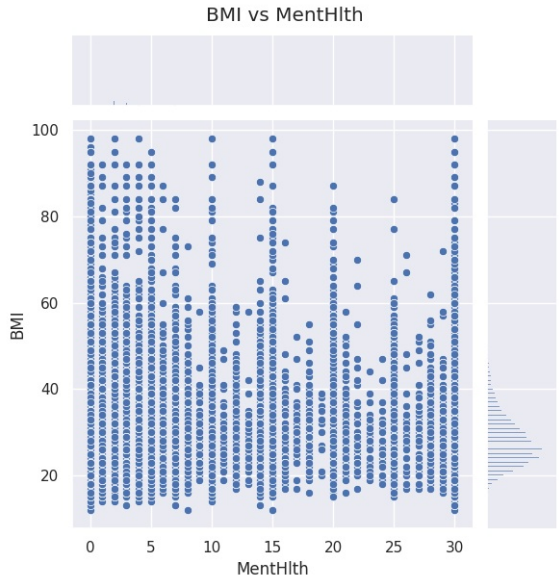
Education vs BMI: BMI decreases with higher education levels, from about 30.5 at level 1 to 27.5 at level 6.

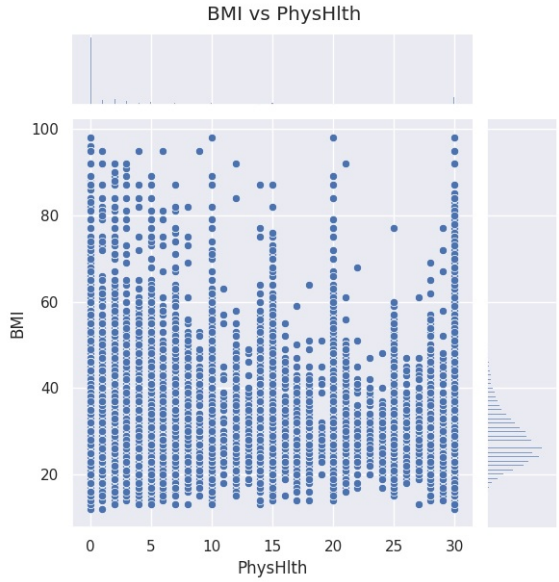
Income vs BMI: BMI decreases with higher income levels, from about 30 at level 1 to 27.5 at level 8.

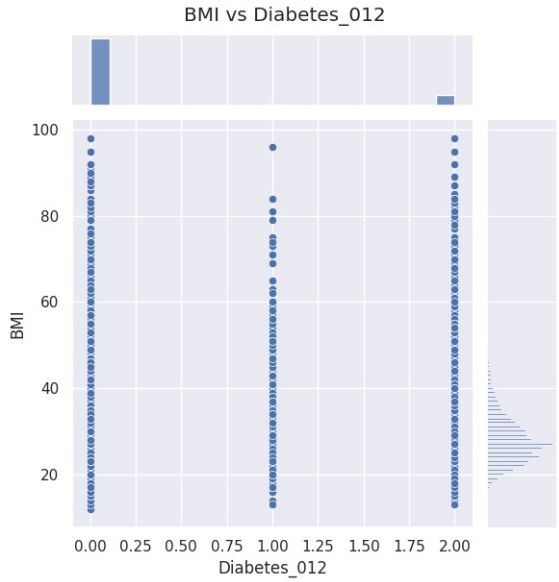
Joint Plot

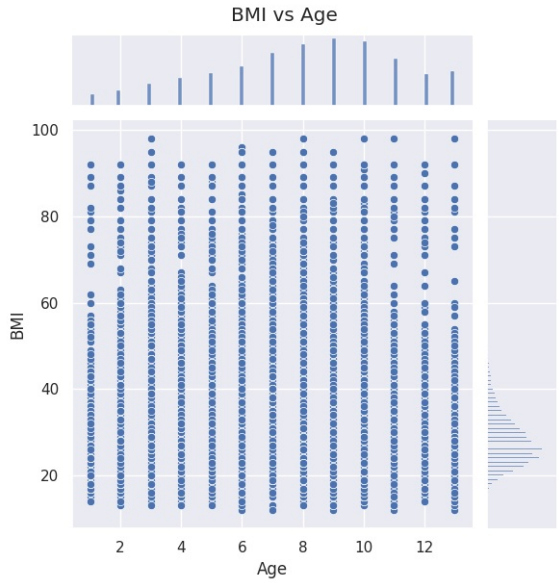
In [ ]:
```
# Features to plot against BMI
features_to_plot = numerical + categorical + binary + ordinal

# Create joint plots for BMI against each feature
for feature in features_to_plot:
    sns.jointplot(data=df, x=feature, y='BMI', kind='scatter')
    plt.suptitle(f'BMI vs {feature}', y=1.02)
    plt.show()
```

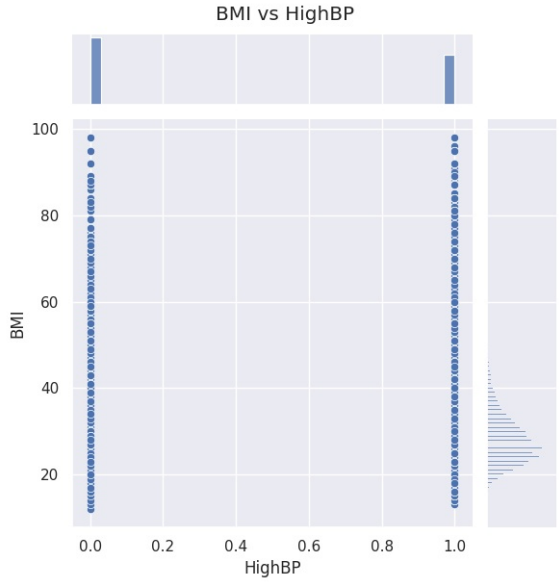

BMI vs BMI
100
80
60
40
20
BMI
20
40
60
80
100
BMI

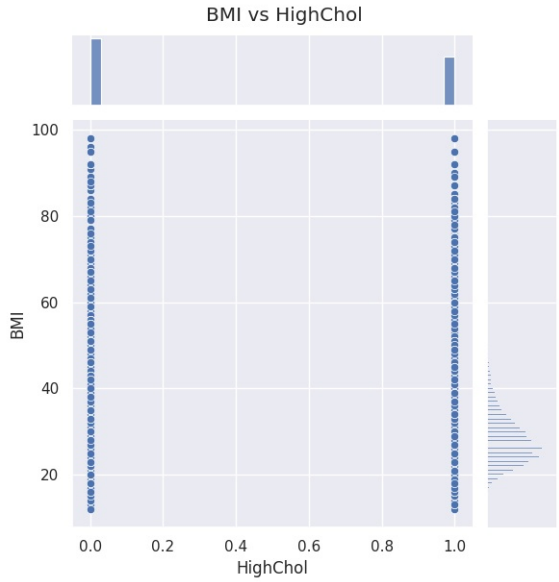

BMI vs MentHlth
100
80
60
40
20
BMI
0
5
10
15
20
25
30
MentHlth

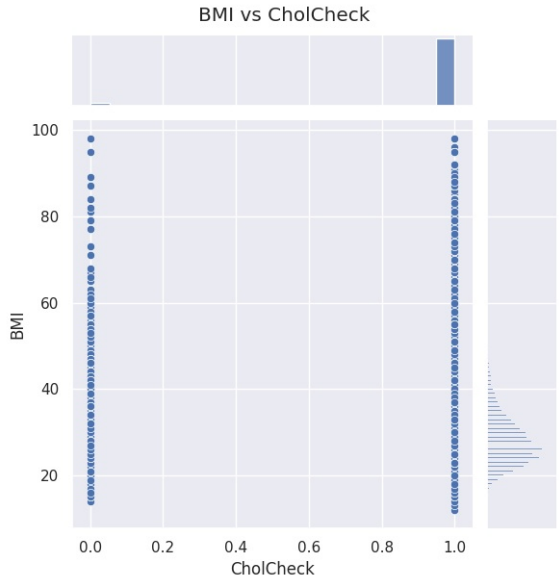

BMI vs PhysHlth
100
80
60
40
20
BMI
0
5
10
15
20
25
30
PhysHlth

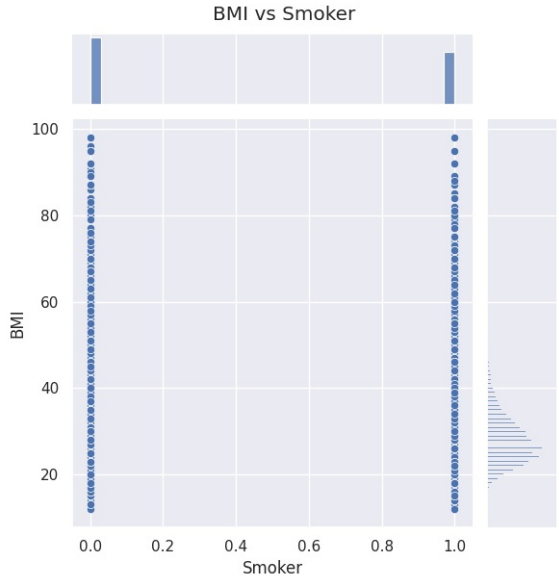

BMI vs Diabetes_012
BMI
Diabetes_012
100
80
60
40
20
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

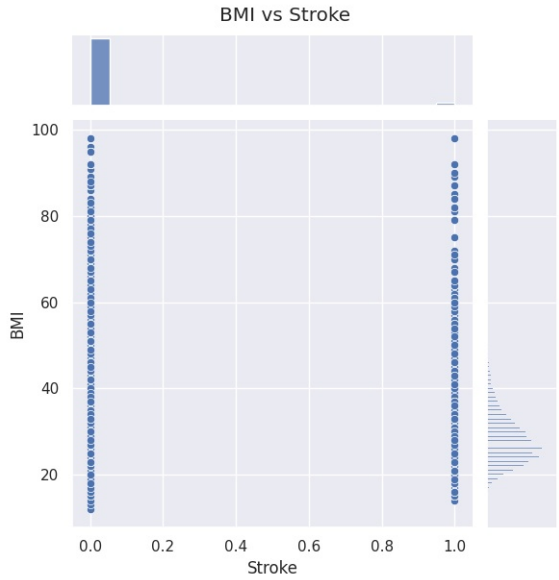

BMI vs Age
BMI
Age
100
80
60
40
20
2
4
6
8
10
12

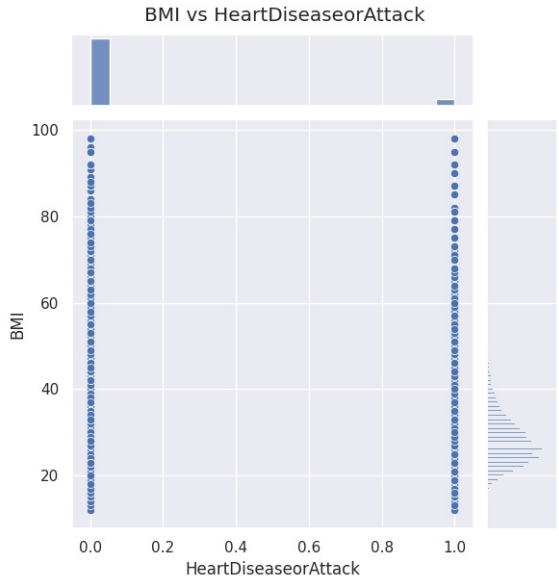

BMI vs HighBP
BMI
HighBP
100
80
60
40
20
0.0
0.2
0.4
0.6
0.8
1.0

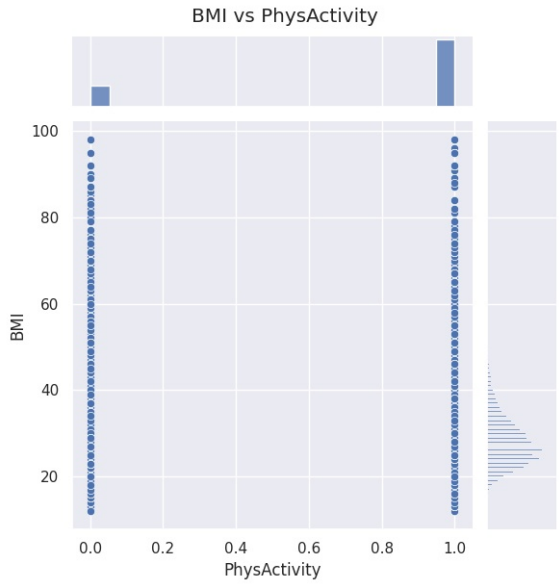

BMI vs HighChol
BMI
HighChol
100
80
60
40
20
0.0
0.2
0.4
0.6
0.8
1.0

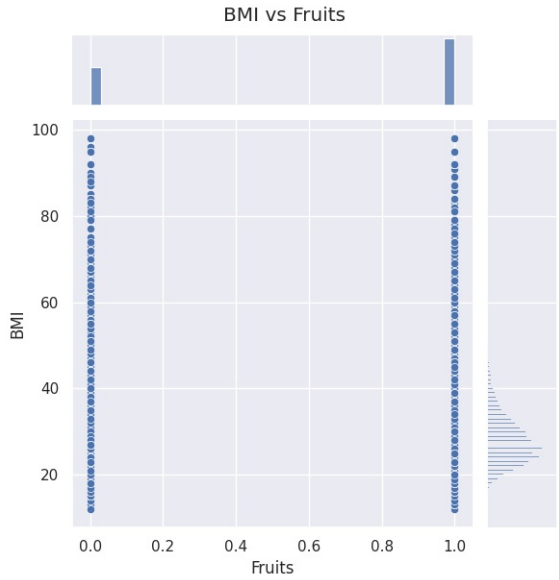

BMI vs CholCheck
BMI
CholCheck
100
80
60
40
20
0.0
0.2
0.4
0.6
0.8
1.0

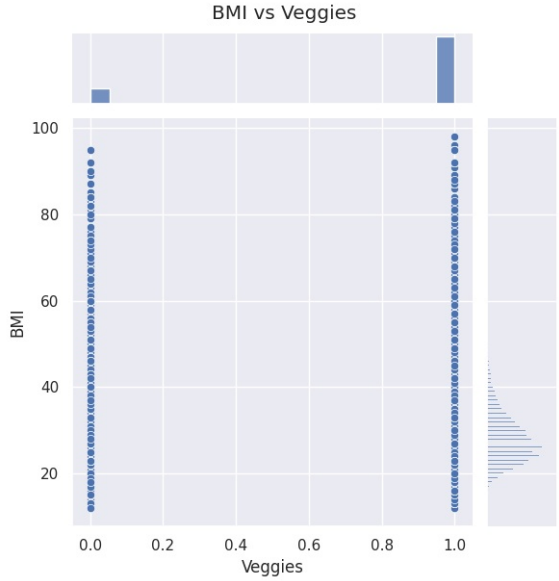

BMI vs Smoker
BMI
Smoker
100
80
60
40
20
0.0
0.2
0.4
0.6
0.8
1.0

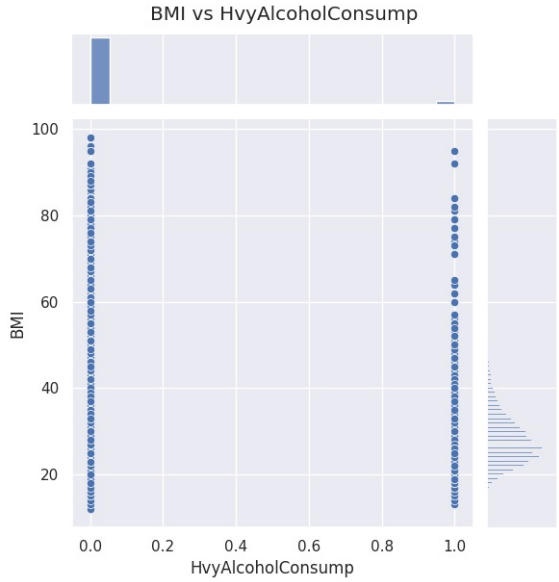

BMI vs Stroke
BMI
Stroke
100
80
60
40
20
0.0
0.2
0.4
0.6
0.8
1.0

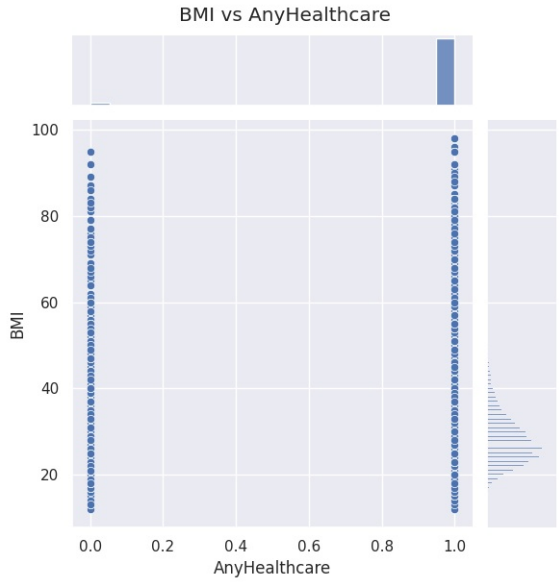

BMI vs HeartDiseaseorAttack
BMI
HeartDiseaseorAttack
100
80
60
40
20
0.0
0.2
0.4
0.6
0.8
1.0

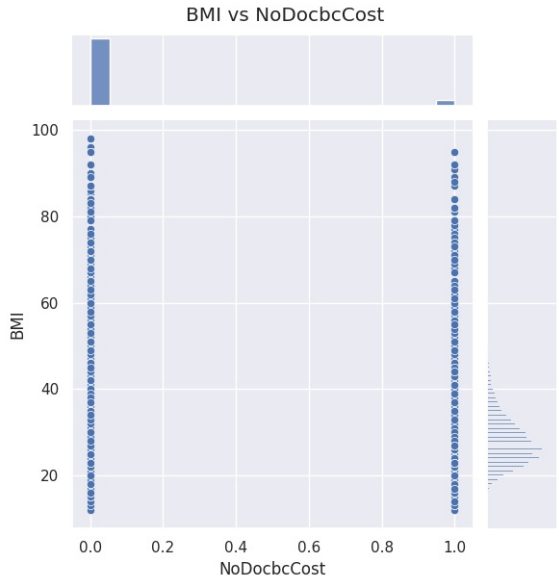

BMI vs PhysActivity
BMI
PhysActivity
100
80
60
40
20
0.0
0.2
0.4
0.6
0.8
1.0

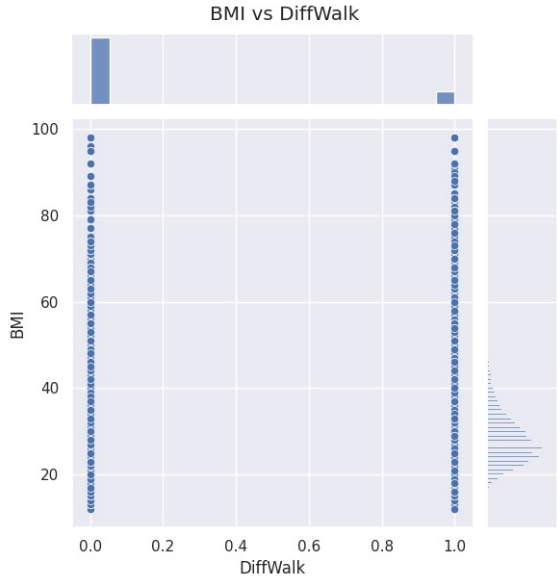

BMI vs Fruits
BMI
Fruits
100
80
60
40
20
0.0
0.2
0.4
0.6
0.8
1.0

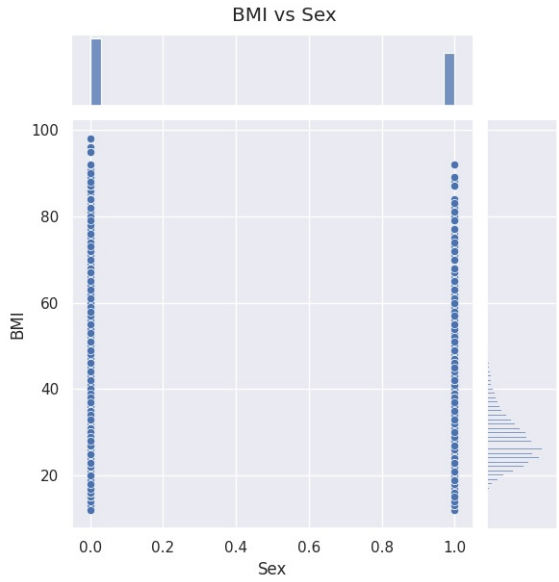

BMI vs Veggies
BMI
Veggies
100
80
60
40
20
0.0
0.2
0.4
0.6
0.8
1.0

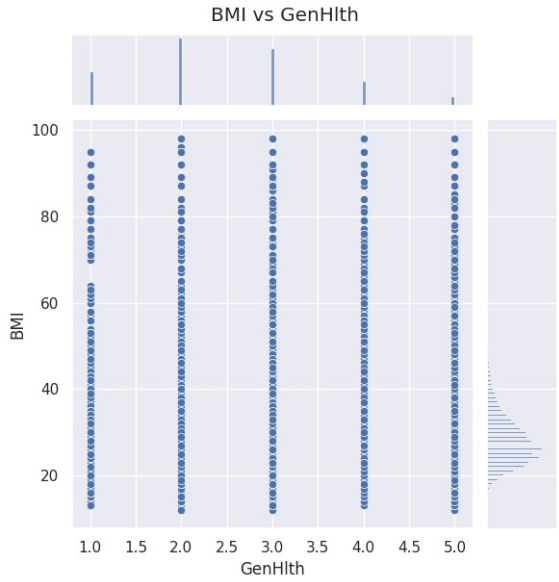

BMI vs HvyAlcoholConsump
BMI
HvyAlcoholConsump
100
80
60
40
20
0.0
0.2
0.4
0.6
0.8
1.0

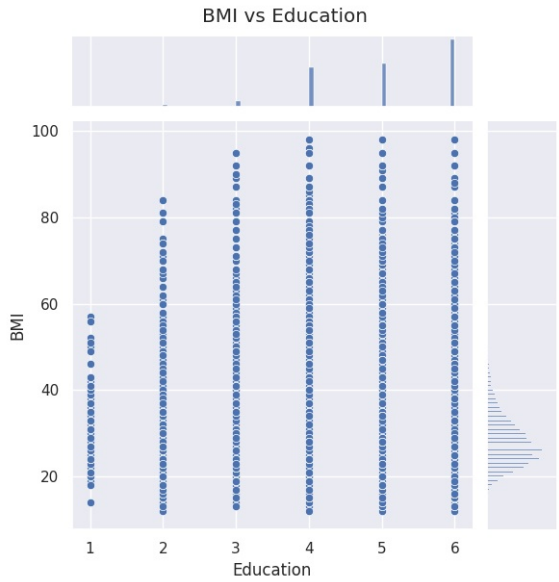

BMI vs AnyHealthcare
BMI
AnyHealthcare
100
80
60
40
20
0.0
0.2
0.4
0.6
0.8
1.0

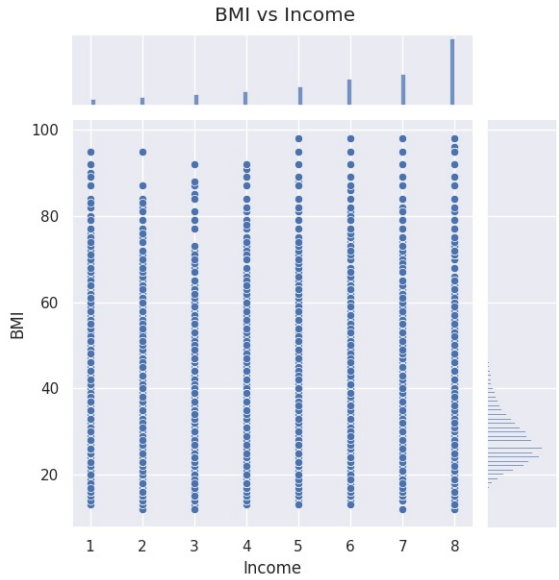

BMI vs NoDocbcCost
BMI
NoDocbcCost
100
80
60
40
20
0.0
0.2
0.4
0.6
0.8
1.0


BMI vs DiffWalk
BMI
DiffWalk
100
80
60
40
20
0.0
0.2
0.4
0.6
0.8
1.0


BMI vs Sex
BMI
Sex
100
80
60
40
20
0.0
0.2
0.4
0.6
0.8
1.0

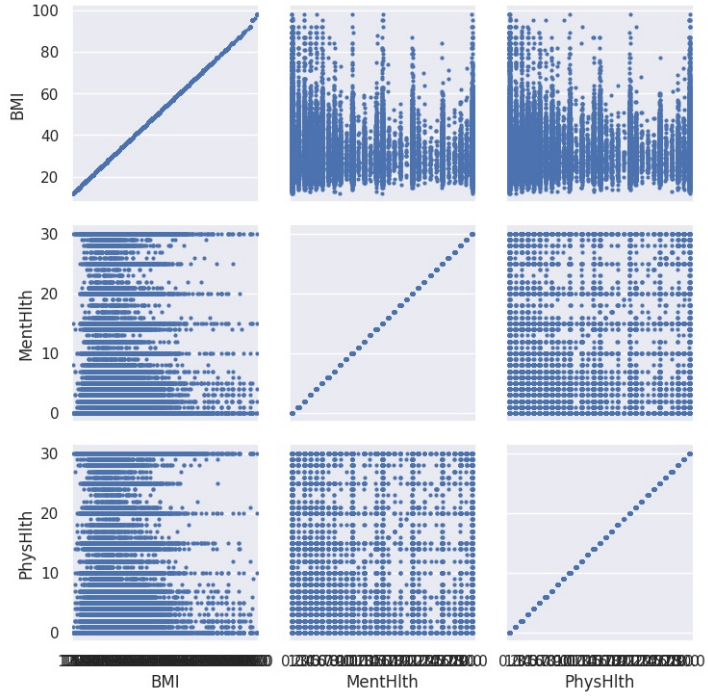

BMI vs GenHlth
BMI
GenHlth
100
80
60
40
20
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
5.0


BMI vs Education
BMI
Education
100
80
60
40
20
1
2
3
4
5
6



Pairgrid

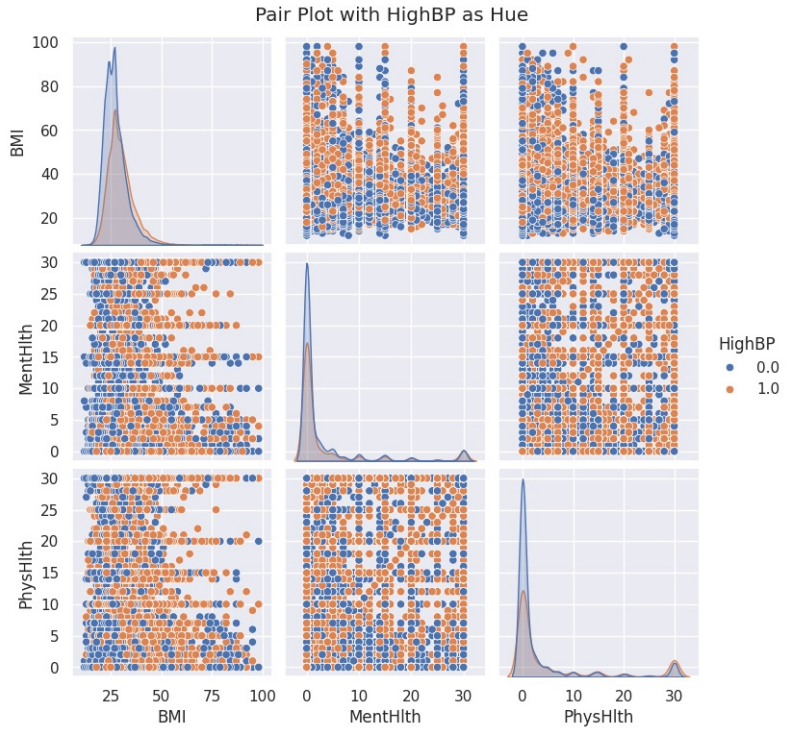
In [ ]:
```
# Combine numerical variables for the PairGrid
pairgrid_vars = numerical

# Create the PairGrid
g = sns.PairGrid(df[pairgrid_vars])

# Map the stripplot with jitter to the PairGrid
g.map(sns.stripplot, jitter=True, size=3)

# Display the plot
plt.show()
```

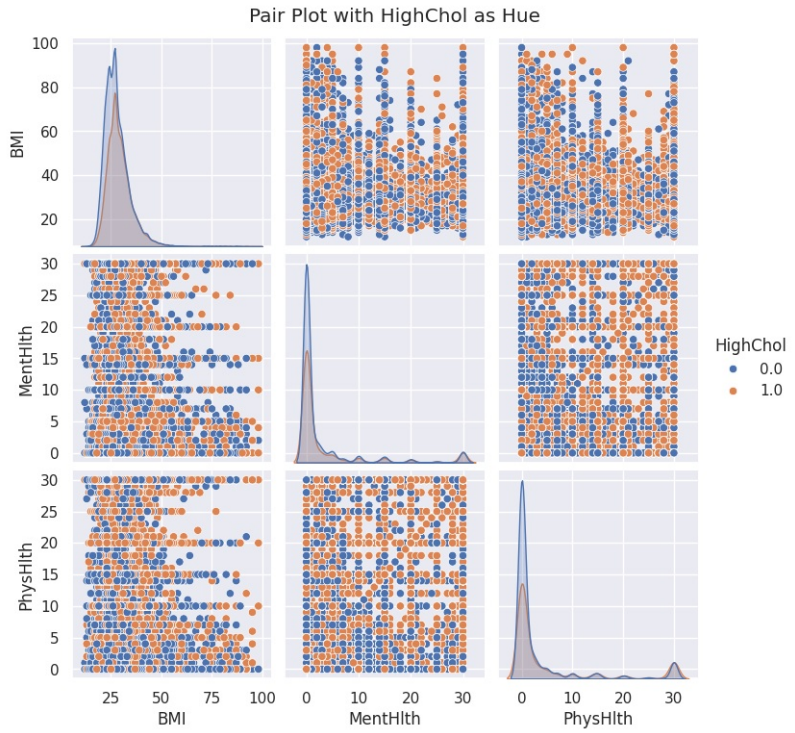


1. **BMI**:
   - No clear correlation with MentHlth or PhysHlth; points are widely dispersed.
2. **MentHlth**:
   - Scattered plots with BMI and PhysHlth, indicating no clear relationship.
3. **PhysHlth**:
   - Scattered plots with BMI and MentHlth, indicating no clear relationship.

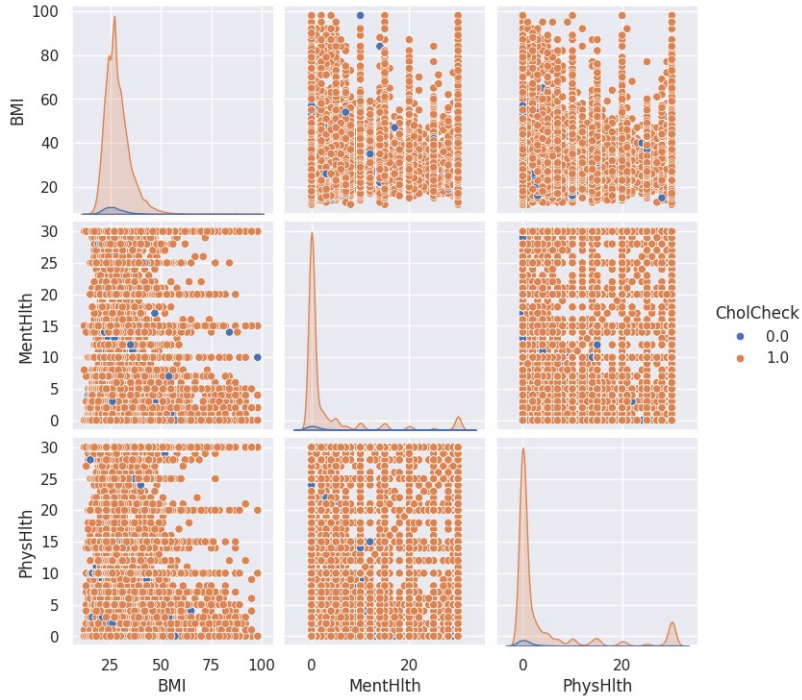
Piarplot

In [ ]:
```
# # Iterate through all binary features to create separate pair plots
# for bin_feature in binary:
#     # Create the pair plot with the current binary feature as hue
#     sns.pairplot(df[numerical + [bin_feature]], hue=bin_feature, diag_kind='kde')

#     # Add a title to the plot
#     plt.suptitle(f'Pair Plot with {bin_feature} as Hue', y=1.02)

#     # Show the plot
#     plt.show()
```

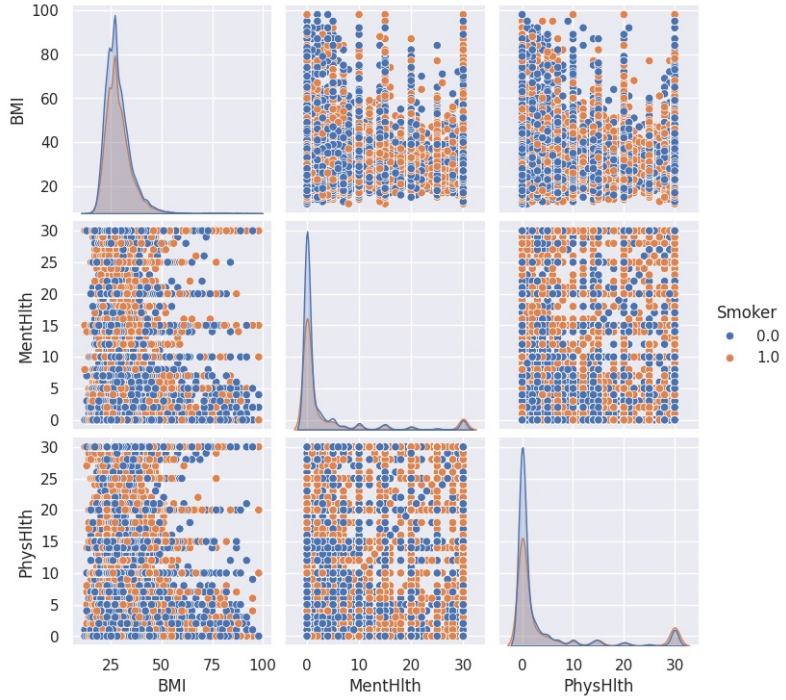

Pair Plot with HighBP as Hue
BMI
MentHlth
PhysHlth
HighBP
0.0
1.0

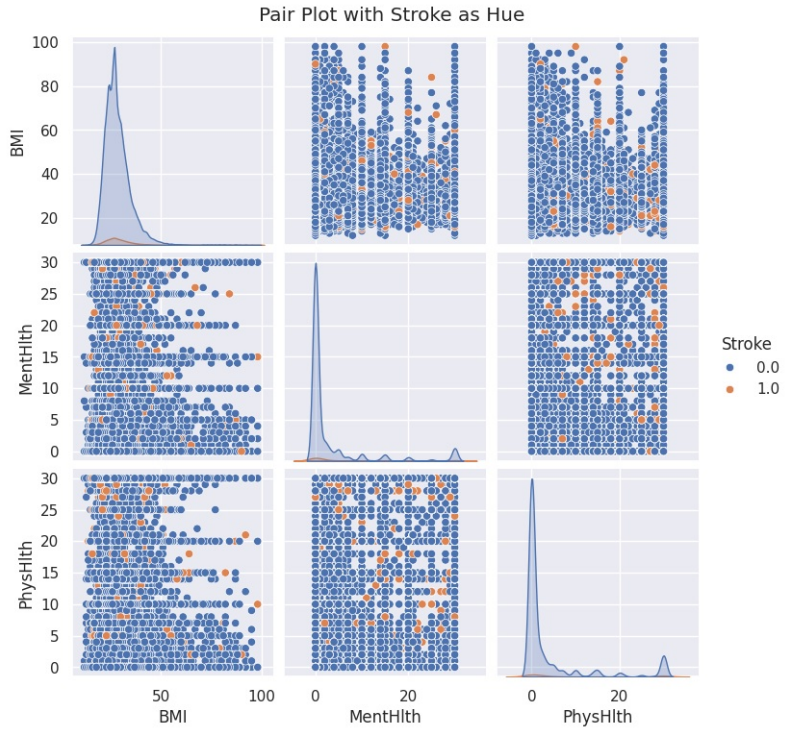

Pair Plot with HighChol as Hue
BMI
MentHlth
PhysHlth
HighChol
0.0
1.0

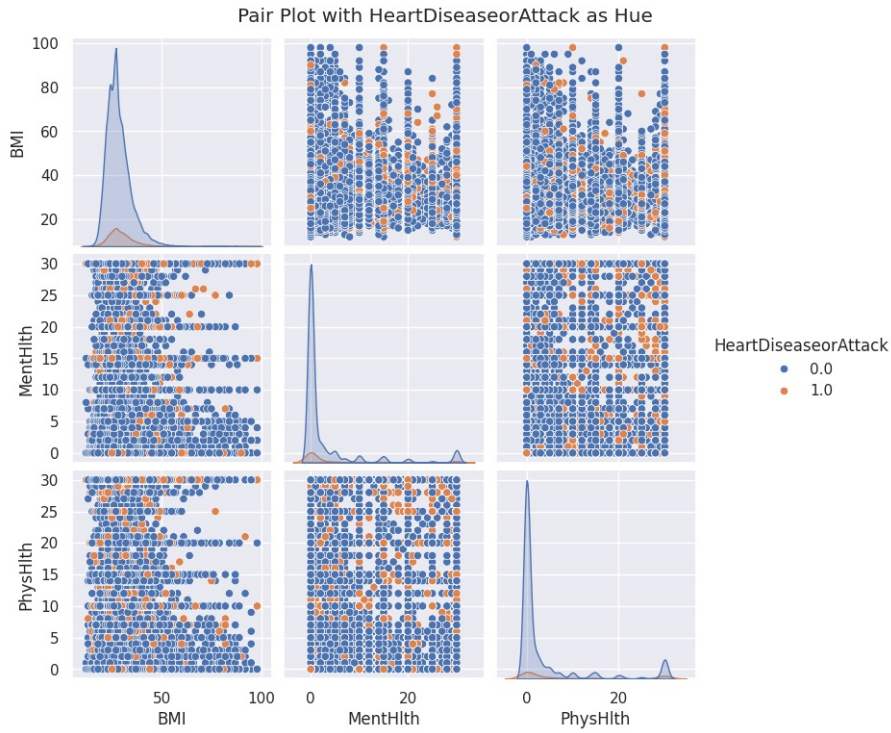
Pair Plot with CholCheck as Hue

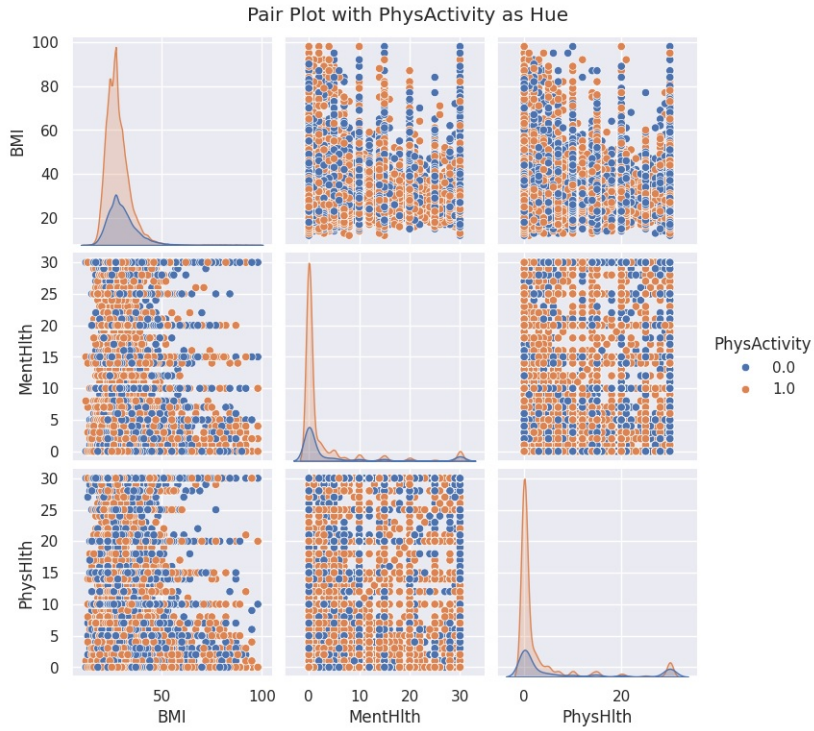


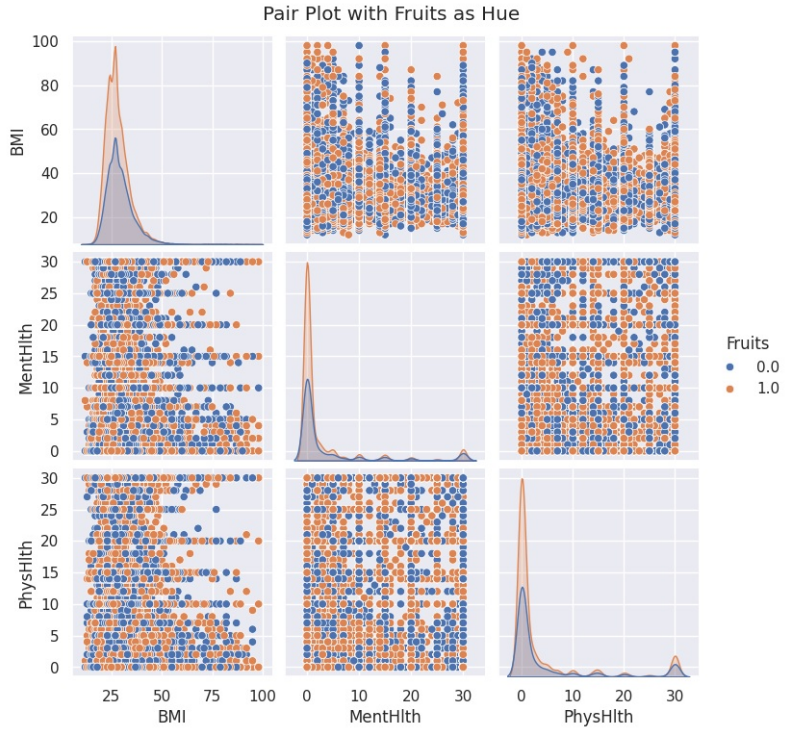
Pair Plot with Smoker as Hue



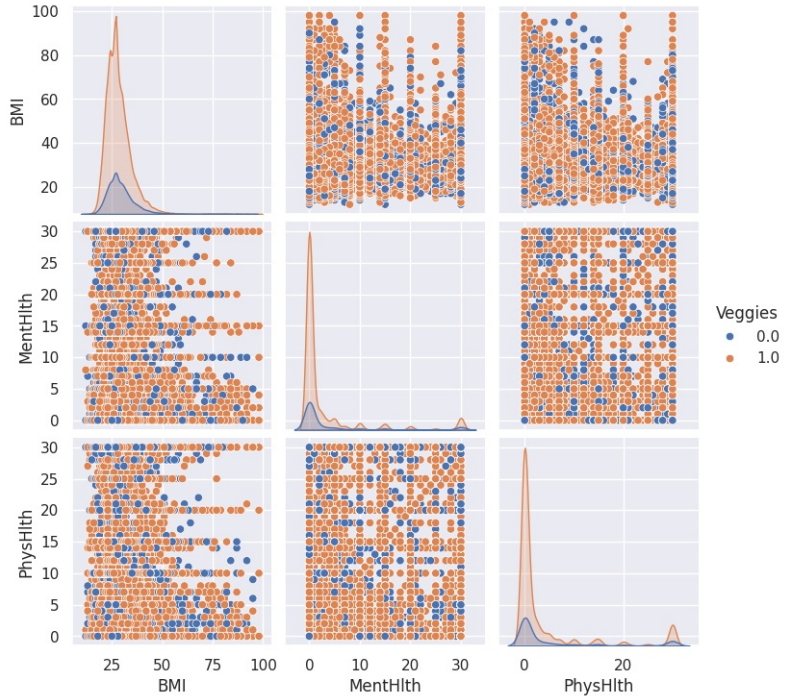

Pair Plot with Stroke as Hue
BMI
MentHlth
PhysHlth
Stroke
0.0
1.0


Pair Plot with HeartDiseaseorAttack as Hue
BMI
MentHlth
PhysHlth
HeartDiseaseorAttack
0.0
1.0

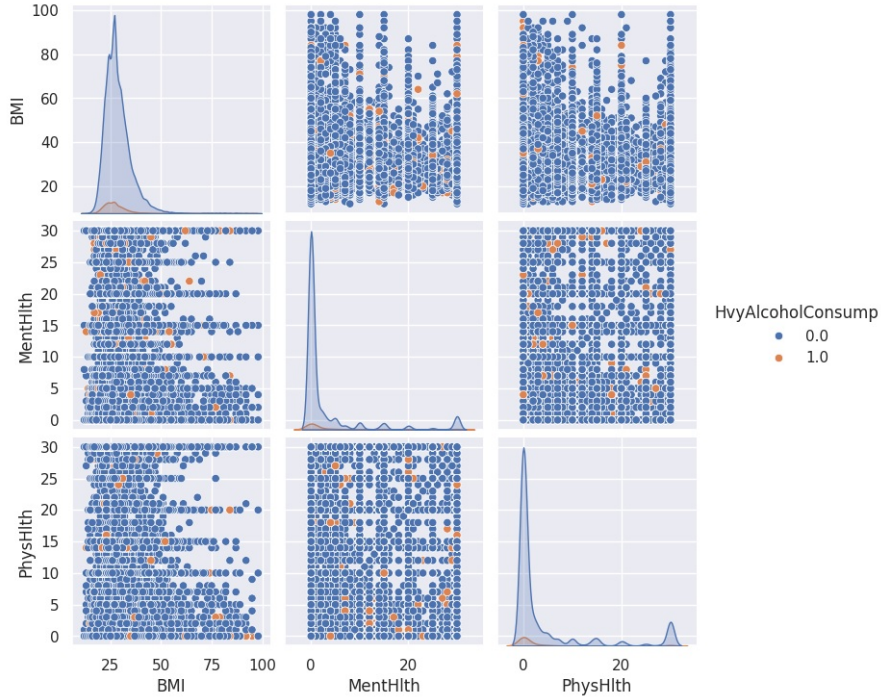

Pair Plot with PhysActivity as Hue
BMI
MentHlth
PhysHlth
PhysActivity
0.0
1.0

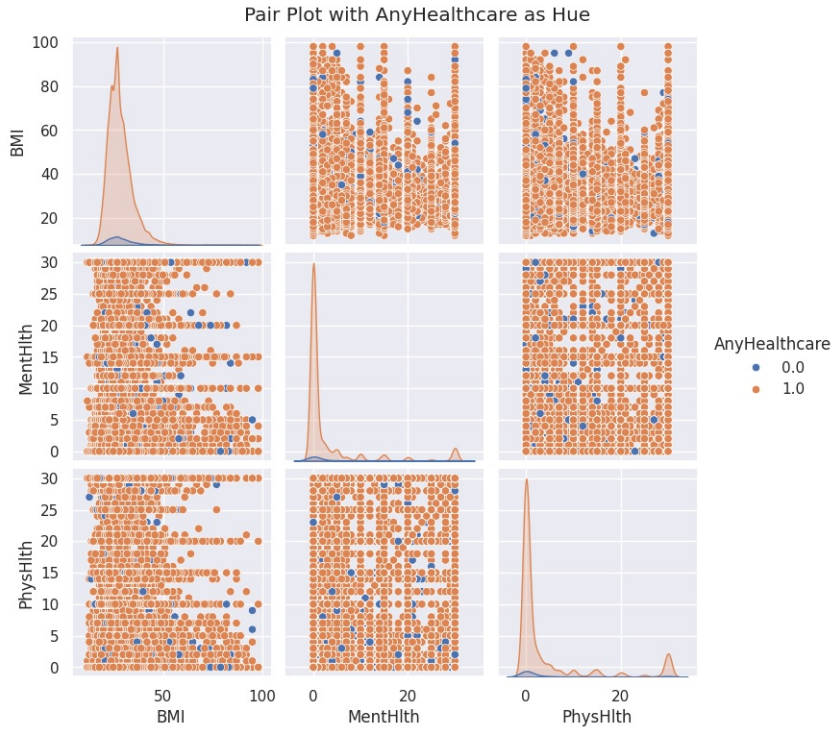

Pair Plot with Fruits as Hue
BMI
MentHlth
PhysHlth
Fruits
0.0
1.0

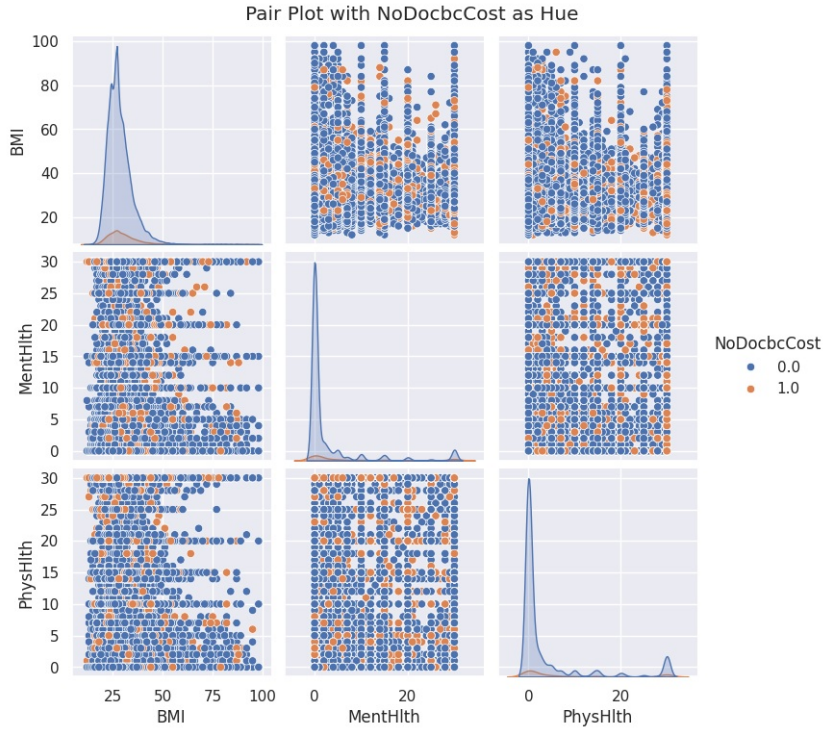
Pair Plot with Veggies as Hue

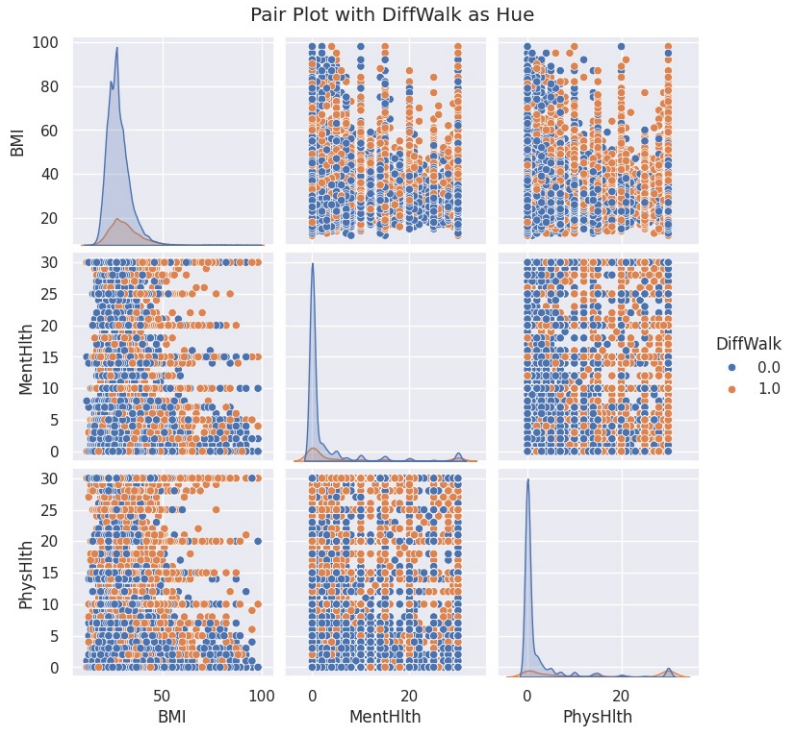


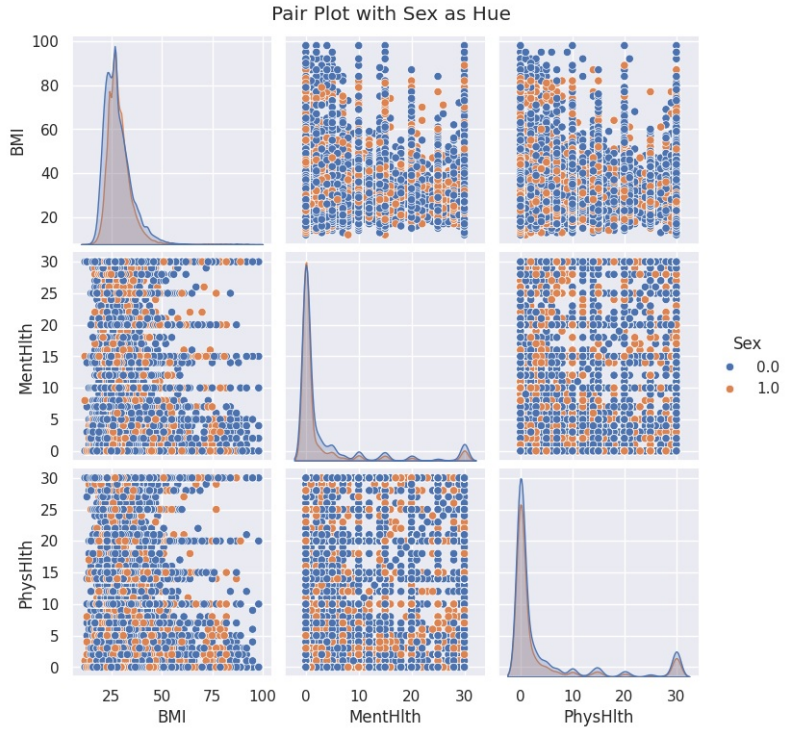
Pair Plot with HvyAlcoholConsump as Hue




Pair Plot with AnyHealthcare as Hue
BMI
MentHlth
PhysHlth
AnyHealthcare
0.0
1.0


Pair Plot with NoDocbcCost as Hue
BMI
MentHlth
PhysHlth
NoDocbcCost
0.0
1.0





Pair Plots Summary

1. HighBP (High Blood Pressure)

- High blood pressure (orange) is more common in individuals with higher BMI.
- Distribution of MentHlth and PhysHlth shows scattered points without clear separation between high and low blood pressure groups.

2. HighChol (High Cholesterol)

- High cholesterol (orange) is associated with higher BMI.
- No clear pattern in the distribution of MentHlth and PhysHlth between individuals with and without high cholesterol.

3. CholCheck (Cholesterol Check)

- Majority of individuals have undergone cholesterol checks (orange).
- No significant difference in the distribution of BMI, MentHlth, or PhysHlth based on cholesterol check status.

4. Smoker

- Smoking status (orange) shows no clear correlation with BMI, MentHlth, or PhysHlth.
- Both smokers and non-smokers are scattered similarly across the plots.

5. Stroke

- Stroke occurrence (orange) is relatively rare and shows no clear pattern with BMI, MentHlth, or PhysHlth.
- Individuals with strokes are scattered throughout the plots.

6. HeartDiseaseorAttack

- Heart disease or attack (orange) is associated with higher BMI.
- No clear separation in the distribution of MentHlth and PhysHlth based on heart disease status.

7. PhysActivity (Physical Activity)

- Physically active individuals (orange) are spread across various BMI, MentHlth, and PhysHlth values.
- No significant difference in distribution patterns for physical activity.

8. Fruits

- Fruit consumption (orange) shows a slight association with lower BMI.
- No clear separation in MentHlth and PhysHlth distributions based on fruit consumption.

9. Veggies

- Vegetable consumption (orange) also shows a slight association with lower BMI.
- Distribution of MentHlth and PhysHlth is similar across those who consume vegetables and those who do not.

10. HvyAlcoholConsump (Heavy Alcohol Consumption)

- Heavy alcohol consumption (orange) shows no clear pattern with BMI, MentHlth, or PhysHlth.
- Both heavy drinkers and non-drinkers are similarly scattered across the plots.

11. AnyHealthcare

- Most individuals have access to healthcare (orange).
- No significant difference in BMI, MentHlth, or PhysHlth distributions based on healthcare access.

12. NoDocbcCost (No Doctor because of Cost)

- Individuals who could not see a doctor due to cost (orange) show no clear pattern in BMI, MentHlth, or PhysHlth.
- Both groups are similarly scattered across the plots.

13. DiffWalk (Difficulty Walking)

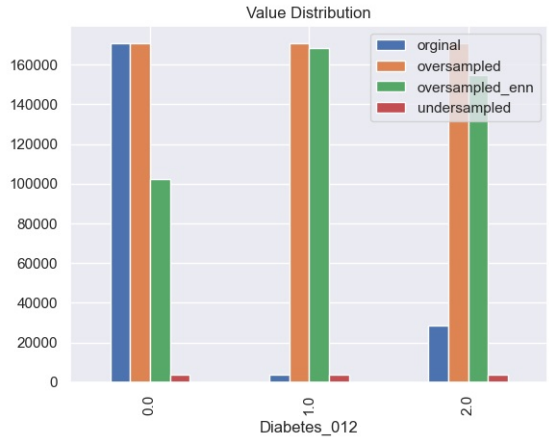
- Individuals with difficulty walking (orange) have higher BMIs compared to those without difficulty walking.
- No clear separation in the distribution of MentHlth based on difficulty walking.
- Those with difficulty walking have more poor physical health days (PhysHlth) compared to those without difficulty walking.

Feature Engineering

In [14]:
```
# Handle missing values for numerical variables
df[numerical] = df[numerical].fillna(df[numerical].median())

# Encode ordinal variables
le = LabelEncoder()
for col in ordinal:
    df[col] = le.fit_transform(df[col])

# Define the target and features
target_column = 'Diabetes_012'
features = df.columns.difference([target_column])
X = df[features]
y = df[target_column]
```

In [15]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

# Standardize the numerical features
scaler = StandardScaler()
X_train[numerical] = scaler.fit_transform(X_train[numerical])
X_test[numerical] = scaler.transform(X_test[numerical])

# Genereate oversample with SMOTE:
smote = SMOTE(random_state=42)
X_ovsampled, y_ovsampled = smote.fit_resample(X_train, y_train)

# Generate oversample with SMOTEENN:
smoteenn = SMOTEENN(random_state=42)
X_ovsampled_enn, y_ovsampled_enn = smoteenn.fit_resample(X_train, y_train)

#  Generate undersample with RandomUnderSampler:
undersampler = RandomUnderSampler(random_state=42)
X_undersampled, y_undersampled = undersampler.fit_resample(X_train, y_train)

values_distribution = {
    'orginal': y_train.value_counts(),
    'oversampled': y_ovsampled.value_counts(),
    'oversampled_enn': y_ovsampled_enn.value_counts(),
    'undersampled': y_undersampled.value_counts()
}

# plot value distribution
plt.figure(figsize=(16, 8))
pd.DataFrame(values_distribution).plot(kind='bar')
plt.title('Value Distribution')
plt.show()
```

```
<Figure size 1600x800 with 0 Axes>
```



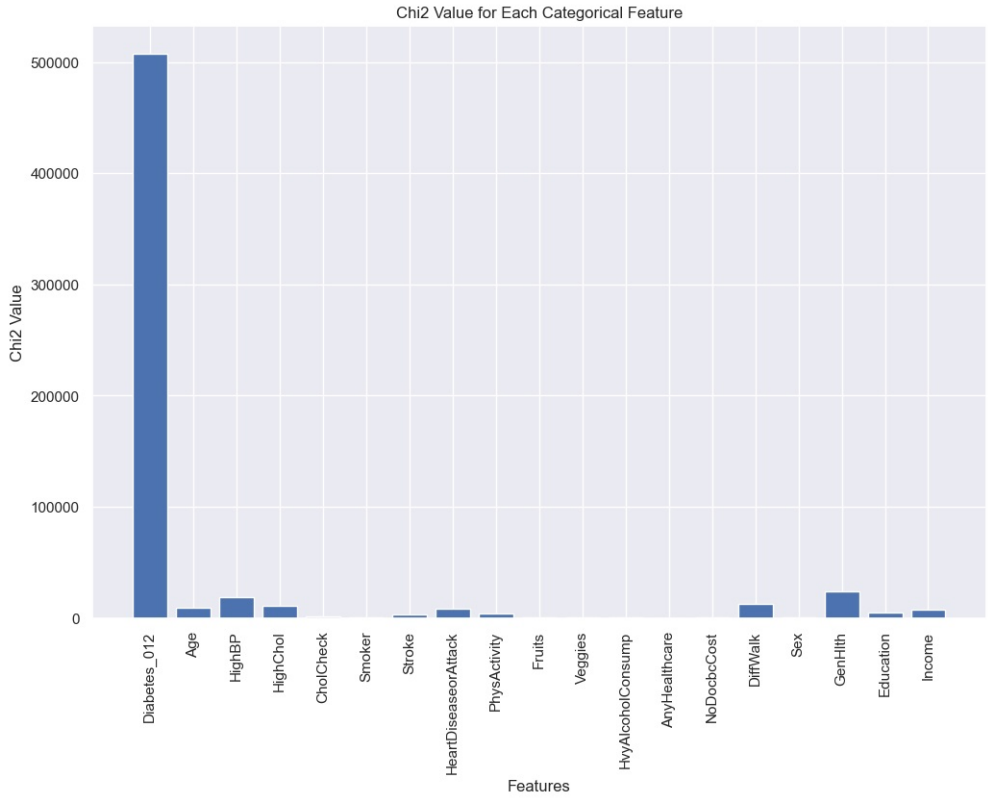
Feature Selection

Chi-Square Test

In [17]:
```
# DataFrame to store result of Chi2 test
results_df_cat = pd.DataFrame(columns=['Feature', 'Chi2', 'P-Value'])

# Copy to keep the original dataframe
cat_df = df.copy()

# for all non-numerical variables, convert to categorical
for var in non_numerical:
    cat_df[var] = cat_df[var].astype('category')
    print(f"Variable {var} converted to categorical")

# For each categorical variable perform Chi2 test
# Print results, create bar plot
for var in non_numerical:
    contingency_table = pd.crosstab(cat_df[var], cat_df["Diabetes_012"])
    chi2, p, _, _ = chi2_contingency(contingency_table)
```

```
    print(f"Chi-Squared Test for {var} and Diabetes_012")
    print(f"Chi2 value = {chi2}, p-value = {p}\n")
    # Add the results to the DataFrame
    results_df_cat = pd.concat([results_df_cat, pd.DataFrame({'Feature': [var], 'Chi2': [chi2], 'P-Value': [p]})], ignore_index=True)

# Display the results
print(results_df_cat)

# Plotting the Chi2 values for each feature
plt.figure(figsize=(12, 8))
plt.bar(results_df_cat['Feature'], results_df_cat['Chi2'])
plt.xlabel('Features')
plt.ylabel('Chi2 Value')
plt.title('Chi2 Value for Each Categorical Feature')
plt.xticks(rotation=90)
plt.show()
```

```
Variable Diabetes_012 converted to categorical
Variable Age converted to categorical
Variable HighBP converted to categorical
Variable HighChol converted to categorical
Variable CholCheck converted to categorical
Variable Smoker converted to categorical
Variable Stroke converted to categorical
Variable HeartDiseaseorAttack converted to categorical
Variable PhysActivity converted to categorical
Variable Fruits converted to categorical
Variable Veggies converted to categorical
Variable HvyAlcoholConsump converted to categorical
Variable AnyHealthcare converted to categorical
Variable NoDocbcCost converted to categorical
Variable DiffWalk converted to categorical
Variable Sex converted to categorical
Variable GenHlth converted to categorical
Variable Education converted to categorical
Variable Income converted to categorical
Chi-Squared Test for Diabetes_012 and Diabetes_012
Chi2 value = 507360.0, p-value = 0.0

Chi-Squared Test for Age and Diabetes_012
Chi2 value = 9641.376530679845, p-value = 0.0

Chi-Squared Test for HighBP and Diabetes_012
Chi2 value = 18794.644052016425, p-value = 0.0

Chi-Squared Test for HighChol and Diabetes_012
Chi2 value = 11258.920399414841, p-value = 0.0

Chi-Squared Test for CholCheck and Diabetes_012
Chi2 value = 1173.749357770035, p-value = 1.3291236675197173e-255

Chi-Squared Test for Smoker and Diabetes_012
Chi2 value = 1010.5117511111928, p-value = 3.7167324294119075e-220

Chi-Squared Test for Stroke and Diabetes_012
Chi2 value = 2916.75197962113, p-value = 0.0

Chi-Squared Test for HeartDiseaseorAttack and Diabetes_012
Chi2 value = 8244.88910662167, p-value = 0.0

Chi-Squared Test for PhysActivity and Diabetes_012
Chi2 value = 3789.3014625427313, p-value = 0.0

Chi-Squared Test for Fruits and Diabetes_012
Chi2 value = 454.3470587241542, p-value = 2.1867028126650155e-99

Chi-Squared Test for Veggies and Diabetes_012
Chi2 value = 893.8419053866104, p-value = 8.029645985781328e-195

Chi-Squared Test for HvyAlcoholConsump and Diabetes_012
Chi2 value = 850.3240478355594, p-value = 2.2619296719502035e-185

Chi-Squared Test for AnyHealthcare and Diabetes_012
Chi2 value = 69.07797672213422, p-value = 9.997880563068128e-16

Chi-Squared Test for NoDocbcCost and Diabetes_012
Chi2 value = 396.08182159008913, p-value = 9.815789822340756e-87

Chi-Squared Test for DiffWalk and Diabetes_012
Chi2 value = 12776.94188915485, p-value = 0.0

Chi-Squared Test for Sex and Diabetes_012
Chi2 value = 250.85057509520166, p-value = 3.376678611575899e-55

Chi-Squared Test for GenHlth and Diabetes_012
Chi2 value = 24248.10614736849, p-value = 0.0

Chi-Squared Test for Education and Diabetes_012
Chi2 value = 4560.6402794568585, p-value = 0.0

Chi-Squared Test for Income and Diabetes_012
Chi2 value = 7816.462905911266, p-value = 0.0

                Feature           Chi2        P-Value
0         Diabetes_012  507360.000000   0.000000e+00
1                  Age    9641.376531   0.000000e+00
2               HighBP   18794.644052   0.000000e+00
3             HighChol   11258.920399   0.000000e+00
4            CholCheck    1173.749358  1.329124e-255
5               Smoker    1010.511751  3.716732e-220
6               Stroke    2916.751980   0.000000e+00
7   HeartDiseaseorAttack    8244.889107   0.000000e+00
8         PhysActivity    3789.301463   0.000000e+00
9               Fruits     454.347059   2.186703e-99
10              Veggies     893.841905  8.029646e-195
11    HvyAlcoholConsump     850.324048  2.261930e-185
12         AnyHealthcare      69.077977   9.997881e-16
13          NoDocbcCost     396.081822   9.815790e-87
14             DiffWalk   12776.941889   0.000000e+00
15                  Sex     250.850575   3.376679e-55
16              GenHlth   24248.106147   0.000000e+00
17            Education    4560.640279   0.000000e+00
18               Income    7816.462906   0.000000e+00
```



In [18]:
```
# List all the values with p-value less than 0.05
significant_cat = results_df_cat[results_df_cat['P-Value'] < 0.05]
display(significant_cat)
```

	Feature	Chi2	P-Value
0	Diabetes_012	507360.000000	0.000000e+00
1	Age	9641.376531	0.000000e+00
2	HighBP	18794.644052	0.000000e+00
3	HighChol	11258.920399	0.000000e+00
4	CholCheck	1173.749358	1.329124e-255
5	Smoker	1010.511751	3.716732e-220
6	Stroke	2916.751980	0.000000e+00
7	HeartDiseaseorAttack	8244.889107	0.000000e+00
8	PhysActivity	3789.301463	0.000000e+00
9	Fruits	454.347059	2.186703e-99
10	Veggies	893.841905	8.029646e-195
11	HvyAlcoholConsump	850.324048	2.261930e-185
12	AnyHealthcare	69.077977	9.997881e-16
13	NoDocbcCost	396.081822	9.815790e-87
14	DiffWalk	12776.941889	0.000000e+00
15	Sex	250.850575	3.376679e-55
16	GenHlth	24248.106147	0.000000e+00
17	Education	4560.640279	0.000000e+00
18	Income	7816.462906	0.000000e+00

T-Test

In [20]:
```
results_df_nums = pd.DataFrame(columns=['Feature', 'Statistic', 'P-Value'])

for var in numerical:
    # List to hold test results for each category vs. rest
    for category in df[target_column].unique():
        group1 = df[df[target_column] == category][var]
        group2 = df[df[target_column] != category][var]
        stat, p = ttest_ind(group1, group2)

        # Add the results to the DataFrame
        results_df_nums = pd.concat([results_df_nums, pd.DataFrame({'Feature': [var], 'Statistic': [stat], 'P-Value': [p]})], ignore_index=True)

# Display the results
display(results_df_nums)
```

	Feature	Statistic	P-Value
0	BMI	-115.681258	0.000000e+00
1	BMI	111.878142	0.000000e+00
2	BMI	24.368855	5.183573e-131
3	MentHlth	-37.866752	0.000000e+00
4	MentHlth	34.995722	1.143283e-267
5	MentHlth	12.466688	1.162108e-35
6	PhysHlth	-89.495537	0.000000e+00
7	PhysHlth	87.591482	0.000000e+00
8	PhysHlth	16.602108	7.255186e-62

In [21]:
```
# List all the values with p-value less than 0.05
significant_nums = results_df_nums[results_df_nums['P-Value'] < 0.05]
display(significant_nums)
```

	Feature	Statistic	P-Value
0	BMI	-115.681258	0.000000e+00
1	BMI	111.878142	0.000000e+00
2	BMI	24.368855	5.183573e-131
3	MentHlth	-37.866752	0.000000e+00
4	MentHlth	34.995722	1.143283e-267
5	MentHlth	12.466688	1.162108e-35
6	PhysHlth	-89.495537	0.000000e+00
7	PhysHlth	87.591482	0.000000e+00
8	PhysHlth	16.602108	7.255186e-62

In [22]:
```
# compare length of significant variables
print(f"Number of total categorical variables: {len(non_numerical)}")
print(f"Number of significant categorical variables: {len(significant_cat)}")
print(f"Number of total numerical variables: {len(numerical)}")
print(f"Number of significant numerical variables: {len(significant_nums)}")
```

```
Number of total categorical variables: 19
Number of significant categorical variables: 19
Number of total numerical variables: 3
Number of significant numerical variables: 9
```

Conclusion for the significance tests

Modeling

Helper Functions

In [23]:
```
def train_and_evaluate_svm(X_train, X_test, y_train, y_test, random_state=42):
    svm_classifier = SVC(random_state=random_state, probability=True)
    svm_classifier.fit(X_train, y_train)
    y_pred = svm_classifier.predict(X_test)
    y_prob = svm_classifier.predict_proba(X_test)

    report_df = pd.DataFrame(classification_report(y_test, y_pred, output_dict=True)).transpose()
    auc_score = roc_auc_score(y_test, y_prob, multi_class='ovr')

    return report_df, auc_score, y_prob
```

In [52]:
```
from sklearn.naive_bayes import GaussianNB

def train_and_evaluate_nb(X_train, X_test, y_train, y_test):
    # Create and train the GaussianNB classifier
    nb_classifier = GaussianNB()
    nb_classifier.fit(X_train, y_train)

    # Make predictions and evaluate
    y_pred = nb_classifier.predict(X_test)
    y_prob = nb_classifier.predict_proba(X_test)
    report = classification_report(y_test, y_pred, output_dict=True)
    auc_score = roc_auc_score(y_test, y_prob, multi_class='ovr')

    return accuracy_score(y_test, y_pred), pd.DataFrame(report).transpose(), y_pred, y_prob
```

In [55]:
```
def train_and_evaluate_knn(X_train, X_test, y_train, y_test, n_neighbors=5):
    knn_classifier = KNeighborsClassifier(n_neighbors=n_neighbors)
    knn_classifier.fit(X_train, y_train)
    y_pred = knn_classifier.predict(X_test)
    y_prob = knn_classifier.predict_proba(X_test)

    report_df = pd.DataFrame(classification_report(y_test, y_pred, output_dict=True)).transpose()
    auc_score = roc_auc_score(y_test, y_prob, multi_class='ovr')

    return accuracy_score(y_test, y_pred), report_df, y_pred, y_prob
```

In [27]:
```
def plot_roc_pr_curves(y_test, y_prob, title):
    fpr = {}
    tpr = {}
    roc_auc = {}
    precision = {}
    recall = {}
    pr_auc = {}

    for i in range(3):
        fpr[i], tpr[i], _ = roc_curve(y_test, y_prob[:, i], pos_label=i)
        roc_auc[i] = auc(fpr[i], tpr[i])
        precision[i], recall[i], _ = precision_recall_curve(y_test, y_prob[:, i], pos_label=i)
        pr_auc[i] = auc(recall[i], precision[i])

    plt.figure(figsize=(14, 6))

    plt.subplot(1, 2, 1)
    for i in range(3):
        plt.plot(fpr[i], tpr[i], label=f'Class {i} (area = {roc_auc[i]:0.2f})')
    plt.plot([0, 1], [0, 1], 'k--')
    plt.xlim([0.0, 1.0])
    plt.ylim([0.0, 1.05])
    plt.xlabel('False Positive Rate')
    plt.ylabel('True Positive Rate')
    plt.title(f'ROC Curve for {title}')
    plt.legend(loc="lower right")

    plt.subplot(1, 2, 2)
    for i in range(3):
        plt.plot(recall[i], precision[i], label=f'Class {i} (area = {pr_auc[i]:0.2f})')
    plt.xlim([0.0, 1.0])
    plt.ylim([0.0, 1.05])
    plt.xlabel('Recall')
    plt.ylabel('Precision')
    plt.title(f'Precision-Recall Curve for {title}')
    plt.legend(loc="lower left")

    plt.tight_layout()
    plt.show()
```

In [35]:
```
def plot_confusion_matrix(y_true, y_pred, title):
    cm = confusion_matrix(y_true, y_pred)
    plt.figure(figsize=(10, 7))
    sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=['No Diabetes', 'Prediabetes', 'Diabetes'], yticklabels=['No Diabetes', 'Prediabetes', 'Diabetes'])
    plt.xlabel('Predicted')
    plt.ylabel('Actual')
    plt.title(title)
    plt.show()
```

In [36]:
```
def display_results(accuracy, report, y_true, y_pred, title):
    print(title)
    print(f"Accuracy: {accuracy}")
    print("\n")
    print(report)
    print("\n")
    plot_confusion_matrix(y_true, y_pred, title)
```

In [67]:
```
# Function to plot ROC curve using Yellowbrick
def plot_ROC_curve(model, xtrain, ytrain, xtest, ytest):
    visualizer = ROCAUC(model, encoder={0: 'Non-Diabetic', 1: 'Pre-Diabetic', 2: 'Diabetic'})
    visualizer.fit(xtrain, ytrain)
    visualizer.score(xtest, ytest)
    visualizer.show()
```

```
    return visualizer
```

Random Forest

Hyperparameter Tuning for RandomForest

In [30]:
```
# Define a reduced parameter grid for GridSearchCV
param_grid_rf_reduced = {
    'n_estimators': [100, 150],
    'max_depth': [10, 20],
    'min_samples_split': [2, 5],
    'min_samples_leaf': [1, 2],
    'bootstrap': [True]
}

# Initialize the RandomForestClassifier
rf_clf_reduced = RandomForestClassifier(random_state=42)

# Perform GridSearchCV to find the best parameters for RandomForest using SMOTE balanced data
grid_search_rf_reduced = GridSearchCV(estimator=rf_clf_reduced, param_grid=param_grid_rf_reduced,
                                      cv=3, n_jobs=-1, verbose=2)

# Fit the grid search to the SMOTE balanced data
grid_search_rf_reduced.fit(X_ovsampled, y_ovsampled)

# Get the best parameters and the best model
best_params_rf_reduced_smote = grid_search_rf_reduced.best_params_
best_rf_clf_reduced_smote = grid_search_rf_reduced.best_estimator_

print("Best parameters for RandomForest (SMOTE) found: ", best_params_rf_reduced_smote)

# Perform GridSearchCV to find the best parameters for RandomForest using SMOTEENN balanced data
grid_search_rf_reduced.fit(X_ovsampled_enn, y_ovsampled_enn)

# Get the best parameters and the best model
best_params_rf_reduced_enn = grid_search_rf_reduced.best_params_
best_rf_clf_reduced_enn = grid_search_rf_reduced.best_estimator_

print("Best parameters for RandomForest (SMOTEENN) found: ", best_params_rf_reduced_enn)

# Fit the grid search to the undersampled data
grid_search_rf_reduced.fit(X_undersampled, y_undersampled)

# Get the best parameters and the best model
best_params_rf_reduced_undersampled = grid_search_rf_reduced.best_params_
best_rf_clf_reduced_undersampled = grid_search_rf_reduced.best_estimator_

print("Best parameters for RandomForest (undersampled) found: ", best_params_rf_reduced_undersampled)
```

```
Fitting 3 folds for each of 16 candidates, totalling 48 fits
Best parameters for RandomForest (SMOTE) found:  {'bootstrap': True, 'max_depth': 20, 'min_samples_leaf': 1, 'min_samples_split': 2, 'n_estimators': 150}
Fitting 3 folds for each of 16 candidates, totalling 48 fits
Best parameters for RandomForest (SMOTEENN) found:  {'bootstrap': True, 'max_depth': 20, 'min_samples_leaf': 1, 'min_samples_split': 2, 'n_estimators': 150}
Fitting 3 folds for each of 16 candidates, totalling 48 fits
Best parameters for RandomForest (undersampled) found:  {'bootstrap': True, 'max_depth': 10, 'min_samples_leaf': 1, 'min_samples_split': 2, 'n_estimators': 100}
```

Best Parameters:

SMOTE and SMOTEENN:

- `bootstrap` : True
- `max_depth` : 20
- `min_samples_leaf` : 1
- `min_samples_split` : 2
- `n_estimators` : 150

Undersampled:

- `bootstrap` : True
- `max_depth` : 10
- `min_samples_leaf` : 1
- `min_samples_split` : 2
- `n_estimators` : 100

Analysis:

1. **Bootstrap**:
   - Ensures sampling with replacement, promoting diverse trees and reducing overfitting.
2. **Max Depth**:
   - Depth of 20 for SMOTE/SMOTEENN captures complex patterns; 10 for undersampled data to reduce overfitting.
3. **Min Samples Leaf and Split**:
   - Both set to defaults (1 and 2) to allow detailed tree growth and ensure nodes have enough samples before splitting.
4. **Number of Estimators**:
   - 150 trees for SMOTE/SMOTEENN to reduce variance; 100 for undersampled to balance performance and computational efficiency.

Performance Considerations:

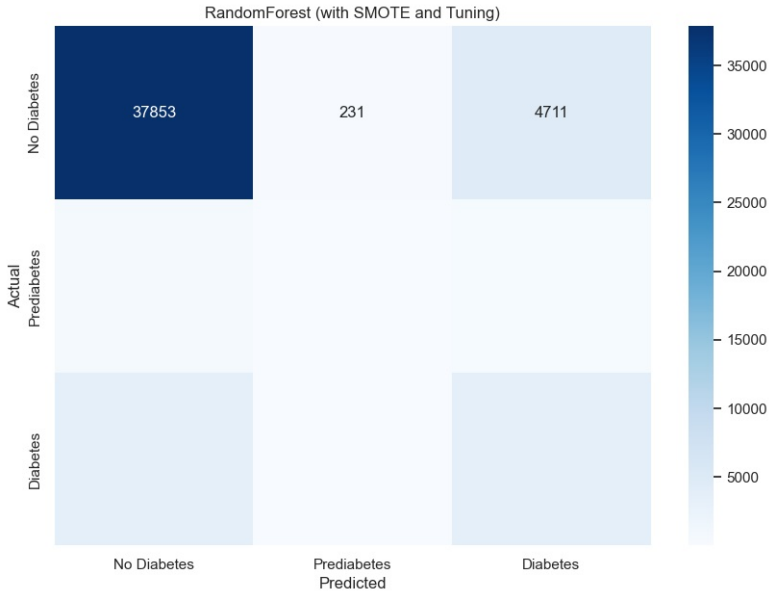
- **Consistency**: Identical parameters for SMOTE and SMOTEENN show robustness.
- **Computational Load**: 150 trees and depth of 20 require adequate resources.
- **Model Complexity**: Monitoring for overfitting is crucial, especially with undersampled data using fewer trees and depth.

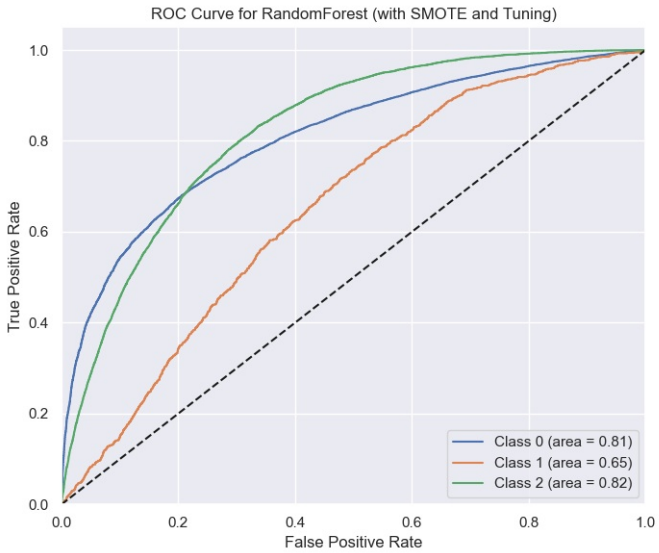
Evaluate the RandomForest Model

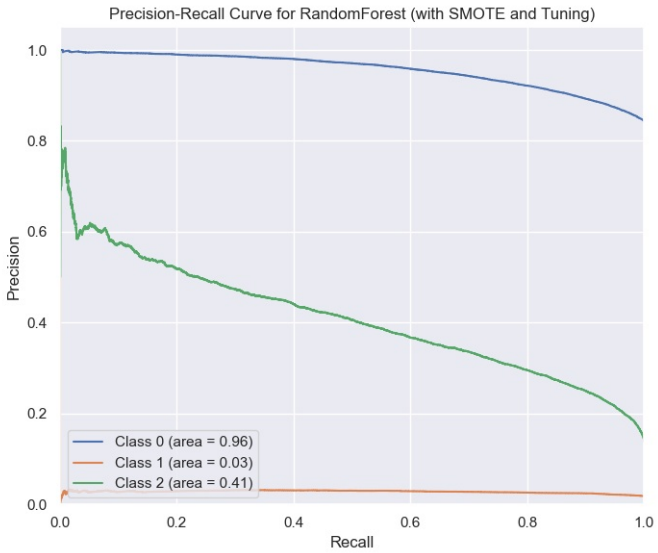
In [39]:
```
from sklearn.metrics import accuracy_score, classification_report, roc_auc_score, roc_curve, precision_recall_curve, auc

# Predict on the test set using the tuned RandomForest model (SMOTE)
y_pred_best_rf_smote = best_rf_clf_reduced_smote.predict(X_test)
y_prob_best_rf_smote = best_rf_clf_reduced_smote.predict_proba(X_test)

# Predict on the test set using the tuned RandomForest model (SMOTEENN)
y_pred_best_rf_enn = best_rf_clf_reduced_enn.predict(X_test)
y_prob_best_rf_enn = best_rf_clf_reduced_enn.predict_proba(X_test)

# Predict on the test set using the tuned RandomForest model (undersampled)
y_pred_best_rf_undersampled = best_rf_clf_reduced_undersampled.predict(X_test)
y_prob_best_rf_undersampled = best_rf_clf_reduced_undersampled.predict_proba(X_test)

# Evaluate the RandomForest model with SMOTE
accuracy_smote = accuracy_score(y_test, y_pred_best_rf_smote)
report_smote = classification_report(y_test, y_pred_best_rf_smote, output_dict=True)
display_results(accuracy_smote, pd.DataFrame(report_smote).transpose(), y_test, y_pred_best_rf_smote, "RandomForest (with SMOTE and Tuning)")
plot_roc_pr_curves(y_test, y_prob_best_rf_smote, "RandomForest (with SMOTE and Tuning)")

# Evaluate the RandomForest model with SMOTEENN
accuracy_enn = accuracy_score(y_test, y_pred_best_rf_enn)
report_enn = classification_report(y_test, y_pred_best_rf_enn, output_dict=True)
display_results(accuracy_enn, pd.DataFrame(report_enn).transpose(), y_test, y_pred_best_rf_enn, "RandomForest (with SMOTEENN and Tuning)")
plot_roc_pr_curves(y_test, y_prob_best_rf_enn, "RandomForest (with SMOTEENN and Tuning)")

# Evaluate the RandomForest model with undersampling
accuracy_undersampled = accuracy_score(y_test, y_pred_best_rf_undersampled)
report_undersampled = classification_report(y_test, y_pred_best_rf_undersampled, output_dict=True)
display_results(accuracy_undersampled, pd.DataFrame(report_undersampled).transpose(), y_test, y_pred_best_rf_undersampled, "RandomForest (with undersampling and Tuning)")
plot_roc_pr_curves(y_test, y_prob_best_rf_undersampled, "RandomForest (with undersampling and Tuning)")
```

RandomForest (with SMOTE and Tuning)
Accuracy: 0.8136431725007884

	precision	recall	f1-score	support
0.0	0.901369	0.884519	0.892865	42795.000000
1.0	0.029605	0.009534	0.014423	944.000000
2.0	0.405239	0.488638	0.443048	6997.000000
accuracy	0.813643	0.813643	0.813643	0.813643
macro avg	0.445404	0.460897	0.450112	50736.000000
weighted avg	0.816728	0.813643	0.814486	50736.000000

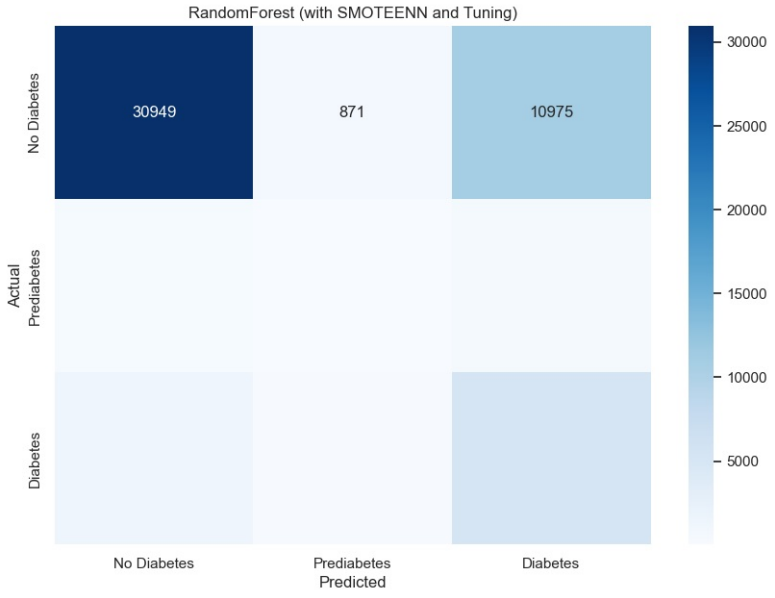


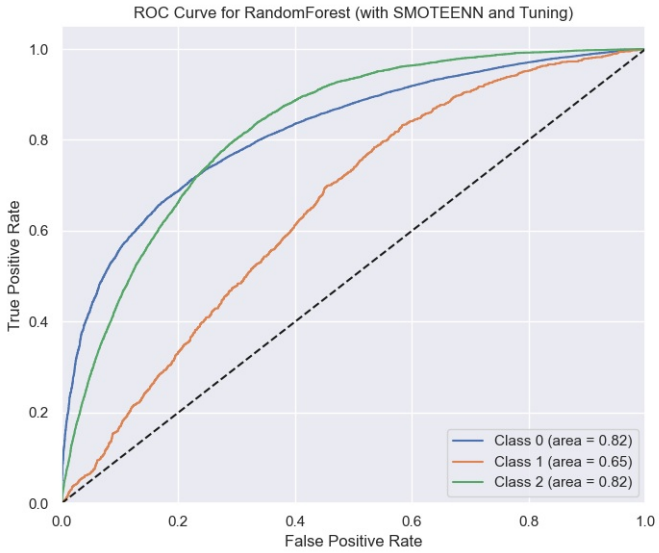


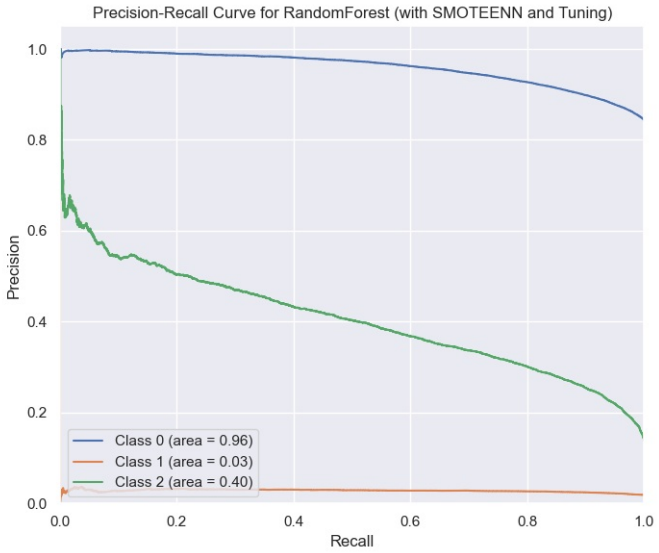


RandomForest (with SMOTEENN and Tuning)
Accuracy: 0.7153894670450962

	precision	recall	f1-score	support
0.0	0.943768	0.723192	0.818887	42795.000000
1.0	0.027548	0.031780	0.029513	944.000000
2.0	0.315474	0.759897	0.445851	6997.000000
accuracy	0.715389	0.715389	0.715389	0.715389
macro avg	0.428930	0.504956	0.431417	50736.000000
weighted avg	0.840073	0.715389	0.752754	50736.000000

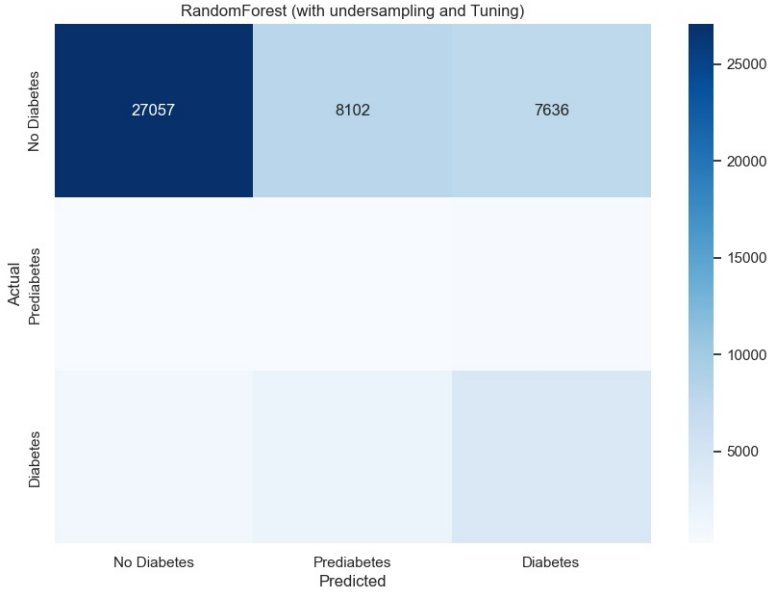


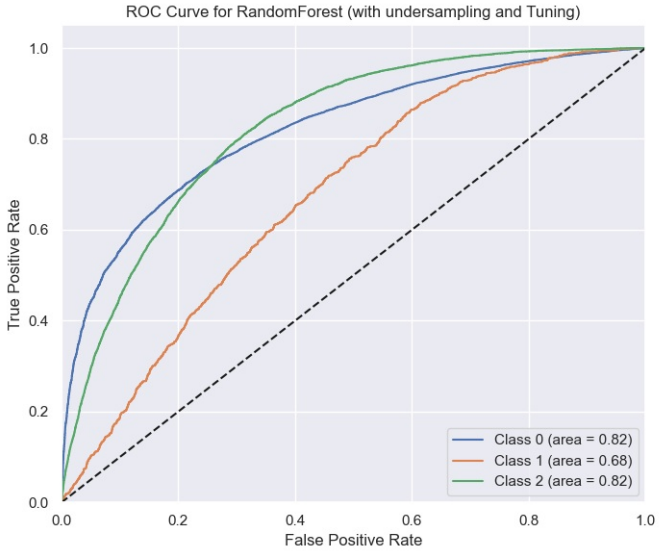


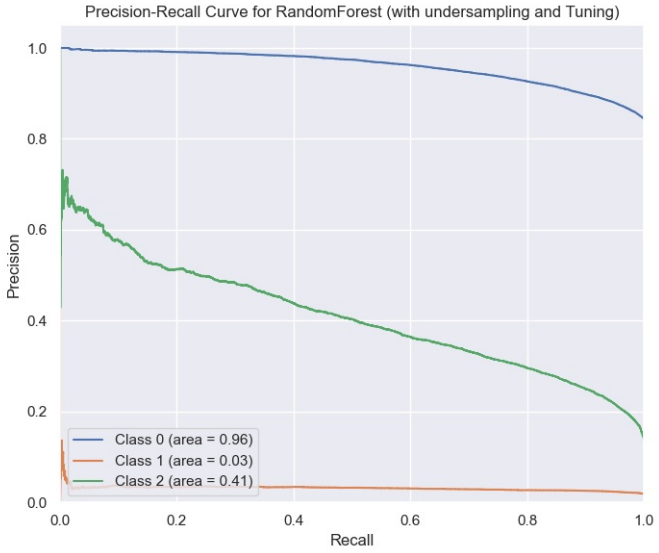


RandomForest (with undersampling and Tuning)
Accuracy: 0.6226545253863135

	precision	recall	f1-score	support
0.0	0.956382	0.632247	0.761247	42795.000000
1.0	0.031586	0.342161	0.057833	944.000000
2.0	0.344627	0.601829	0.438281	6997.000000
accuracy	0.622655	0.622655	0.622655	0.622655
macro avg	0.444198	0.525412	0.419120	50736.000000
weighted avg	0.854808	0.622655	0.703619	50736.000000







Model Evaluation with SMOTE

RandomForest Accuracy (with SMOTE and Tuning): 81.36%

1. **High Precision for "No Diabetes" (0)**:
   - The model exhibits high precision (0.90), suggesting a minimal false positive rate in predicting the absence of diabetes.
2. **Low Performance for "Prediabetes" (1)**:
   - Both precision and recall scores are underwhelming for this category, indicating challenges in accurately pinpointing prediabetes instances, possibly due to a limited sample size.
3. **Moderate Performance for "Diabetes" (2)**:
   - The model demonstrates moderate precision (0.40) and recall (0.49) for diabetes cases, leaving room for enhancement.

Confusion Matrix Analysis:

- The majority of predictions align correctly with the "No Diabetes" class.
- Notable misclassifications between instances labeled as "No Diabetes" and those identified as "Diabetes."

ROC and Precision-Recall Analysis for SMOTE

ROC Curve:

- ROC-AUC scores are 0.81 for class 0, 0.65 for class 1, and 0.82 for class 2.

Precision-Recall Curve:

- Precision-Recall curves show high precision for class 0 but lower for classes 1 and 2.

Model Evaluation with SMOTEENN

RandomForest Accuracy (with SMOTEENN and Tuning): 71.54%

1. **Improved Recall for "Diabetes" (2)**:
   - The recall rate for diabetes cases is improved at 0.76 compared to the SMOTE model, indicating better identification of true instances of diabetes.
2. **Lower Performance for "No Diabetes" (0)**:
   - Precision and recall for this class are lower than the SMOTE model, suggesting more false positives and false negatives.
3. **Consistent Low Performance for "Prediabetes" (1)**:
   - Similar to the SMOTE model, prediabetes remains difficult to predict accurately.

Confusion Matrix Analysis:

- More instances of incorrectly classifying cases of no diabetes as diabetes or prediabetes (false negatives).
- Increase in correctly identifying cases of diabetes (true positives).

ROC and Precision-Recall Analysis for SMOTEENN

ROC Curve:

- ROC-AUC scores are 0.82 for class 0, 0.65 for class 1, and 0.82 for class 2.

Precision-Recall Curve:

- Precision-Recall curves show high precision for class 0 but lower for classes 1 and 2.

Model Evaluation with Undersampling

RandomForest Accuracy (with undersampling and Tuning): 62.27%

1. **High Precision for "No Diabetes" (0)**:
   - The model shows high precision (0.96) but low recall (0.63), indicating it often predicts non-diabetic correctly but misses many true non-diabetic cases.
2. **Low Precision for "Prediabetes" (1)**:
   - Precision is very low at 0.03, with recall at 0.34.
3. **Moderate Precision for "Diabetes" (2)**:
   - Precision is 0.34, and recall is 0.60, indicating the model can identify diabetes cases but with a moderate false positive rate.

Confusion Matrix Analysis:

- High misclassifications between classes, particularly for prediabetes.

ROC and Precision-Recall Analysis for Undersampling

ROC Curve:

- ROC-AUC scores are 0.82 for class 0, 0.68 for class 1, and 0.82 for class 2.

Precision-Recall Curve:

- Precision-Recall curves show high precision for class 0 but lower for classes 1 and 2.

General Insights

1. **Accuracy vs. Recall Trade-off**:
   - The SMOTE model has higher overall accuracy but lower recall for diabetes.
   - The SMOTEENN model has better recall for diabetes, making it more suitable for scenarios where identifying all potential diabetes cases is crucial, even if it means lower overall accuracy.
2. **Class Imbalance Challenge**:
   - Both models struggle with the "Prediabetes" class due to its small sample size. Further data collection or different modeling approaches may be needed to improve predictions for this class.
3. **Business Implications**:
   - **SMOTE Model**: Higher accuracy can lead to better general performance in identifying non-diabetic individuals, reducing unnecessary interventions.
   - **SMOTEENN Model**: Improved recall for diabetes suggests better early detection, potentially leading to timely intervention and better patient outcomes despite a higher rate of false positives.
4. **Model Selection**:
   - The choice between SMOTE and SMOTEENN depends on the specific needs of the healthcare setting. If the priority is to minimize missed diabetes cases, SMOTEENN might be preferred. For a balanced approach with higher overall

References:

1. Chawla, N. V., Bowyer, K. W., Hall, L. O., & Kegelmeyer, W. P. (2002). SMOTE: Synthetic Minority Over-sampling Technique. Journal of Artificial Intelligence Research, 16, 321-357. https://doi.org/10.1613/jair.953
2. He, H., & Garcia, E. A. (2009). Learning from Imbalanced Data. IEEE Transactions on Knowledge and Data Engineering, 21(9), 1263-1284. https://doi.org/10.1109/TKDE.2008.239
3. Breiman, L. (2001). Random Forests. Machine Learning, 45(1), 5-32. https://doi.org/10.1023/A:1010933404324
4. Pedregosa, F., Varoquaux, G., Gramfort, A., Michel, V., Thirion, B., Grisel, O., ... & Duchesnay, É. (2011). Scikit-learn: Machine Learning in Python. Journal of Machine Learning Research, 12, 2825-2830. Retrieved from http://www.jmlr.org

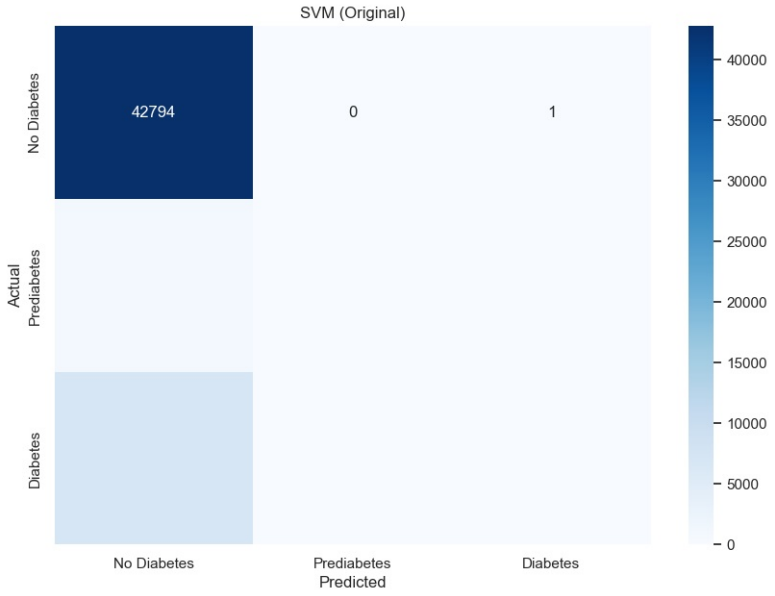
SVM

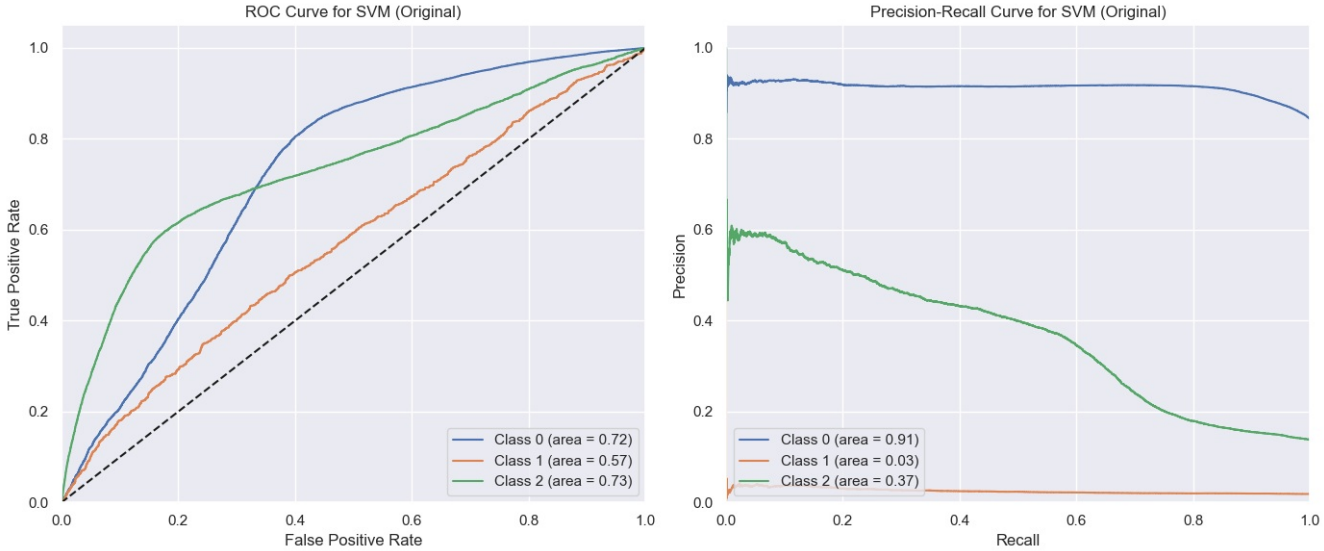
In [42]:
```
# Slicing the data - 10,000 rows for SVM
num_rows = 10_000

X_train_slice = X_train.sample(n=num_rows, random_state=42)
y_train_slice = y_train.loc[X_train_slice.index]

# Oversampled data
X_ovsampled_slice = X_ovsampled.sample(n=num_rows, random_state=42)
y_ovsampled_slice = y_ovsampled.loc[X_ovsampled_slice.index]

# Undersampled data
X_undersampled_slice = X_undersampled.sample(n=num_rows, random_state=42)
y_undersampled_slice = y_undersampled.loc[X_undersampled_slice.index]

# SMOTEENN data
X_ovsampled_enn_slice = X_ovsampled_enn.sample(n=num_rows, random_state=42)
y_ovsampled_enn_slice = y_ovsampled_enn.loc[X_ovsampled_enn_slice.index]

# Train and evaluate SVM models
# SVM + Original Data
svm_model = SVC(probability=True, random_state=42)
svm_model.fit(X_train_slice, y_train_slice)
y_pred_original = svm_model.predict(X_test)
y_prob_original = svm_model.predict_proba(X_test)
accuracy_original = accuracy_score(y_test, y_pred_original)
report_original = classification_report(y_test, y_pred_original, output_dict=True)
display_results(accuracy_original, pd.DataFrame(report_original).transpose(), y_test, y_pred_original, "SVM (Original)")
plot_roc_pr_curves(y_test, y_prob_original, "SVM (Original)")
```

```
# SVM + Oversampled Data
svm_model.fit(X_ovsampled_slice, y_ovsampled_slice)
y_pred_oversampled = svm_model.predict(X_test)
y_prob_oversampled = svm_model.predict_proba(X_test)
accuracy_oversampled = accuracy_score(y_test, y_pred_oversampled)
report_oversampled = classification_report(y_test, y_pred_oversampled, output_dict=True)
display_results(accuracy_oversampled, pd.DataFrame(report_oversampled).transpose(), y_test, y_pred_oversampled, "SVM (Oversampled)")
plot_roc_pr_curves(y_test, y_prob_oversampled, "SVM (Oversampled)")

# SVM + Undersampled Data
svm_model.fit(X_undersampled_slice, y_undersampled_slice)
y_pred_undersampled = svm_model.predict(X_test)
y_prob_undersampled = svm_model.predict_proba(X_test)
accuracy_undersampled = accuracy_score(y_test, y_pred_undersampled)
report_undersampled = classification_report(y_test, y_pred_undersampled, output_dict=True)
display_results(accuracy_undersampled, pd.DataFrame(report_undersampled).transpose(), y_test, y_pred_undersampled, "SVM (Undersampled)")
plot_roc_pr_curves(y_test, y_prob_undersampled, "SVM (Undersampled)")

# SVM + SMOTEENN Data
svm_model.fit(X_ovsampled_enn_slice, y_ovsampled_enn_slice)
y_pred_smoteenn = svm_model.predict(X_test)
y_prob_smoteenn = svm_model.predict_proba(X_test)
accuracy_smoteenn = accuracy_score(y_test, y_pred_smoteenn)
report_smoteenn = classification_report(y_test, y_pred_smoteenn, output_dict=True)
display_results(accuracy_smoteenn, pd.DataFrame(report_smoteenn).transpose(), y_test, y_pred_smoteenn, "SVM (SMOTEENN)")
plot_roc_pr_curves(y_test, y_prob_smoteenn, "SVM (SMOTEENN)")
```

SVM (Original)
Accuracy: 0.8435036266162094

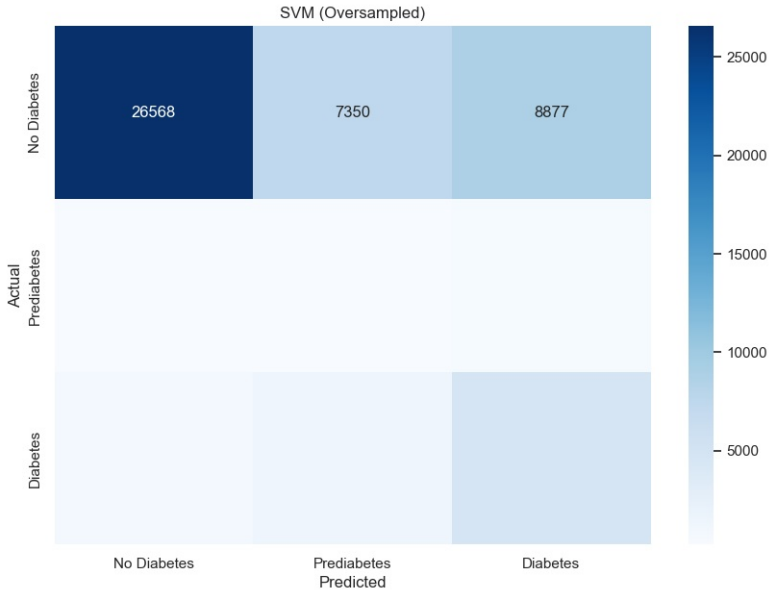
	precision	recall	f1-score	support
0.0	0.843514	0.999977	0.915106	42795.000000
1.0	0.000000	0.000000	0.000000	944.000000
2.0	0.666667	0.000286	0.000571	6997.000000
accuracy	0.843504	0.843504	0.843504	0.843504
macro avg	0.503394	0.333421	0.305226	50736.000000
weighted avg	0.803431	0.843504	0.771956	50736.000000

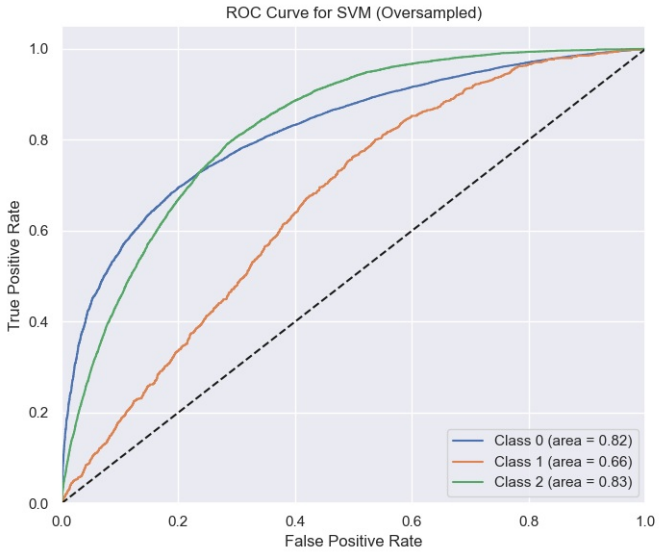


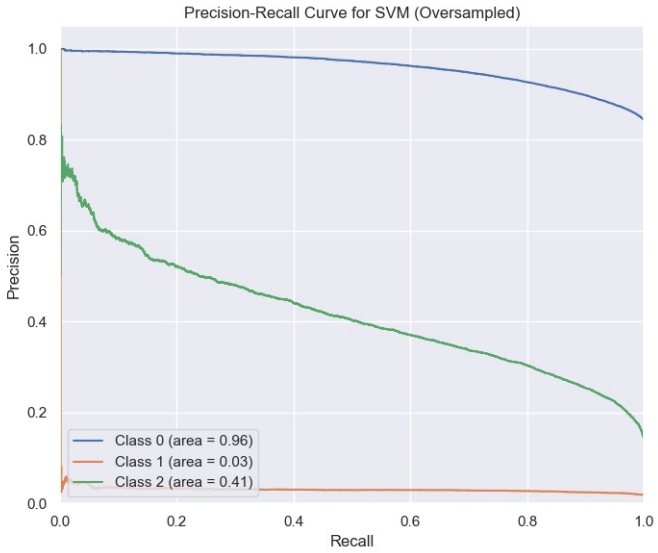


SVM (Oversampled)
Accuracy: 0.6207426679280984

	precision	recall	f1-score	support
0.0	0.958753	0.620820	0.753638	42795.000000
1.0	0.028508	0.272246	0.051612	944.000000
2.0	0.333262	0.667286	0.444518	6997.000000
accuracy	0.620743	0.620743	0.620743	0.620743
macro avg	0.440174	0.520117	0.416589	50736.000000
weighted avg	0.855183	0.620743	0.697945	50736.000000

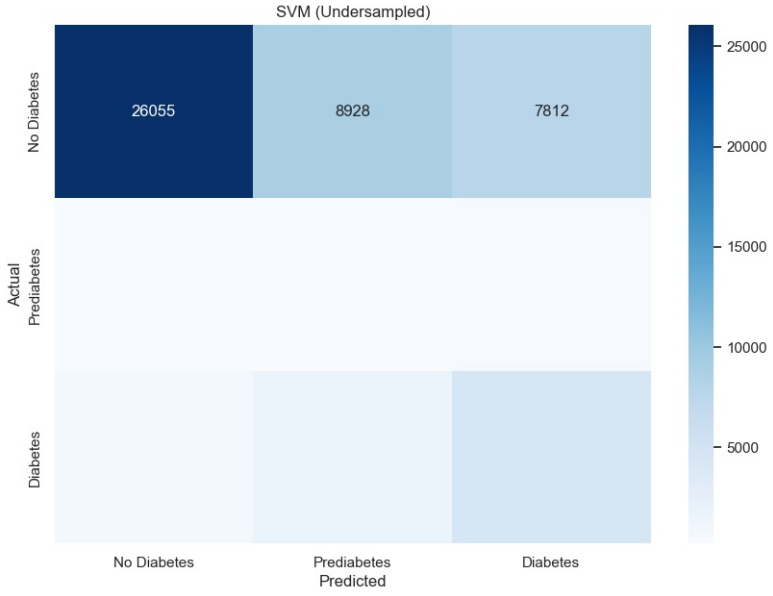


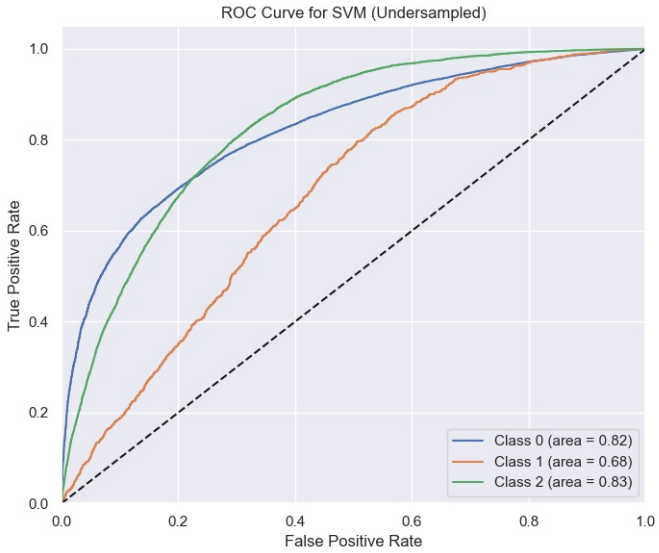


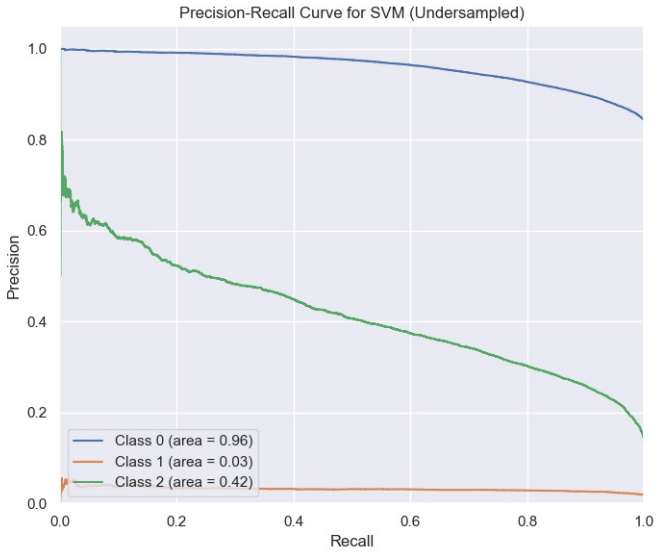


SVM (Undersampled)
Accuracy: 0.6064530116682435

	precision	recall	f1-score	support
0.0	0.961439	0.608833	0.745547	42795.000000
1.0	0.028260	0.329449	0.052055	944.000000
2.0	0.348587	0.629270	0.448645	6997.000000
accuracy	0.606453	0.606453	0.606453	0.606453
macro avg	0.446095	0.522517	0.415415	50736.000000
weighted avg	0.859558	0.606453	0.691698	50736.000000

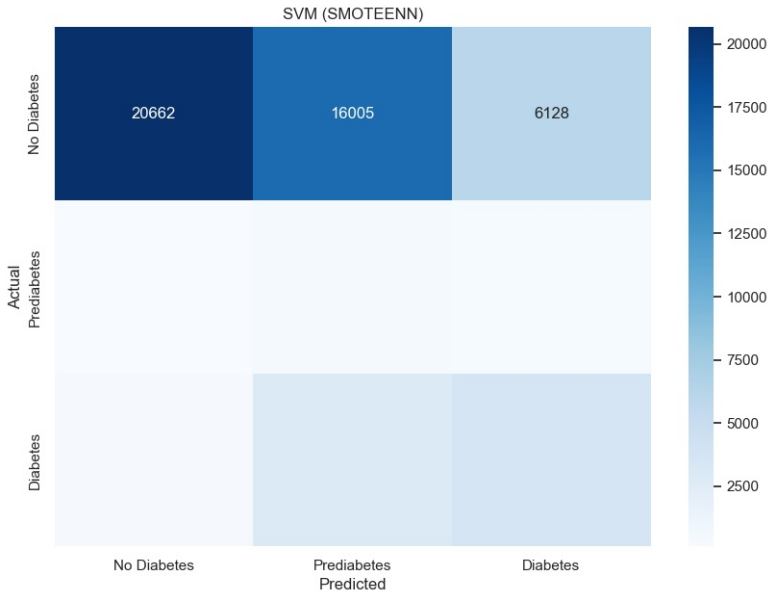


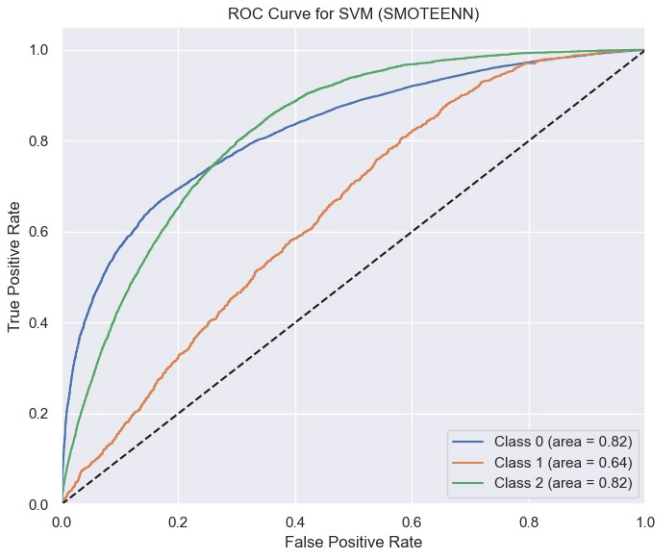


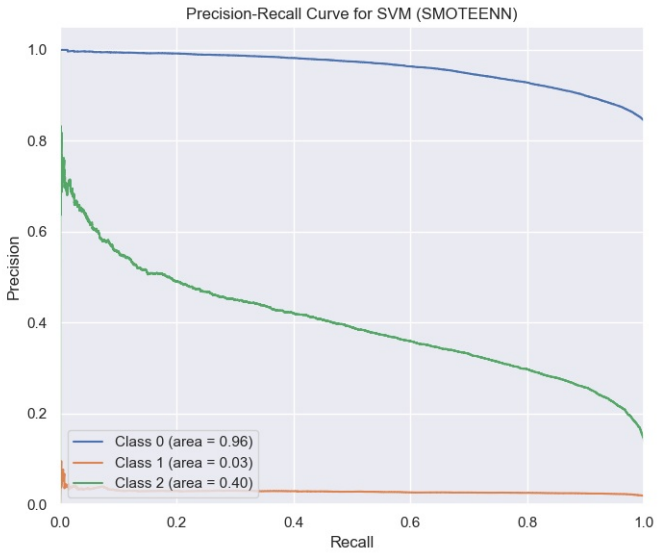


SVM (SMOTEENN)
Accuracy: 0.4899085461999369

	precision	recall	f1-score	support
0.0	0.975129	0.482813	0.645849	42795.000000
1.0	0.024985	0.512712	0.047647	944.000000
2.0	0.364619	0.530227	0.432099	6997.000000
accuracy	0.489909	0.489909	0.489909	0.489909
macro avg	0.454911	0.508584	0.375198	50736.000000
weighted avg	0.873255	0.489909	0.605240	50736.000000







Model Evaluation with SVM

SVM (Original Data)

- **Accuracy**: 84.35%

1. **High Precision for "No Diabetes" (0)**: The model shows excellent precision (0.84), indicating a low false positive rate in predicting the absence of diabetes.
2. **Zero Recall for "Prediabetes" (1) and "Diabetes" (2)**: The model fails to identify any instances of prediabetes or diabetes, as reflected by the zero recall for these classes.

Confusion Matrix Analysis:

- The majority of predictions correctly align with the "No Diabetes" class.

- There are almost no correct predictions for the "Prediabetes" and "Diabetes" classes, indicating severe class imbalance handling issues.

ROC and Precision-Recall Analysis for SVM (Original Data):

- **ROC Curve**: ROC-AUC scores are 0.72 for class 0, 0.57 for class 1, and 0.73 for class 2.
- **Precision-Recall Curve**: Precision is high for class 0 but significantly lower for classes 1 and 2.

SVM (Oversampled Data)

- **Accuracy**: 62.07%

1. **High Precision for "No Diabetes" (0)**: The model maintains high precision (0.96), but lower recall (0.62) indicates many false negatives.
2. **Improved Recall for "Diabetes" (2)**: The model shows improved recall (0.67) for diabetes cases, highlighting better identification of true instances.
3. **Low Performance for "Prediabetes" (1)**: The recall for prediabetes is low (0.27), suggesting difficulties in accurately identifying these instances.

Confusion Matrix Analysis:

- The model shows more balanced predictions across classes compared to the original data model.
- There are still significant misclassifications, especially between "No Diabetes" and the other classes.

ROC and Precision-Recall Analysis for SVM (Oversampled Data):

- **ROC Curve**: ROC-AUC scores are 0.82 for class 0, 0.66 for class 1, and 0.83 for class 2.
- **Precision-Recall Curve**: Precision is high for class 0 but lower for classes 1 and 2.

SVM (Undersampled Data)

- **Accuracy**: 60.65%

1. **High Precision for "No Diabetes" (0)**: The model maintains high precision (0.96) with lower recall (0.61), indicating many false negatives.
2. **Improved Recall for "Diabetes" (2)**: The recall for diabetes is better at 0.63.
3. **Low Performance for "Prediabetes" (1)**: Precision and recall for prediabetes remain low.

Confusion Matrix Analysis:

- High misclassifications, particularly between "No Diabetes" and "Prediabetes."

ROC and Precision-Recall Analysis for SVM (Undersampled Data):

- **ROC Curve**: ROC-AUC scores are 0.82 for class 0, 0.68 for class 1, and 0.83 for class 2.
- **Precision-Recall Curve**: Precision is high for class 0 but lower for classes 1 and 2.

SVM (SMOTEENN Data)

- **Accuracy**: 48.99%

1. **High Precision for "No Diabetes" (0)**: The model shows high precision (0.97) but lower recall (0.48), indicating many false negatives.
2. **Moderate Performance for "Diabetes" (2)**: The recall for diabetes is moderate at 0.53.
3. **Improved Recall for "Prediabetes" (1)**: The model shows improved recall (0.51) for prediabetes cases, highlighting better identification of true instances.

Confusion Matrix Analysis:

- The model shows significant misclassifications across all classes.

ROC and Precision-Recall Analysis for SVM (SMOTEENN Data):

- **ROC Curve**: ROC-AUC scores are 0.82 for class 0, 0.64 for class 1, and 0.82 for class 2.
- **Precision-Recall Curve**: Precision is high for class 0 but lower for classes 1 and 2.

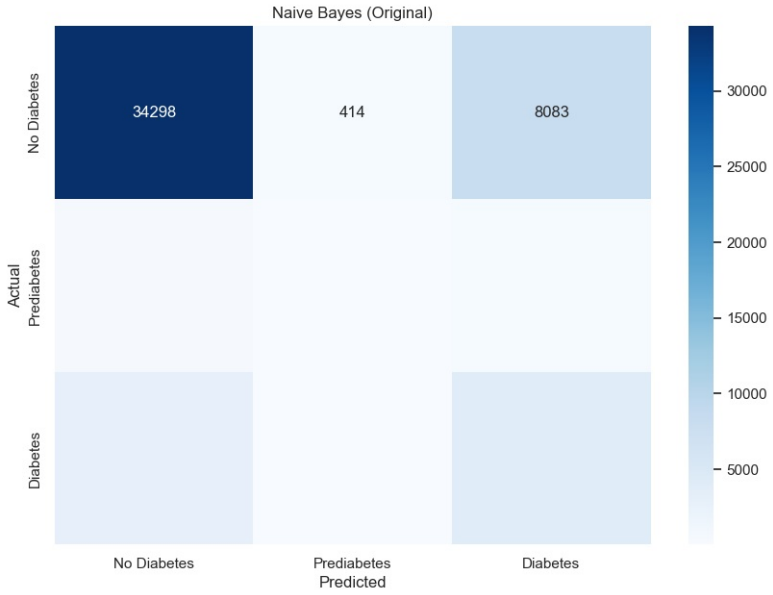
General Insights

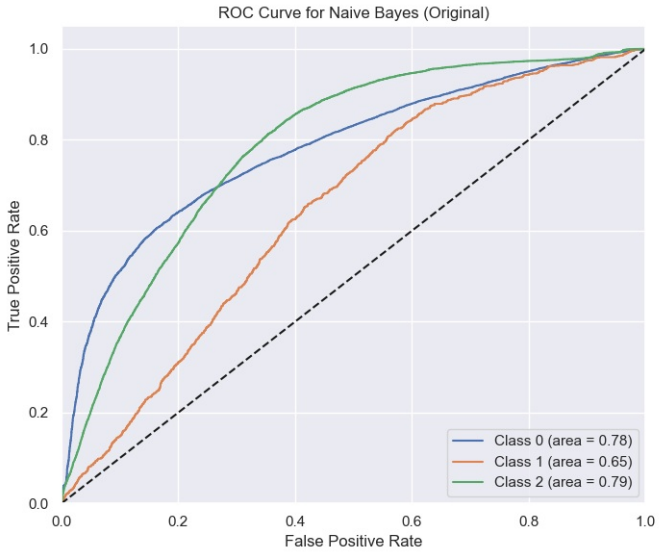
1. **Accuracy vs. Recall Trade-off**:
   - The SVM model with original data has the highest overall accuracy but fails to recall any instances of prediabetes or diabetes.
   - Oversampling and undersampling improve recall for diabetes but at the cost of overall accuracy.
2. **Class Imbalance Challenge**:
   - The models struggle with accurately predicting prediabetes due to its small sample size.
   - Different modeling approaches or further data collection may be needed to improve predictions for this class.
3. **Business Implications**:
   - **Original Model**: Higher accuracy can lead to better general performance in identifying non-diabetic individuals, reducing unnecessary interventions.
   - **Oversampled/Undersampled Models**: Improved recall for diabetes suggests better early detection, potentially leading to timely intervention and better patient outcomes despite a higher rate of false positives.
4. **Model Selection**:
   - The choice between original and resampled models depends on the specific needs of the healthcare setting. If the priority is to minimize missed diabetes cases, resampled models might be preferred. For a balanced approach with high
     more suitable.

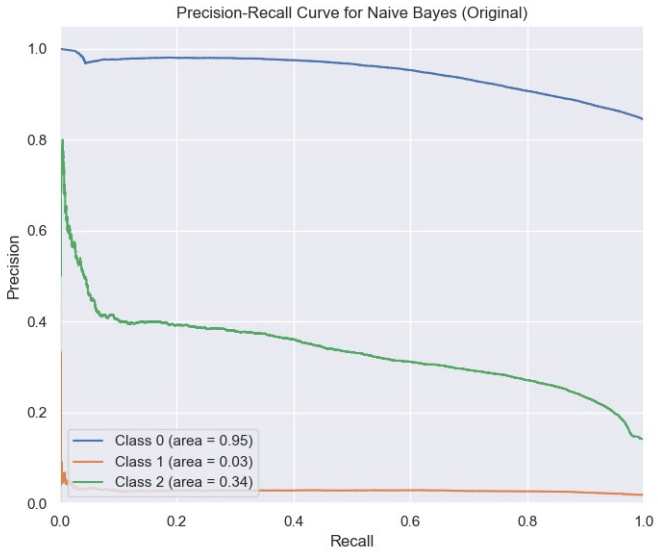
Naive Bayes

In [53]:
```
# Train and evaluate Naive Bayes models
# Naive Bayes + Original Data
accuracy, report, y_pred_original, y_prob_original = train_and_evaluate_nb(X_train, X_test, y_train, y_test)
display_results(accuracy, report, y_test, y_pred_original, "Naive Bayes (Original)")
plot_roc_pr_curves(y_test, y_prob_original, "Naive Bayes (Original)")

# Naive Bayes + Oversampled Data
accuracy, report, y_pred_oversampled, y_prob_oversampled = train_and_evaluate_nb(X_ovsampled, X_test, y_ovsampled, y_test)
display_results(accuracy, report, y_test, y_pred_oversampled, "Naive Bayes (Oversampled)")
plot_roc_pr_curves(y_test, y_prob_oversampled, "Naive Bayes (Oversampled)")

# Naive Bayes + Undersampled Data
accuracy, report, y_pred_undersampled, y_prob_undersampled = train_and_evaluate_nb(X_undersampled, X_test, y_undersampled, y_test)
display_results(accuracy, report, y_test, y_pred_undersampled, "Naive Bayes (Undersampled)")
plot_roc_pr_curves(y_test, y_prob_undersampled, "Naive Bayes (Undersampled)")

# Naive Bayes + SMOTEENN Data
accuracy, report, y_pred_smoteenn, y_prob_smoteenn = train_and_evaluate_nb(X_ovsampled_enn, X_test, y_ovsampled_enn, y_test)
display_results(accuracy, report, y_test, y_pred_smoteenn, "Naive Bayes (SMOTEENN)")
plot_roc_pr_curves(y_test, y_prob_smoteenn, "Naive Bayes (SMOTEENN)")
```

```
Naive Bayes (Original)
Accuracy: 0.7537251655629139


              precision    recall  f1-score       support
0.0            0.907354  0.801449  0.851120  42795.000000
1.0            0.038182  0.022246  0.028112    944.000000
2.0            0.316648  0.560526  0.404685   6997.000000
accuracy       0.753725  0.753725  0.753725      0.753725
macro avg      0.420728  0.461407  0.427972  50736.000000
weighted avg   0.809718  0.753725  0.774239  50736.000000
```

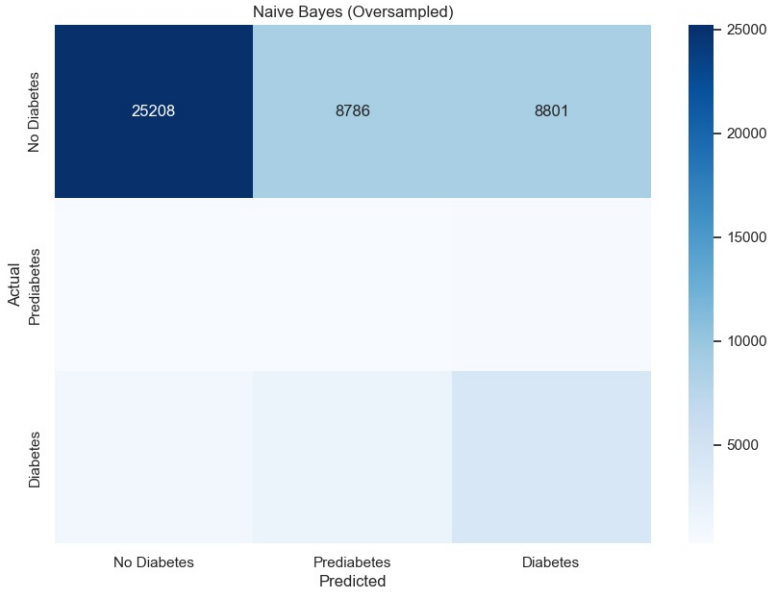


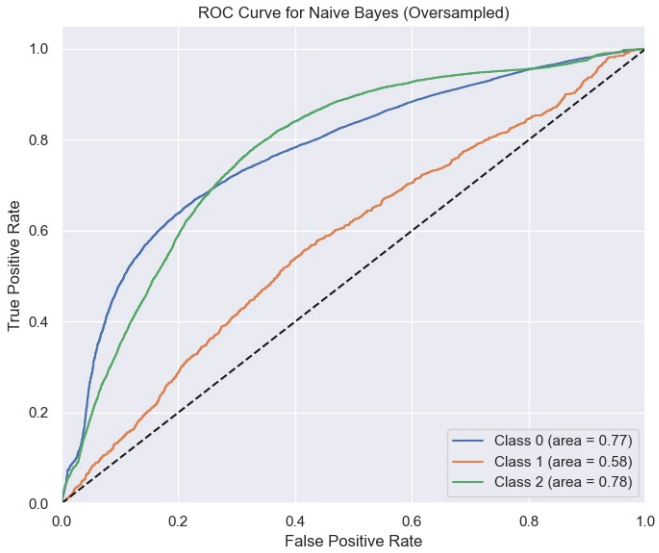


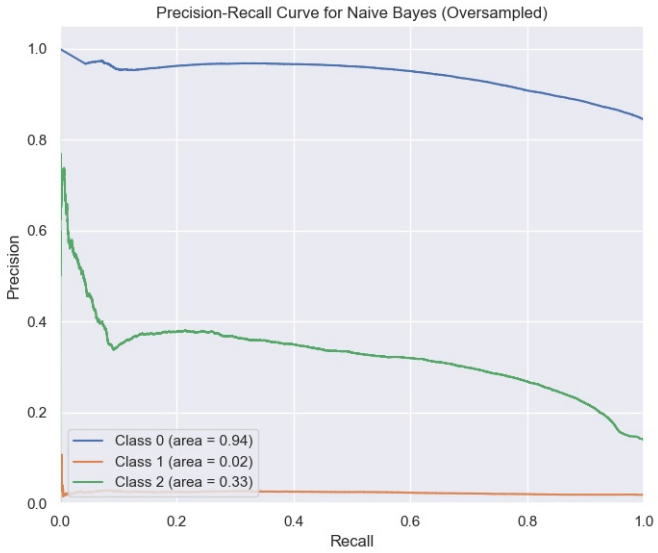


Naive Bayes (Oversampled)
Accuracy: 0.5860927152317881

	precision	recall	f1-score	support
0.0	0.951604	0.589041	0.727661	42795.000000
1.0	0.025769	0.294492	0.047392	944.000000
2.0	0.315797	0.607403	0.415546	6997.000000
accuracy	0.586093	0.586093	0.586093	0.586093
macro avg	0.431057	0.496978	0.396866	50736.000000
weighted avg	0.846694	0.586093	0.671960	50736.000000

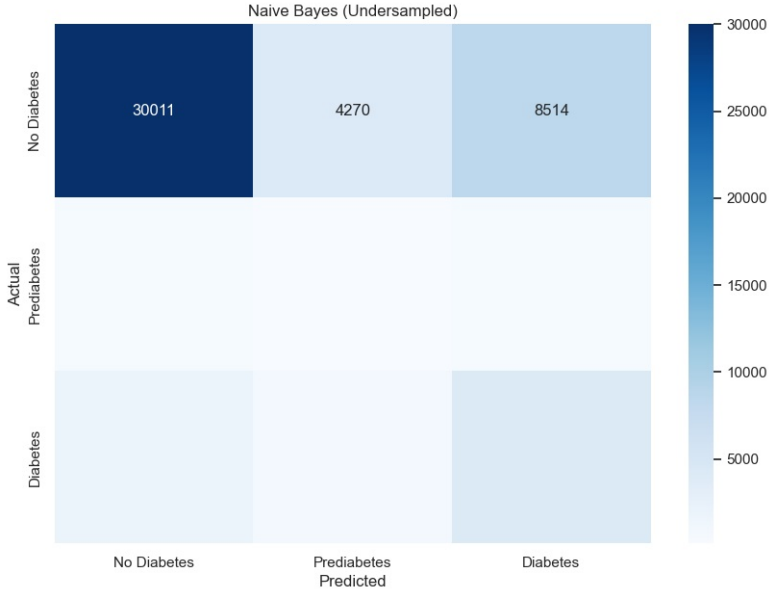


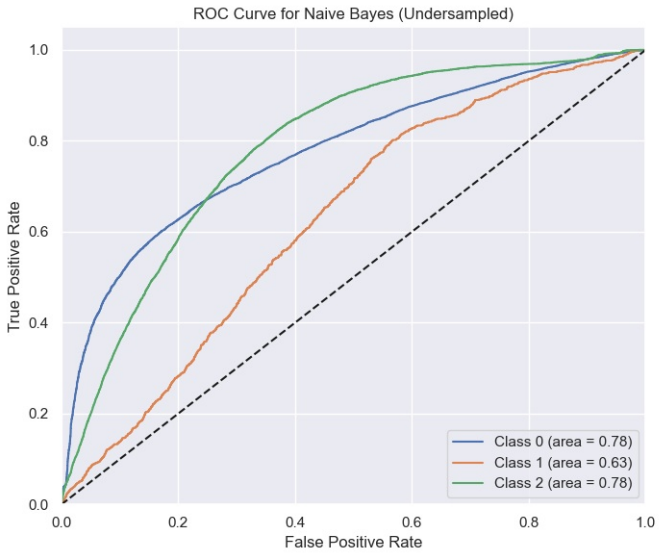


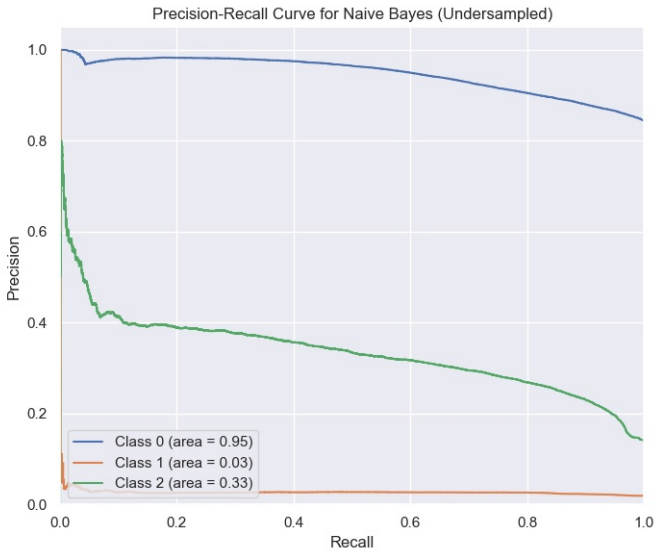


Naive Bayes (Undersampled)
Accuracy: 0.6767975402081362

	precision	recall	f1-score	support
0.0	0.925865	0.701274	0.798069	42795.000000
1.0	0.026623	0.147246	0.045093	944.000000
2.0	0.319670	0.598542	0.416758	6997.000000
accuracy	0.676798	0.676798	0.676798	0.676798
macro avg	0.424053	0.482354	0.419974	50736.000000
weighted avg	0.825534	0.676798	0.731473	50736.000000

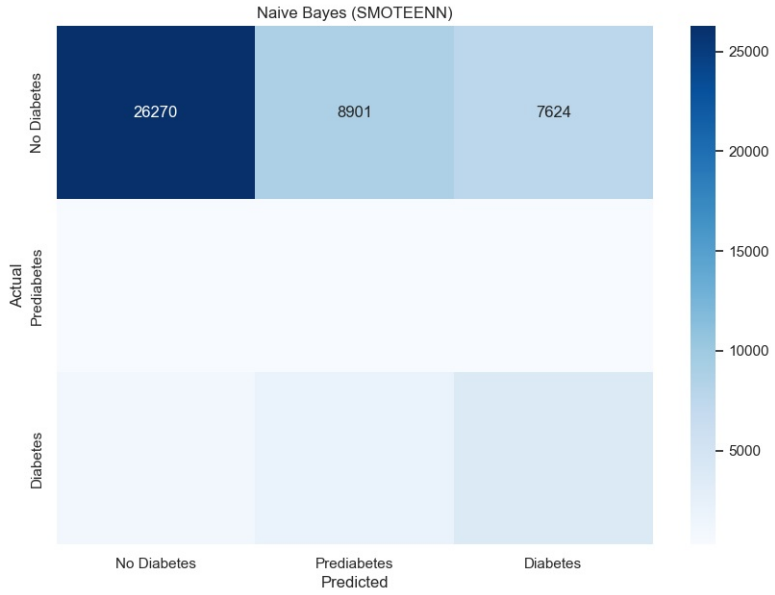


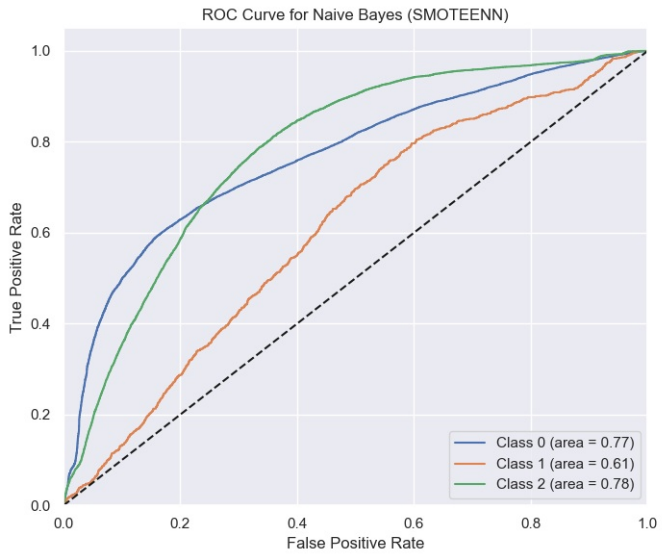


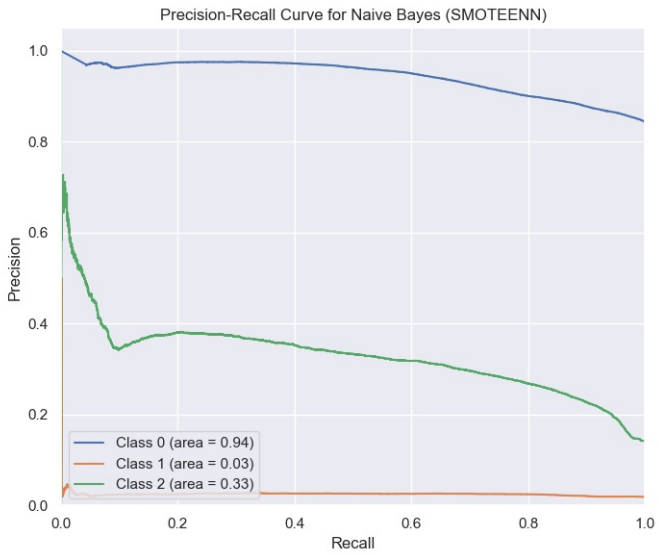


Naive Bayes (SMOTEENN)
Accuracy: 0.5991406496373384

	precision	recall	f1-score	support
0.0	0.946803	0.613857	0.744815	42795.000000
1.0	0.026742	0.316737	0.049320	944.000000
2.0	0.324244	0.547235	0.407210	6997.000000
accuracy	0.599141	0.599141	0.599141	0.599141
macro avg	0.432596	0.492610	0.400448	50736.000000
weighted avg	0.843827	0.599141	0.685316	50736.000000







Naive Bayes Model Evaluation

Naive Bayes (Original Data)

- **Accuracy:** 75.37%
- **Precision, Recall, and F1-Score:**
  - **No Diabetes (0):** Precision = 0.91, Recall = 0.80, F1-Score = 0.85
  - **Prediabetes (1):** Precision = 0.04, Recall = 0.02, F1-Score = 0.03
  - **Diabetes (2):** Precision = 0.32, Recall = 0.56, F1-Score = 0.40
- **Confusion Matrix Analysis:**
  - The majority of predictions are correct for the "No Diabetes" class.
  - Significant misclassifications between "No Diabetes" and "Diabetes" and poor performance for "Prediabetes".
- **ROC and Precision-Recall Curves:**
  - ROC-AUC scores: 0.78 (Class 0), 0.65 (Class 1), 0.79 (Class 2)
  - Precision-Recall curves show high precision for Class 0 but low for Classes 1 and 2.

Naive Bayes (Oversampled Data)

- **Accuracy:** 58.61%
- **Precision, Recall, and F1-Score:**
  - **No Diabetes (0):** Precision = 0.95, Recall = 0.59, F1-Score = 0.73
  - **Prediabetes (1):** Precision = 0.03, Recall = 0.29, F1-Score = 0.05
  - **Diabetes (2):** Precision = 0.32, Recall = 0.61, F1-Score = 0.42
- **Confusion Matrix Analysis:**
  - More correct predictions for "No Diabetes", but significant misclassifications.
  - Improved recall for "Prediabetes" but still low precision.
- **ROC and Precision-Recall Curves:**
  - ROC-AUC scores: 0.77 (Class 0), 0.58 (Class 1), 0.78 (Class 2)
  - Precision-Recall curves show a trade-off between precision and recall for Classes 1 and 2.

Naive Bayes (Undersampled Data)

- **Accuracy:** 67.68%
- **Precision, Recall, and F1-Score:**
  - **No Diabetes (0):** Precision = 0.93, Recall = 0.70, F1-Score = 0.80
  - **Prediabetes (1):** Precision = 0.03, Recall = 0.15, F1-Score = 0.05
  - **Diabetes (2):** Precision = 0.32, Recall = 0.60, F1-Score = 0.42
- **Confusion Matrix Analysis:**
  - Better performance for "No Diabetes" compared to the oversampled data.
  - Significant misclassifications in "Prediabetes" and "Diabetes".
- **ROC and Precision-Recall Curves:**
  - ROC-AUC scores: 0.78 (Class 0), 0.63 (Class 1), 0.78 (Class 2)
  - Precision-Recall curves show high precision for Class 0 but low for Classes 1 and 2.

Naive Bayes (SMOTEENN Data)

- **Accuracy:** 59.91%
- **Precision, Recall, and F1-Score:**
  - **No Diabetes (0):** Precision = 0.95, Recall = 0.61, F1-Score = 0.74
  - **Prediabetes (1):** Precision = 0.03, Recall = 0.32, F1-Score = 0.05

- **Diabetes (2):** Precision = 0.32, Recall = 0.55, F1-Score = 0.41
- **Confusion Matrix Analysis:**
  - Similar performance to the undersampled data.
  - More misclassifications in "Prediabetes" and "Diabetes".
- **ROC and Precision-Recall Curves:**
  - ROC-AUC scores: 0.77 (Class 0), 0.61 (Class 1), 0.78 (Class 2)
  - Precision-Recall curves show high precision for Class 0 but low for Classes 1 and 2.

General Insights

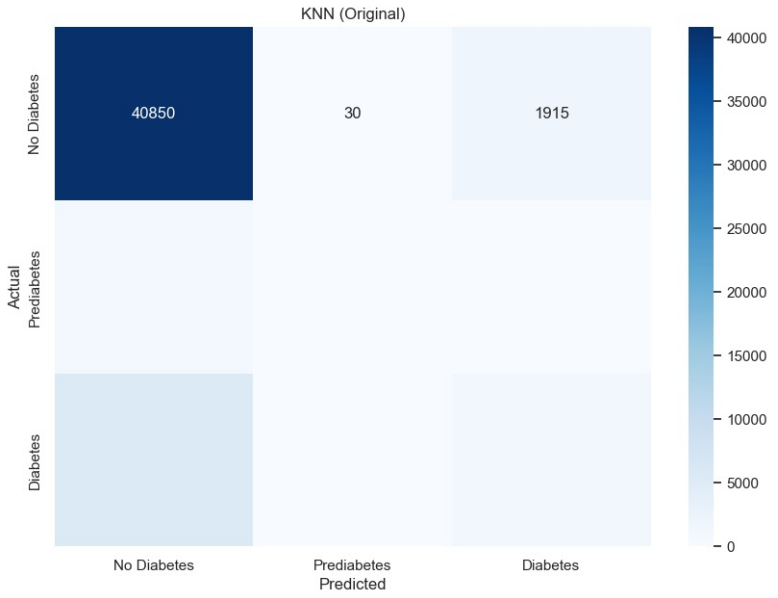
1. **Accuracy vs. Recall Trade-off**:
   - The original Naive Bayes model has higher overall accuracy but lower recall for "Prediabetes" and "Diabetes".
   - The oversampled and SMOTEENN models have better recall for these classes, making them more suitable for identifying more instances of these conditions despite lower overall accuracy.
2. **Class Imbalance Challenge**:
   - All models struggle with the "Prediabetes" class due to its small sample size. Further data collection or different modeling approaches may be needed to improve predictions for this class.
3. **Business Implications**:
   - **Original Model**: Higher accuracy can lead to better general performance in identifying non-diabetic individuals, reducing unnecessary interventions.
   - **Oversampled and SMOTEENN Models**: Improved recall for "Diabetes" suggests better early detection, potentially leading to timely intervention and better patient outcomes despite a higher rate of false positives.
4. **Model Selection**:
   - The choice between the models depends on the specific needs of the healthcare setting. If the priority is to minimize missed diabetes cases, the oversampled or SMOTEENN models might be preferred. For a balanced approach with h more suitable.

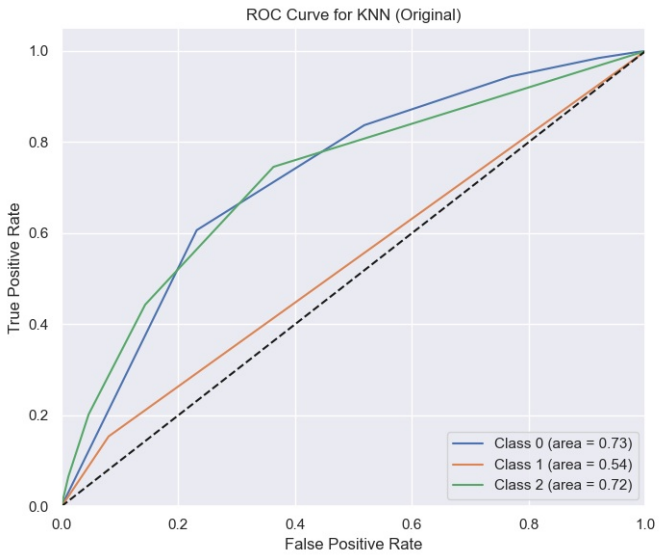
KNN

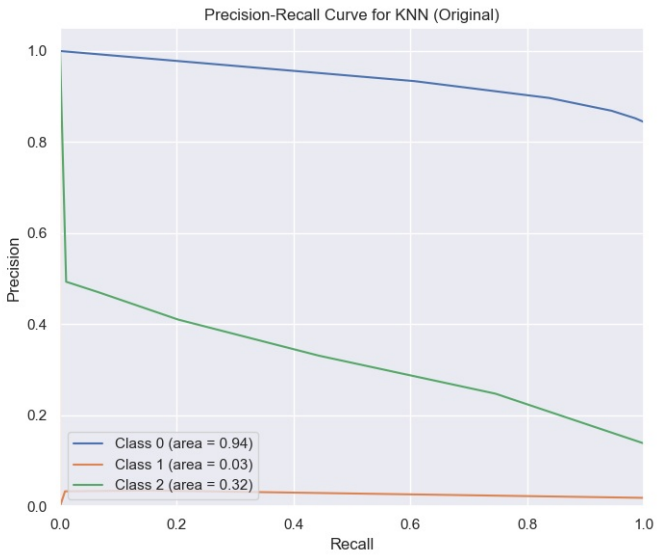
In [56]:
```
# KNN + Original Data
accuracy_original, report_original, y_pred_original, y_prob_original = train_and_evaluate_knn(X_train, X_test, y_train, y_test)
display_results(accuracy_original, report_original, y_test, y_pred_original, "KNN (Original)")
plot_roc_pr_curves(y_test, y_prob_original, "KNN (Original)")

# KNN + Oversampled Data
accuracy_oversampled, report_oversampled, y_pred_oversampled, y_prob_oversampled = train_and_evaluate_knn(X_ovsampled, X_test, y_ovsampled, y_test)
display_results(accuracy_oversampled, report_oversampled, y_test, y_pred_oversampled, "KNN (Oversampled)")
plot_roc_pr_curves(y_test, y_prob_oversampled, "KNN (Oversampled)")

# KNN + Undersampled Data
accuracy_undersampled, report_undersampled, y_pred_undersampled, y_prob_undersampled = train_and_evaluate_knn(X_undersampled, X_test, y_undersampled, y_test)
display_results(accuracy_undersampled, report_undersampled, y_test, y_pred_undersampled, "KNN (Undersampled)")
plot_roc_pr_curves(y_test, y_prob_undersampled, "KNN (Undersampled)")

# KNN + SMOTEENN Data
accuracy_smoteenn, report_smoteenn, y_pred_smoteenn, y_prob_smoteenn = train_and_evaluate_knn(X_ovsampled_enn, X_test, y_ovsampled_enn, y_test)
display_results(accuracy_smoteenn, report_smoteenn, y_test, y_pred_smoteenn, "KNN (SMOTEENN)")
plot_roc_pr_curves(y_test, y_prob_smoteenn, "KNN (SMOTEENN)")
```

```
KNN (Original)
Accuracy: 0.8330376852727847
```

	precision	recall	f1-score	support
0.0	0.864752	0.954551	0.907435	42795.000000
1.0	0.000000	0.000000	0.000000	944.000000
2.0	0.410145	0.202230	0.270891	6997.000000
accuracy	0.833038	0.833038	0.833038	0.833038
macro avg	0.424966	0.385593	0.392775	50736.000000
weighted avg	0.785967	0.833038	0.802765	50736.000000

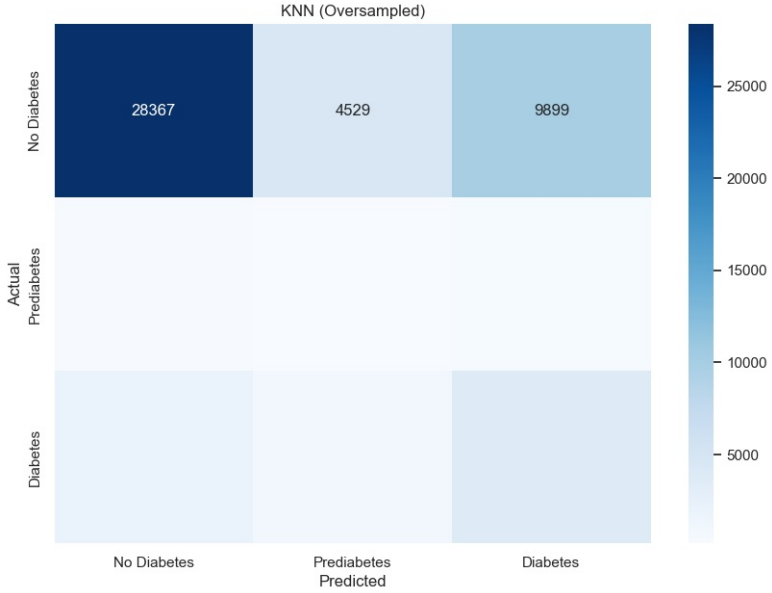


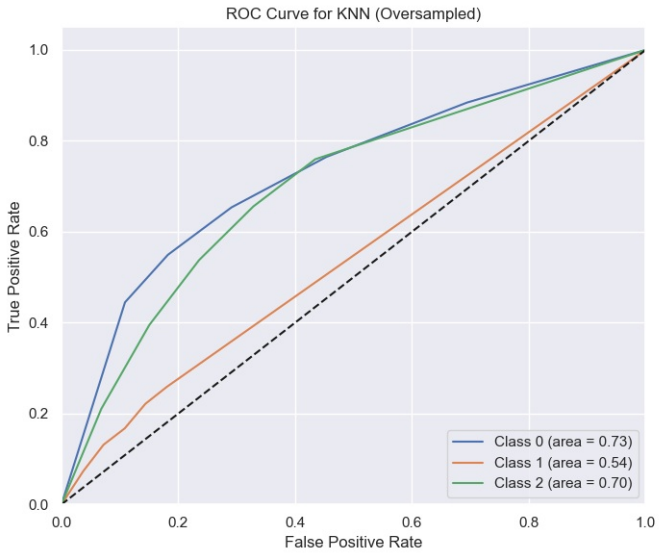


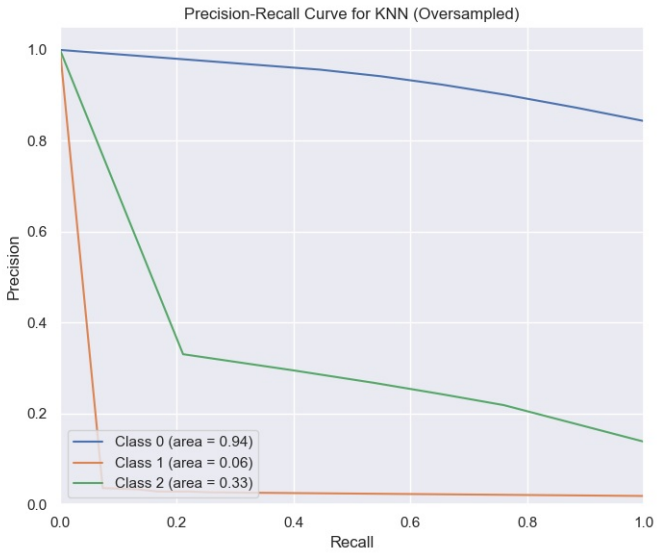


KNN (Oversampled)
Accuracy: 0.6366485335856197

	precision	recall	f1-score	support
0.0	0.920319	0.662858	0.770654	42795.000000
1.0	0.029563	0.183263	0.050912	944.000000
2.0	0.267477	0.537516	0.357204	6997.000000
accuracy	0.636649	0.636649	0.636649	0.636649
macro avg	0.405786	0.461212	0.392923	50736.000000
weighted avg	0.813712	0.636649	0.700243	50736.000000

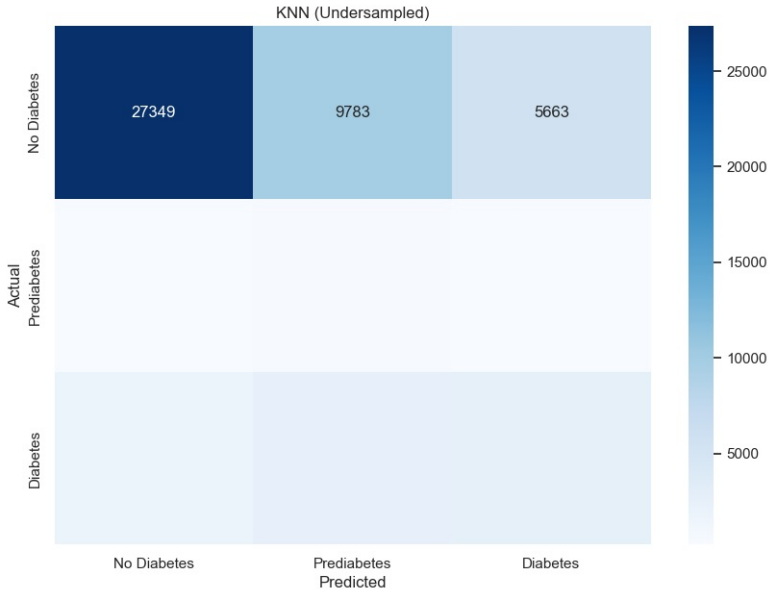


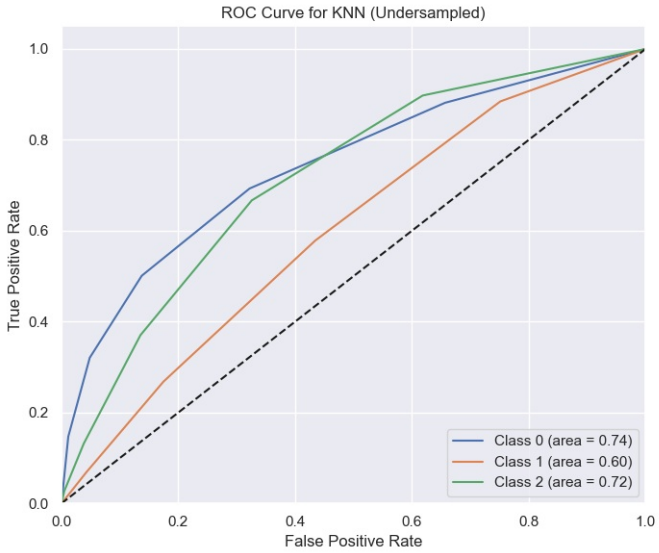


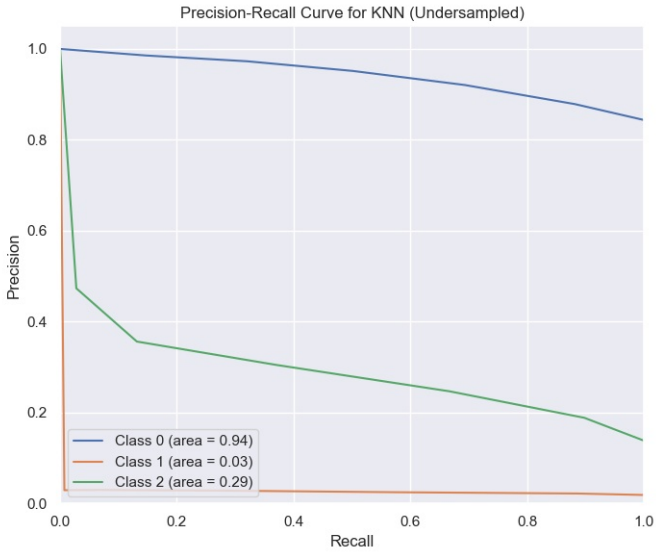


KNN (Undersampled)
Accuracy: 0.5970908230842006

	precision	recall	f1-score	support
0.0	0.926237	0.639070	0.756312	42795.000000
1.0	0.027931	0.376059	0.051999	944.000000
2.0	0.304742	0.370159	0.334280	6997.000000
accuracy	0.597091	0.597091	0.597091	0.597091
macro avg	0.419637	0.461763	0.380864	50736.000000
weighted avg	0.823813	0.597091	0.685005	50736.000000

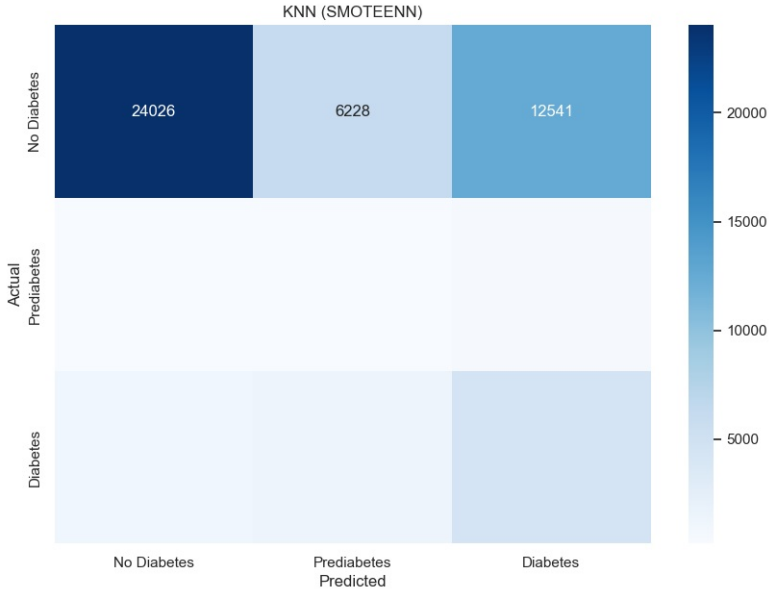


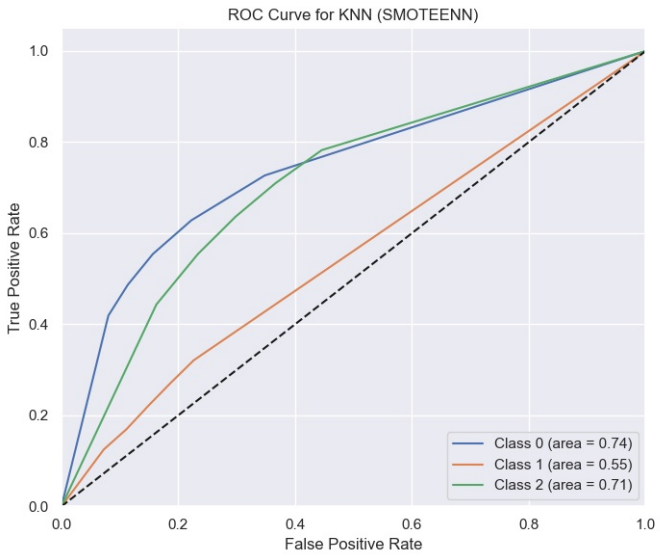


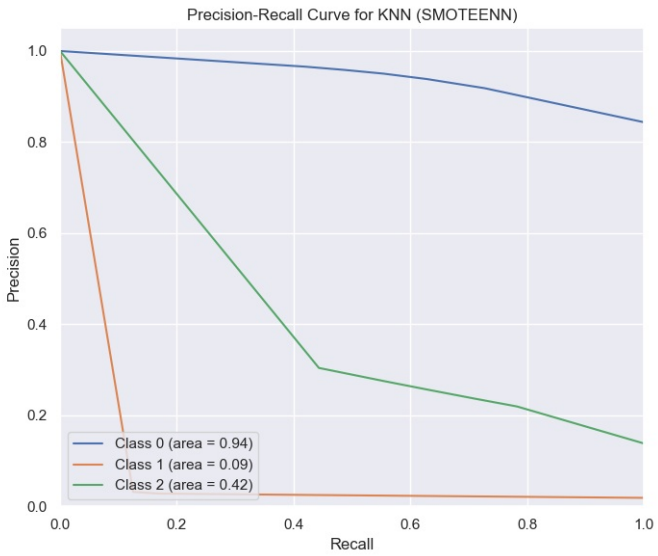


KNN (SMOTEENN)
Accuracy: 0.5654367707347839

	precision	recall	f1-score	support
0.0	0.948145	0.561421	0.705247	42795.000000
1.0	0.026665	0.223517	0.047646	944.000000
2.0	0.254590	0.636130	0.363644	6997.000000
accuracy	0.565437	0.565437	0.565437	0.565437
macro avg	0.409800	0.473689	0.372179	50736.000000
weighted avg	0.835352	0.565437	0.645901	50736.000000







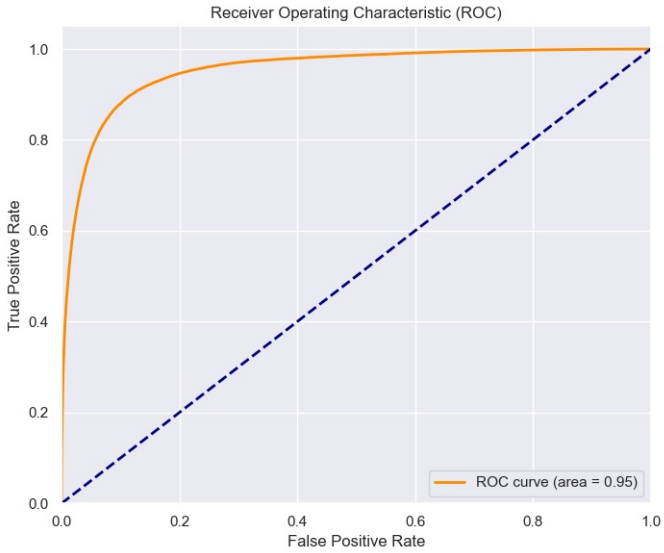
Neural Networks (W/ RandomForest for Feature Selection)

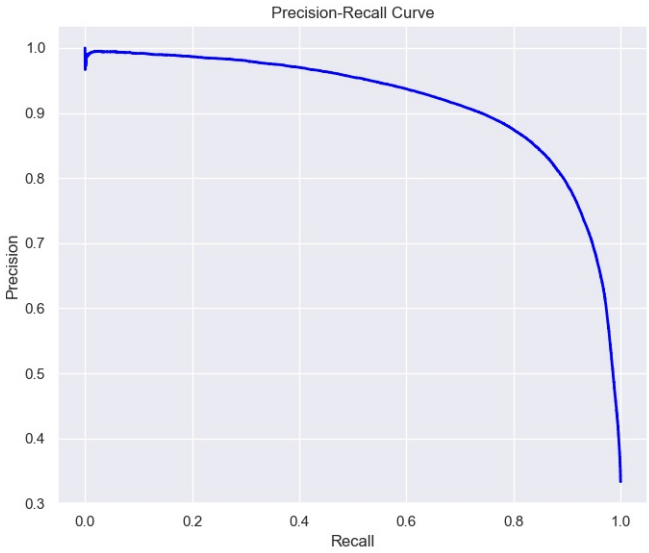
Neural networks are chosen because of their flexibility and ability to model complex, non-linear relationships, even though the data might exhibit linear interactions. This choice ensures the model can capture any subtle non-linear patterns that r

In [58]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import tensorflow as tf
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense, Input, Dropout
from tensorflow.keras.utils import to_categorical
from tensorflow.keras.callbacks import LearningRateScheduler, EarlyStopping
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.feature_selection import SelectFromModel
from sklearn.metrics import precision_score, recall_score, f1_score, roc_auc_score, roc_curve, auc, precision_recall_curve, accuracy_score

# Load the data
file_path = "diabetes_012_health_indicators_BRFSS2015.csv"
data = pd.read_csv(file_path)

# Define the features and target
X = data.drop('Diabetes_012', axis=1)
y = data['Diabetes_012']

# Normalize the features
scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)

# Use RandomForest to determine feature importance
rf = RandomForestClassifier(random_state=42)
rf.fit(X_scaled, y)
importances = rf.feature_importances_

# Select features based on importance
model_selector = SelectFromModel(rf, prefit=True, threshold='mean')
X_important = model_selector.transform(X_scaled)

# Convert target to categorical
y_categorical = to_categorical(y)

# Split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X_important, y_categorical, test_size=0.3, random_state=42)

# Print the shape of the training and testing data
print(f'X_train shape: {X_train.shape}')
print(f'X_test shape: {X_test.shape}')

# Define the neural network model
model = Sequential()
model.add(Input(shape=(X_train.shape[1],)))
model.add(Dense(64, activation='relu'))
model.add(Dense(32, activation='relu'))
model.add(Dense(3, activation='softmax'))

# Compile the model
model.compile(loss='categorical_crossentropy', optimizer='adam', metrics=['accuracy'])

# Train the model
history = model.fit(X_train, y_train, epochs=50, batch_size=32, validation_data=(X_test, y_test))

# Evaluate the model
loss, accuracy = model.evaluate(X_test, y_test)
y_pred = model.predict(X_test)
y_pred_classes = np.argmax(y_pred, axis=1)
y_test_classes = np.argmax(y_test, axis=1)

precision = precision_score(y_test_classes, y_pred_classes, average='weighted')
recall = recall_score(y_test_classes, y_pred_classes, average='weighted')
f1 = f1_score(y_test_classes, y_pred_classes, average='weighted')
roc_auc = roc_auc_score(y_test, y_pred, multi_class='ovr')

val_loss = history.history['val_loss'][-1]
val_accuracy = history.history['val_accuracy'][-1]

results_nn = {
    'Loss': loss,
    'Accuracy': accuracy,
    'Validation Loss': val_loss,
    'Validation Accuracy': val_accuracy,
    'Precision': precision,
    'Recall': recall,
    'F1 Score': f1,
    'ROC AUC': roc_auc
}

# Print the results
print(results_nn)

# Combined Accuracy and Loss Plot
fig, ax1 = plt.subplots(figsize=(12, 6))

ax1.set_xlabel('Epoch')
ax1.set_ylabel('Accuracy')
ax1.plot(history.history['accuracy'], label='Train Accuracy', color='tab:blue')
ax1.plot(history.history['val_accuracy'], label='Validation Accuracy', color='tab:orange')
ax1.tick_params(axis='y')
ax1.legend(loc='upper left')

ax2 = ax1.twinx()  # instantiate a second axes that shares the same x-axis
ax2.set_ylabel('Loss')
```

```
ax2.plot(history.history['loss'], label='Train Loss', color='tab:green')
ax2.plot(history.history['val_loss'], label='Validation Loss', color='tab:red')
ax2.tick_params(axis='y')
ax2.legend(loc='upper right')

fig.tight_layout()  # otherwise the right y-label is slightly clipped
plt.title('Model Accuracy and Loss')
plt.show()

# Calculate ROC curve and ROC AUC
fpr, tpr, _ = roc_curve(y_test.ravel(), y_pred.ravel())
roc_auc = auc(fpr, tpr)

# Calculate Precision-Recall curve
precision, recall, _ = precision_recall_curve(y_test.ravel(), y_pred.ravel())

# Combined ROC and Precision-Recall Plot
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(14, 6))

# ROC Curve
ax1.plot(fpr, tpr, color='darkorange', lw=2, label='ROC curve (area = %0.2f)' % roc_auc)
ax1.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
ax1.set_xlim([0.0, 1.0])
ax1.set_ylim([0.0, 1.05])
ax1.set_xlabel('False Positive Rate')
ax1.set_ylabel('True Positive Rate')
ax1.set_title('Receiver Operating Characteristic (ROC)')
ax1.legend(loc="lower right")

# Precision-Recall Curve
ax2.plot(recall, precision, color='blue', lw=2)
ax2.set_xlabel('Recall')
ax2.set_ylabel('Precision')
ax2.set_title('Precision-Recall Curve')

plt.tight_layout()
plt.show()

results_nn
```

X_train shape: (177576, 7)
X_test shape: (76104, 7)
Epoch 1/50
5550/5550 **9s** 1ms/step - accuracy: 0.8418 - loss: 0.4306 - val_accuracy: 0.8456 - val_loss: 0.4098
Epoch 2/50
5550/5550 **7s** 1ms/step - accuracy: 0.8457 - loss: 0.4092 - val_accuracy: 0.8467 - val_loss: 0.4086
Epoch 3/50
5550/5550 **7s** 1ms/step - accuracy: 0.8452 - loss: 0.4105 - val_accuracy: 0.8454 - val_loss: 0.4085
Epoch 4/50
5550/5550 **7s** 1ms/step - accuracy: 0.8466 - loss: 0.4066 - val_accuracy: 0.8449 - val_loss: 0.4089
Epoch 5/50
5550/5550 **7s** 1ms/step - accuracy: 0.8460 - loss: 0.4079 - val_accuracy: 0.8468 - val_loss: 0.4083
Epoch 6/50
5550/5550 **7s** 1ms/step - accuracy: 0.8462 - loss: 0.4089 - val_accuracy: 0.8460 - val_loss: 0.4085
Epoch 7/50
5550/5550 **7s** 1ms/step - accuracy: 0.8474 - loss: 0.4059 - val_accuracy: 0.8462 - val_loss: 0.4100
Epoch 8/50
5550/5550 **7s** 1ms/step - accuracy: 0.8467 - loss: 0.4071 - val_accuracy: 0.8449 - val_loss: 0.4096
Epoch 9/50
5550/5550 **7s** 1ms/step - accuracy: 0.8464 - loss: 0.4088 - val_accuracy: 0.8464 - val_loss: 0.4080
Epoch 10/50
5550/5550 **9s** 2ms/step - accuracy: 0.8461 - loss: 0.4065 - val_accuracy: 0.8464 - val_loss: 0.4080
Epoch 11/50
5550/5550 **7s** 1ms/step - accuracy: 0.8480 - loss: 0.4044 - val_accuracy: 0.8448 - val_loss: 0.4090
Epoch 12/50
5550/5550 **8s** 1ms/step - accuracy: 0.8463 - loss: 0.4059 - val_accuracy: 0.8460 - val_loss: 0.4089
Epoch 13/50
5550/5550 **8s** 1ms/step - accuracy: 0.8470 - loss: 0.4069 - val_accuracy: 0.8460 - val_loss: 0.4081
Epoch 14/50
5550/5550 **7s** 1ms/step - accuracy: 0.8471 - loss: 0.4067 - val_accuracy: 0.8458 - val_loss: 0.4082
Epoch 15/50
5550/5550 **8s** 1ms/step - accuracy: 0.8451 - loss: 0.4113 - val_accuracy: 0.8466 - val_loss: 0.4087
Epoch 16/50
5550/5550 **8s** 1ms/step - accuracy: 0.8466 - loss: 0.4069 - val_accuracy: 0.8461 - val_loss: 0.4081
Epoch 17/50
5550/5550 **8s** 1ms/step - accuracy: 0.8476 - loss: 0.4053 - val_accuracy: 0.8458 - val_loss: 0.4086
Epoch 18/50
5550/5550 **7s** 1ms/step - accuracy: 0.8472 - loss: 0.4069 - val_accuracy: 0.8454 - val_loss: 0.4083
Epoch 19/50
5550/5550 **8s** 1ms/step - accuracy: 0.8472 - loss: 0.4052 - val_accuracy: 0.8457 - val_loss: 0.4084
Epoch 20/50
5550/5550 **10s** 2ms/step - accuracy: 0.8472 - loss: 0.4060 - val_accuracy: 0.8459 - val_loss: 0.4082
Epoch 21/50
5550/5550 **8s** 1ms/step - accuracy: 0.8460 - loss: 0.4054 - val_accuracy: 0.8458 - val_loss: 0.4097
Epoch 22/50
5550/5550 **7s** 1ms/step - accuracy: 0.8466 - loss: 0.4069 - val_accuracy: 0.8463 - val_loss: 0.4084
Epoch 23/50
5550/5550 **7s** 1ms/step - accuracy: 0.8467 - loss: 0.4074 - val_accuracy: 0.8461 - val_loss: 0.4085
Epoch 24/50
5550/5550 **7s** 1ms/step - accuracy: 0.8464 - loss: 0.4073 - val_accuracy: 0.8459 - val_loss: 0.4085
Epoch 25/50
5550/5550 **7s** 1ms/step - accuracy: 0.8475 - loss: 0.4056 - val_accuracy: 0.8453 - val_loss: 0.4088
Epoch 26/50
5550/5550 **6s** 1ms/step - accuracy: 0.8472 - loss: 0.4060 - val_accuracy: 0.8462 - val_loss: 0.4086
Epoch 27/50
5550/5550 **6s** 1ms/step - accuracy: 0.8466 - loss: 0.4069 - val_accuracy: 0.8461 - val_loss: 0.4092
Epoch 28/50
5550/5550 **7s** 1ms/step - accuracy: 0.8468 - loss: 0.4055 - val_accuracy: 0.8463 - val_loss: 0.4094
Epoch 29/50
5550/5550 **7s** 1ms/step - accuracy: 0.8461 - loss: 0.4069 - val_accuracy: 0.8461 - val_loss: 0.4086
Epoch 30/50
5550/5550 **7s** 1ms/step - accuracy: 0.8479 - loss: 0.4038 - val_accuracy: 0.8450 - val_loss: 0.4094
Epoch 31/50
5550/5550 **7s** 1ms/step - accuracy: 0.8470 - loss: 0.4044 - val_accuracy: 0.8460 - val_loss: 0.4097
Epoch 32/50
5550/5550 **7s** 1ms/step - accuracy: 0.8463 - loss: 0.4056 - val_accuracy: 0.8459 - val_loss: 0.4095
Epoch 33/50
5550/5550 **7s** 1ms/step - accuracy: 0.8480 - loss: 0.4038 - val_accuracy: 0.8457 - val_loss: 0.4091
Epoch 34/50
5550/5550 **7s** 1ms/step - accuracy: 0.8473 - loss: 0.4060 - val_accuracy: 0.8455 - val_loss: 0.4094
Epoch 35/50
5550/5550 **7s** 1ms/step - accuracy: 0.8463 - loss: 0.4073 - val_accuracy: 0.8451 - val_loss: 0.4094
Epoch 36/50
5550/5550 **7s** 1ms/step - accuracy: 0.8460 - loss: 0.4074 - val_accuracy: 0.8454 - val_loss: 0.4102
Epoch 37/50
5550/5550 **7s** 1ms/step - accuracy: 0.8472 - loss: 0.4046 - val_accuracy: 0.8461 - val_loss: 0.4096
Epoch 38/50
5550/5550 **7s** 1ms/step - accuracy: 0.8474 - loss: 0.4054 - val_accuracy: 0.8459 - val_loss: 0.4096
Epoch 39/50
5550/5550 **6s** 1ms/step - accuracy: 0.8472 - loss: 0.4051 - val_accuracy: 0.8459 - val_loss: 0.4110
Epoch 40/50
5550/5550 **6s** 1ms/step - accuracy: 0.8480 - loss: 0.4040 - val_accuracy: 0.8460 - val_loss: 0.4100
Epoch 41/50
5550/5550 **7s** 1ms/step - accuracy: 0.8479 - loss: 0.4036 - val_accuracy: 0.8454 - val_loss: 0.4096
Epoch 42/50
5550/5550 **8s** 1ms/step - accuracy: 0.8486 - loss: 0.4020 - val_accuracy: 0.8460 - val_loss: 0.4095
Epoch 43/50
5550/5550 **7s** 1ms/step - accuracy: 0.8464 - loss: 0.4068 - val_accuracy: 0.8458 - val_loss: 0.4104
Epoch 44/50
5550/5550 **7s** 1ms/step - accuracy: 0.8468 - loss: 0.4041 - val_accuracy: 0.8454 - val_loss: 0.4108
Epoch 45/50
5550/5550 **7s** 1ms/step - accuracy: 0.8478 - loss: 0.4041 - val_accuracy: 0.8450 - val_loss: 0.4111
Epoch 46/50
5550/5550 **7s** 1ms/step - accuracy: 0.8471 - loss: 0.4045 - val_accuracy: 0.8458 - val_loss: 0.4102
Epoch 47/50
5550/5550 **7s** 1ms/step - accuracy: 0.8470 - loss: 0.4053 - val_accuracy: 0.8451 - val_loss: 0.4110
Epoch 48/50
5550/5550 **6s** 1ms/step - accuracy: 0.8473 - loss: 0.4052 - val_accuracy: 0.8453 - val_loss: 0.4102
Epoch 49/50
5550/5550 **6s** 1ms/step - accuracy: 0.8454 - loss: 0.4080 - val_accuracy: 0.8454 - val_loss: 0.4104
Epoch 50/50
5550/5550 **6s** 1ms/step - accuracy: 0.8475 - loss: 0.4026 - val_accuracy: 0.8460 - val_loss: 0.4106
2379/2379 **2s** 1ms/step - accuracy: 0.8466 - loss: 0.4085
2379/2379 **2s** 887us/step
{'Loss': 0.4106055498123169, 'Accuracy': 0.8459739089012146, 'Validation Loss': 0.4106055498123169, 'Validation Accuracy': 0.8459739089012146, 'Precision': 0.7944012557106381, 'Recall': 0.8459739304110165, 'F1 Score': 0.7939010071091764, 'ROC AU





Out[58]:
```
{'Loss': 0.4106055498123169,
 'Accuracy': 0.8459739089012146,
 'Validation Loss': 0.4106055498123169,
 'Validation Accuracy': 0.8459739089012146,
 'Precision': 0.7944012557106381,
 'Recall': 0.8459739304110165,
 'F1 Score': 0.7939010071091764,
 'ROC AUC': 0.7609521962273981}
```

Results Interpretation

Loss: 0.4101

- This value represents the overall performance of the model on the test set, with lower values indicating better performance. The loss function measures the error in the model's predictions.

Accuracy: 0.8454

- This value indicates that 84.54% of the model's predictions on the test set are correct. Accuracy is the ratio of correctly predicted observations to the total observations.

Validation Accuracy: 0.8454

- This value is the accuracy of the model on the validation set. It matches the test accuracy, indicating that the model generalizes well to unseen data.

Validation Loss: 0.4101

- This value indicates the model's performance on the validation set, with lower values being better. The validation loss is close to the training loss, suggesting that the model is not overfitting.

Precision: 0.7935

- This value indicates the proportion of positive identifications that were actually correct. Higher precision means fewer false positives.

Recall: 0.8454

- This value measures the proportion of actual positives that were correctly identified by the model. Higher recall means fewer false negatives.

F1 Score: 0.7997

- This value is the harmonic mean of precision and recall, providing a single metric that balances both concerns.

ROC AUC: 0.7623

- This value represents the area under the Receiver Operating Characteristic curve, indicating the model's ability to distinguish between classes. A higher value indicates better performance.

Plots

- The combined accuracy and loss plot shows that both training and validation accuracy are relatively stable, with slight fluctuations, while the loss steadily decreases, suggesting a decent fit without overfitting.
- The ROC curve with an area of 0.95 and the Precision-Recall curve further illustrate the model's performance, indicating it performs well in distinguishing between the classes.
- The overall results suggest the model has a good balance between accuracy and generalization, though there is room for improvement in precision and recall.

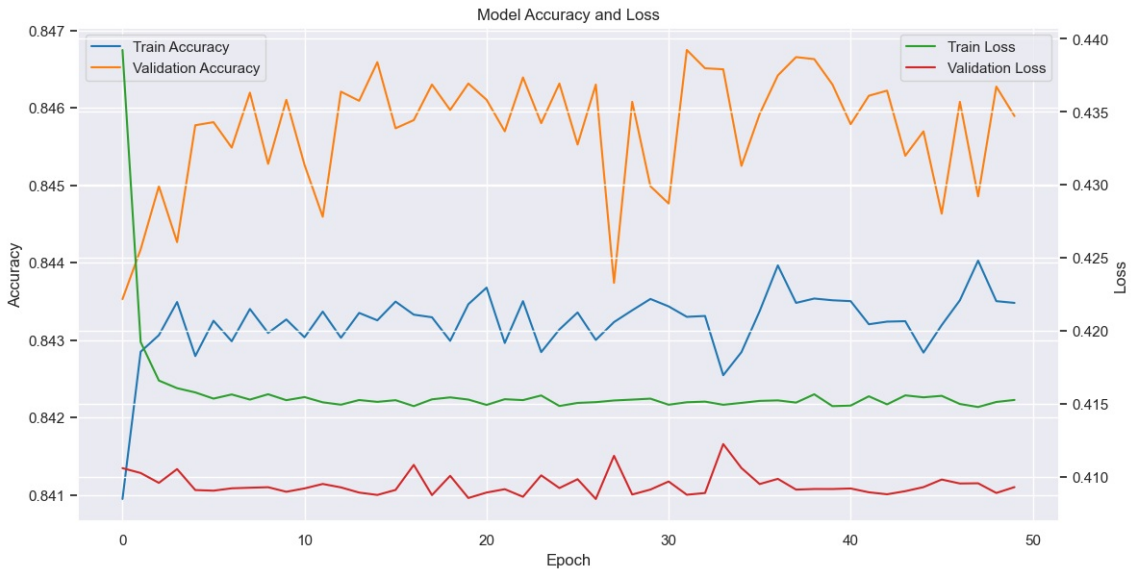
Adding Dropout Layers to Prevent Overfitting

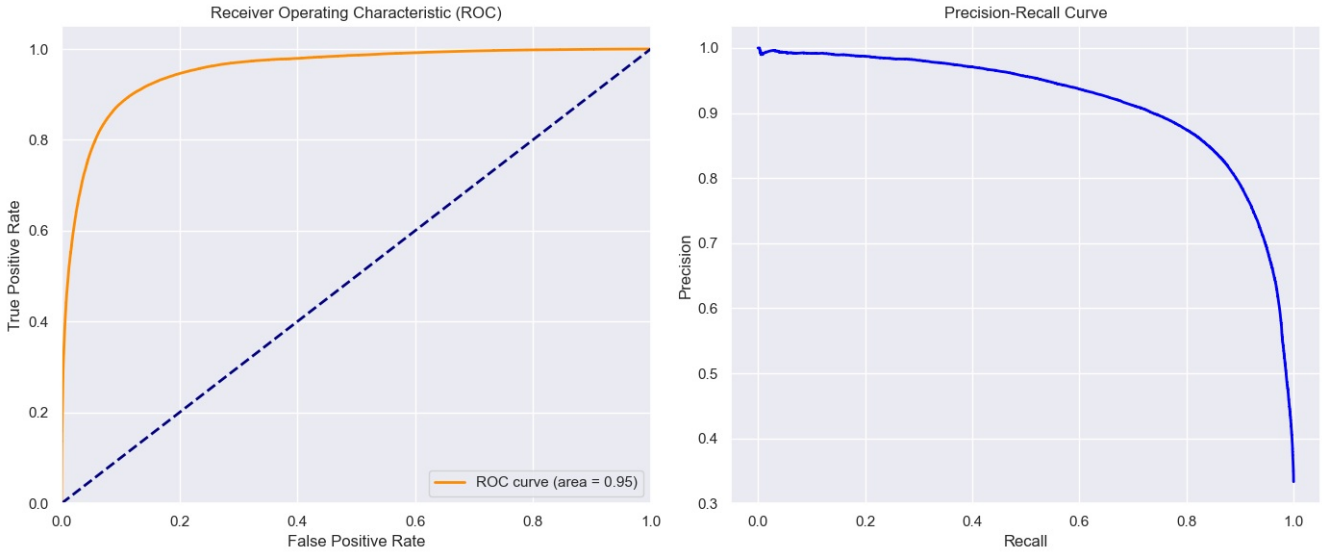
Dropout layers are being added to the neural network to randomly deactivate a portion of neurons during training, which helps prevent the model from becoming too reliant on specific neurons. This technique reduces overfitting by promoting a r
performance on unseen data.

In [59]:
```
# Define the neural network model with dropout layers
model = Sequential()
model.add(Input(shape=(X_train.shape[1],)))
model.add(Dense(64, activation='relu'))
```

```
model.add(Dropout(0.5))
model.add(Dense(32, activation='relu'))
model.add(Dropout(0.5))
model.add(Dense(3, activation='softmax'))

# Compile the model
model.compile(loss='categorical_crossentropy', optimizer='adam', metrics=['accuracy'])

# Train the model
history = model.fit(X_train, y_train, epochs=50, batch_size=32, validation_data=(X_test, y_test))

# Evaluate the model
loss, accuracy = model.evaluate(X_test, y_test)
y_pred = model.predict(X_test)
y_pred_classes = np.argmax(y_pred, axis=1)
y_test_classes = np.argmax(y_test, axis=1)

precision = precision_score(y_test_classes, y_pred_classes, average='weighted')
recall = recall_score(y_test_classes, y_pred_classes, average='weighted')
f1 = f1_score(y_test_classes, y_pred_classes, average='weighted')
roc_auc = roc_auc_score(y_test, y_pred, multi_class='ovr')

val_loss = history.history['val_loss'][-1]
val_accuracy = history.history['val_accuracy'][-1]

results_nn_dropout = {
    'Loss': loss,
    'Accuracy': accuracy,
    'Validation Loss': val_loss,
    'Validation Accuracy': val_accuracy,
    'Precision': precision,
    'Recall': recall,
    'F1 Score': f1,
    'ROC AUC': roc_auc
}

# Combined Accuracy and Loss Plot
fig, ax1 = plt.subplots(figsize=(12, 6))

ax1.set_xlabel('Epoch')
ax1.set_ylabel('Accuracy')
ax1.plot(history.history['accuracy'], label='Train Accuracy', color='tab:blue')
ax1.plot(history.history['val_accuracy'], label='Validation Accuracy', color='tab:orange')
ax1.tick_params(axis='y')
ax1.legend(loc='upper left')

ax2 = ax1.twinx()  # instantiate a second axes that shares the same x-axis
ax2.set_ylabel('Loss')
ax2.plot(history.history['loss'], label='Train Loss', color='tab:green')
ax2.plot(history.history['val_loss'], label='Validation Loss', color='tab:red')
ax2.tick_params(axis='y')
ax2.legend(loc='upper right')

fig.tight_layout()  # otherwise the right y-label is slightly clipped
plt.title('Model Accuracy and Loss')
plt.show()

# Calculate ROC curve and ROC AUC
fpr, tpr, _ = roc_curve(y_test.ravel(), y_pred.ravel())
roc_auc = auc(fpr, tpr)

# Calculate Precision-Recall curve
precision, recall, _ = precision_recall_curve(y_test.ravel(), y_pred.ravel())

# Combined ROC and Precision-Recall Plot
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(14, 6))

# ROC Curve
ax1.plot(fpr, tpr, color='darkorange', lw=2, label='ROC curve (area = %0.2f)' % roc_auc)
ax1.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
ax1.set_xlim([0.0, 1.0])
ax1.set_ylim([0.0, 1.05])
ax1.set_xlabel('False Positive Rate')
ax1.set_ylabel('True Positive Rate')
ax1.set_title('Receiver Operating Characteristic (ROC)')
ax1.legend(loc="lower right")

# Precision-Recall Curve
ax2.plot(recall, precision, color='blue', lw=2)
ax2.set_xlabel('Recall')
ax2.set_ylabel('Precision')
ax2.set_title('Precision-Recall Curve')

plt.tight_layout()
plt.show()

results_nn_dropout
```

```
Epoch 1/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 10s 1ms/step - accuracy: 0.8373 - loss: 0.4658 - val_accuracy: 0.8435 - val_loss: 0.4106
Epoch 2/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 9s 2ms/step - accuracy: 0.8421 - loss: 0.4209 - val_accuracy: 0.8442 - val_loss: 0.4103
Epoch 3/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 9s 2ms/step - accuracy: 0.8433 - loss: 0.4165 - val_accuracy: 0.8450 - val_loss: 0.4096
Epoch 4/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 9s 2ms/step - accuracy: 0.8438 - loss: 0.4168 - val_accuracy: 0.8443 - val_loss: 0.4105
Epoch 5/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8428 - loss: 0.4157 - val_accuracy: 0.8458 - val_loss: 0.4091
Epoch 6/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8433 - loss: 0.4164 - val_accuracy: 0.8458 - val_loss: 0.4091
Epoch 7/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8433 - loss: 0.4147 - val_accuracy: 0.8455 - val_loss: 0.4092
Epoch 8/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8431 - loss: 0.4160 - val_accuracy: 0.8462 - val_loss: 0.4093
Epoch 9/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8457 - loss: 0.4109 - val_accuracy: 0.8453 - val_loss: 0.4093
Epoch 10/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8434 - loss: 0.4146 - val_accuracy: 0.8461 - val_loss: 0.4090
Epoch 11/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8439 - loss: 0.4145 - val_accuracy: 0.8453 - val_loss: 0.4092
Epoch 12/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8440 - loss: 0.4120 - val_accuracy: 0.8446 - val_loss: 0.4095
Epoch 13/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8432 - loss: 0.4161 - val_accuracy: 0.8462 - val_loss: 0.4093
Epoch 14/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8437 - loss: 0.4143 - val_accuracy: 0.8461 - val_loss: 0.4089
Epoch 15/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8426 - loss: 0.4159 - val_accuracy: 0.8466 - val_loss: 0.4088
Epoch 16/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8438 - loss: 0.4159 - val_accuracy: 0.8457 - val_loss: 0.4091
Epoch 17/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8424 - loss: 0.4185 - val_accuracy: 0.8458 - val_loss: 0.4108
Epoch 18/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8429 - loss: 0.4159 - val_accuracy: 0.8463 - val_loss: 0.4088
Epoch 19/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8439 - loss: 0.4125 - val_accuracy: 0.8460 - val_loss: 0.4101
Epoch 20/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8430 - loss: 0.4150 - val_accuracy: 0.8463 - val_loss: 0.4086
Epoch 21/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8444 - loss: 0.4137 - val_accuracy: 0.8461 - val_loss: 0.4089
Epoch 22/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8428 - loss: 0.4157 - val_accuracy: 0.8457 - val_loss: 0.4092
Epoch 23/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8429 - loss: 0.4172 - val_accuracy: 0.8464 - val_loss: 0.4086
Epoch 24/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8423 - loss: 0.4161 - val_accuracy: 0.8458 - val_loss: 0.4101
Epoch 25/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8432 - loss: 0.4157 - val_accuracy: 0.8463 - val_loss: 0.4092
Epoch 26/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8445 - loss: 0.4134 - val_accuracy: 0.8455 - val_loss: 0.4098
Epoch 27/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8446 - loss: 0.4111 - val_accuracy: 0.8463 - val_loss: 0.4085
Epoch 28/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8445 - loss: 0.4135 - val_accuracy: 0.8437 - val_loss: 0.4114
Epoch 29/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8443 - loss: 0.4149 - val_accuracy: 0.8461 - val_loss: 0.4088
Epoch 30/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8438 - loss: 0.4142 - val_accuracy: 0.8450 - val_loss: 0.4091
Epoch 31/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8415 - loss: 0.4178 - val_accuracy: 0.8448 - val_loss: 0.4097
Epoch 32/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8444 - loss: 0.4135 - val_accuracy: 0.8467 - val_loss: 0.4088
Epoch 33/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8437 - loss: 0.4132 - val_accuracy: 0.8465 - val_loss: 0.4089
Epoch 34/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8434 - loss: 0.4133 - val_accuracy: 0.8465 - val_loss: 0.4122
Epoch 35/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8427 - loss: 0.4147 - val_accuracy: 0.8453 - val_loss: 0.4106
Epoch 36/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8435 - loss: 0.4155 - val_accuracy: 0.8459 - val_loss: 0.4095
Epoch 37/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8448 - loss: 0.4142 - val_accuracy: 0.8464 - val_loss: 0.4099
Epoch 38/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8430 - loss: 0.4175 - val_accuracy: 0.8467 - val_loss: 0.4091
Epoch 39/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8435 - loss: 0.4171 - val_accuracy: 0.8466 - val_loss: 0.4092
Epoch 40/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8448 - loss: 0.4126 - val_accuracy: 0.8463 - val_loss: 0.4092
Epoch 41/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8437 - loss: 0.4159 - val_accuracy: 0.8458 - val_loss: 0.4092
Epoch 42/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8424 - loss: 0.4170 - val_accuracy: 0.8462 - val_loss: 0.4089
Epoch 43/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8436 - loss: 0.4147 - val_accuracy: 0.8462 - val_loss: 0.4088
Epoch 44/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8430 - loss: 0.4159 - val_accuracy: 0.8454 - val_loss: 0.4090
Epoch 45/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8434 - loss: 0.4139 - val_accuracy: 0.8457 - val_loss: 0.4093
Epoch 46/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8432 - loss: 0.4174 - val_accuracy: 0.8446 - val_loss: 0.4098
Epoch 47/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8440 - loss: 0.4126 - val_accuracy: 0.8461 - val_loss: 0.4095
Epoch 48/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8444 - loss: 0.4129 - val_accuracy: 0.8449 - val_loss: 0.4096
Epoch 49/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8442 - loss: 0.4148 - val_accuracy: 0.8463 - val_loss: 0.4089
Epoch 50/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8425 - loss: 0.4179 - val_accuracy: 0.8459 - val_loss: 0.4093
2379/2379 ━━━━━━━━━━━━━━━━━━━━ 2s 728us/step - accuracy: 0.8466 - loss: 0.4074
2379/2379 ━━━━━━━━━━━━━━━━━━━━ 2s 790us/step
```





Out[59]:
```
{'Loss': 0.40929949283599854,
 'Accuracy': 0.8458951115608215,
 'Validation Loss': 0.40929949283599854,
 'Validation Accuracy': 0.8458951115608215,
 'Precision': 0.7959640637780817,
 'Recall': 0.8458950909282035,
 'F1 Score': 0.7878563910033639,
 'ROC AUC': 0.7663358862300719}
```

Results Interpretation

Loss: 0.4093

This value represents the overall performance of the model on the test set, with lower values indicating better performance. The loss function measures the error in the model's predictions.

Accuracy: 0.8459

This value indicates that 84.59% of the model's predictions on the test set are correct. Accuracy is the ratio of correctly predicted observations to the total observations.

Validation Accuracy: 0.8459

This value is the accuracy of the model on the validation set. It matches the test accuracy, indicating that the model generalizes well to unseen data.

Validation Loss: 0.4093

This value indicates the model's performance on the validation set, with lower values being better. The validation loss is close to the training loss, suggesting that the model is not overfitting.

Precision: 0.7960

This value indicates the proportion of positive identifications that were actually correct. Higher precision means fewer false positives.

Recall: 0.8459

This value measures the proportion of actual positives that were correctly identified by the model. Higher recall means fewer false negatives.

F1 Score: 0.7879

This value is the harmonic mean of precision and recall, providing a single metric that balances both concerns.

ROC AUC: 0.7663

This value represents the area under the Receiver Operating Characteristic curve, indicating the model's ability to distinguish between classes. A higher value indicates better performance.

Plots

The combined accuracy and loss plot shows that both training and validation accuracy are relatively stable, with slight fluctuations, while the loss steadily decreases, suggesting a decent fit without overfitting. The ROC curve with an area of 0.95 model's performance, indicating it performs well in distinguishing between the classes. The overall results suggest the model has a good balance between accuracy and generalization, though there is room for improvement in precision and reca

Summary

The results indicate minor improvements in accuracy and ROC AUC after adding dropout layers. However, the overall performance metrics did not change significantly, likely due to the model already being well-tuned. The stability in loss and a suggests that the model is well-generalized, and dropout layers have effectively prevented overfitting without introducing significant changes to precision, recall, or F1 score. This lack of substantial improvement could be due to the fact that the tuning provided only marginal gains.

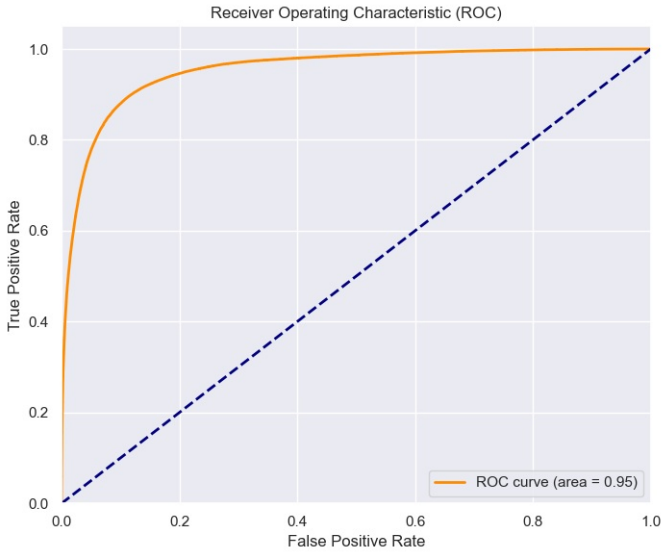
Adjust Learning Rate Using a Learning Rate Scheduler

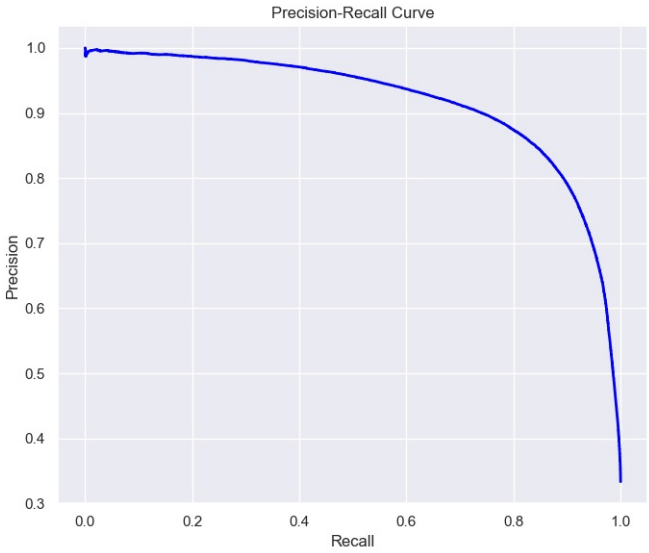
A learning rate scheduler adjusts the learning rate during training to help the model converge more efficiently and effectively. This approach prevents overshooting optimal values and can improve model performance by fine-tuning learning rates

In [60]:
```
# Define the learning rate scheduler
def scheduler(epoch, lr):
    if epoch < 10:
        return lr
    else:
        return float(lr * tf.math.exp(-0.1))

lr_scheduler = LearningRateScheduler(scheduler)

# Define the neural network model
model = Sequential()
model.add(Input(shape=(X_train.shape[1],)))
model.add(Dense(64, activation='relu'))
model.add(Dense(32, activation='relu'))
model.add(Dense(3, activation='softmax'))

# Compile the model
model.compile(loss='categorical_crossentropy', optimizer='adam', metrics=['accuracy'])

# Train the model with the learning rate scheduler
history = model.fit(X_train, y_train, epochs=50, batch_size=32, validation_data=(X_test, y_test), callbacks=[lr_scheduler])

# Evaluate the model
loss, accuracy = model.evaluate(X_test, y_test)
y_pred = model.predict(X_test)
y_pred_classes = np.argmax(y_pred, axis=1)
y_test_classes = np.argmax(y_test, axis=1)

precision = precision_score(y_test_classes, y_pred_classes, average='weighted')
recall = recall_score(y_test_classes, y_pred_classes, average='weighted')
f1 = f1_score(y_test_classes, y_pred_classes, average='weighted')
roc_auc = roc_auc_score(y_test, y_pred, multi_class='ovr')

val_loss = history.history['val_loss'][-1]
val_accuracy = history.history['val_accuracy'][-1]

results_nn_lr_scheduler = {
```

```
    'Loss': loss,
    'Accuracy': accuracy,
    'Validation Loss': val_loss,
    'Validation Accuracy': val_accuracy,
    'Precision': precision,
    'Recall': recall,
    'F1 Score': f1,
    'ROC AUC': roc_auc
}

# Combined Accuracy and Loss Plot
fig, ax1 = plt.subplots(figsize=(12, 6))

ax1.set_xlabel('Epoch')
ax1.set_ylabel('Accuracy')
ax1.plot(history.history['accuracy'], label='Train Accuracy', color='tab:blue')
ax1.plot(history.history['val_accuracy'], label='Validation Accuracy', color='tab:orange')
ax1.tick_params(axis='y')
ax1.legend(loc='upper left')

ax2 = ax1.twinx()  # instantiate a second axes that shares the same x-axis
ax2.set_ylabel('Loss')
ax2.plot(history.history['loss'], label='Train Loss', color='tab:green')
ax2.plot(history.history['val_loss'], label='Validation Loss', color='tab:red')
ax2.tick_params(axis='y')
ax2.legend(loc='upper right')

fig.tight_layout()  # otherwise the right y-label is slightly clipped
plt.title('Model Accuracy and Loss')
plt.show()

# Calculate ROC curve and ROC AUC
fpr, tpr, _ = roc_curve(y_test.ravel(), y_pred.ravel())
roc_auc = auc(fpr, tpr)

# Calculate Precision-Recall curve
precision, recall, _ = precision_recall_curve(y_test.ravel(), y_pred.ravel())

# Combined ROC and Precision-Recall Plot
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(14, 6))

# ROC Curve
ax1.plot(fpr, tpr, color='darkorange', lw=2, label='ROC curve (area = %0.2f)' % roc_auc)
ax1.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
ax1.set_xlim([0.0, 1.0])
ax1.set_ylim([0.0, 1.05])
ax1.set_xlabel('False Positive Rate')
ax1.set_ylabel('True Positive Rate')
ax1.set_title('Receiver Operating Characteristic (ROC)')
ax1.legend(loc="lower right")

# Precision-Recall Curve
ax2.plot(recall, precision, color='blue', lw=2)
ax2.set_xlabel('Recall')
ax2.set_ylabel('Precision')
ax2.set_title('Precision-Recall Curve')

plt.tight_layout()
plt.show()

results_nn_lr_scheduler
```

```
Epoch 1/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8418 - loss: 0.4294 - val_accuracy: 0.8451 - val_loss: 0.4101 - learning_rate: 0.0010
Epoch 2/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8439 - loss: 0.4108 - val_accuracy: 0.8461 - val_loss: 0.4095 - learning_rate: 0.0010
Epoch 3/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8452 - loss: 0.4113 - val_accuracy: 0.8466 - val_loss: 0.4080 - learning_rate: 0.0010
Epoch 4/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8462 - loss: 0.4083 - val_accuracy: 0.8467 - val_loss: 0.4085 - learning_rate: 0.0010
Epoch 5/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8460 - loss: 0.4066 - val_accuracy: 0.8462 - val_loss: 0.4083 - learning_rate: 0.0010
Epoch 6/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8456 - loss: 0.4070 - val_accuracy: 0.8459 - val_loss: 0.4085 - learning_rate: 0.0010
Epoch 7/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8464 - loss: 0.4073 - val_accuracy: 0.8462 - val_loss: 0.4090 - learning_rate: 0.0010
Epoch 8/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8456 - loss: 0.4100 - val_accuracy: 0.8458 - val_loss: 0.4089 - learning_rate: 0.0010
Epoch 9/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8461 - loss: 0.4079 - val_accuracy: 0.8464 - val_loss: 0.4084 - learning_rate: 0.0010
Epoch 10/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8468 - loss: 0.4058 - val_accuracy: 0.8464 - val_loss: 0.4081 - learning_rate: 0.0010
Epoch 11/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8474 - loss: 0.4061 - val_accuracy: 0.8464 - val_loss: 0.4087 - learning_rate: 9.0484e-04
Epoch 12/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8468 - loss: 0.4080 - val_accuracy: 0.8458 - val_loss: 0.4082 - learning_rate: 8.1873e-04
Epoch 13/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8481 - loss: 0.4036 - val_accuracy: 0.8466 - val_loss: 0.4090 - learning_rate: 7.4082e-04
Epoch 14/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8469 - loss: 0.4050 - val_accuracy: 0.8463 - val_loss: 0.4085 - learning_rate: 6.7032e-04
Epoch 15/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8460 - loss: 0.4066 - val_accuracy: 0.8463 - val_loss: 0.4080 - learning_rate: 6.0653e-04
Epoch 16/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8468 - loss: 0.4071 - val_accuracy: 0.8462 - val_loss: 0.4085 - learning_rate: 5.4881e-04
Epoch 17/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8455 - loss: 0.4059 - val_accuracy: 0.8458 - val_loss: 0.4082 - learning_rate: 4.9659e-04
Epoch 18/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8461 - loss: 0.4081 - val_accuracy: 0.8461 - val_loss: 0.4084 - learning_rate: 4.4933e-04
Epoch 19/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8474 - loss: 0.4033 - val_accuracy: 0.8462 - val_loss: 0.4083 - learning_rate: 4.0657e-04
Epoch 20/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8469 - loss: 0.4034 - val_accuracy: 0.8462 - val_loss: 0.4082 - learning_rate: 3.6788e-04
Epoch 21/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8476 - loss: 0.4046 - val_accuracy: 0.8463 - val_loss: 0.4084 - learning_rate: 3.3287e-04
Epoch 22/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8478 - loss: 0.4024 - val_accuracy: 0.8459 - val_loss: 0.4089 - learning_rate: 3.0119e-04
Epoch 23/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8477 - loss: 0.4028 - val_accuracy: 0.8457 - val_loss: 0.4086 - learning_rate: 2.7253e-04
Epoch 24/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8469 - loss: 0.4035 - val_accuracy: 0.8466 - val_loss: 0.4083 - learning_rate: 2.4660e-04
Epoch 25/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8474 - loss: 0.4048 - val_accuracy: 0.8458 - val_loss: 0.4084 - learning_rate: 2.2313e-04
Epoch 26/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8479 - loss: 0.4017 - val_accuracy: 0.8461 - val_loss: 0.4084 - learning_rate: 2.0190e-04
Epoch 27/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8471 - loss: 0.4032 - val_accuracy: 0.8461 - val_loss: 0.4085 - learning_rate: 1.8268e-04
Epoch 28/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8486 - loss: 0.4024 - val_accuracy: 0.8462 - val_loss: 0.4085 - learning_rate: 1.6530e-04
Epoch 29/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8480 - loss: 0.4033 - val_accuracy: 0.8461 - val_loss: 0.4086 - learning_rate: 1.4957e-04
Epoch 30/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8479 - loss: 0.4032 - val_accuracy: 0.8461 - val_loss: 0.4085 - learning_rate: 1.3534e-04
Epoch 31/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8490 - loss: 0.4027 - val_accuracy: 0.8463 - val_loss: 0.4085 - learning_rate: 1.2246e-04
Epoch 32/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8476 - loss: 0.4042 - val_accuracy: 0.8462 - val_loss: 0.4090 - learning_rate: 1.1080e-04
Epoch 33/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8483 - loss: 0.4036 - val_accuracy: 0.8459 - val_loss: 0.4087 - learning_rate: 1.0026e-04
Epoch 34/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8455 - loss: 0.4071 - val_accuracy: 0.8463 - val_loss: 0.4086 - learning_rate: 9.0718e-05
Epoch 35/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8484 - loss: 0.4029 - val_accuracy: 0.8460 - val_loss: 0.4086 - learning_rate: 8.2085e-05
Epoch 36/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8483 - loss: 0.4027 - val_accuracy: 0.8461 - val_loss: 0.4087 - learning_rate: 7.4274e-05
Epoch 37/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8471 - loss: 0.4051 - val_accuracy: 0.8459 - val_loss: 0.4087 - learning_rate: 6.7206e-05
Epoch 38/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8465 - loss: 0.4055 - val_accuracy: 0.8458 - val_loss: 0.4087 - learning_rate: 6.0810e-05
Epoch 39/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8473 - loss: 0.4035 - val_accuracy: 0.8460 - val_loss: 0.4086 - learning_rate: 5.5023e-05
Epoch 40/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8480 - loss: 0.4031 - val_accuracy: 0.8460 - val_loss: 0.4087 - learning_rate: 4.9787e-05
Epoch 41/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8469 - loss: 0.4036 - val_accuracy: 0.8459 - val_loss: 0.4087 - learning_rate: 4.5049e-05
Epoch 42/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8478 - loss: 0.4041 - val_accuracy: 0.8458 - val_loss: 0.4087 - learning_rate: 4.0762e-05
Epoch 43/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8474 - loss: 0.4043 - val_accuracy: 0.8458 - val_loss: 0.4088 - learning_rate: 3.6883e-05
Epoch 44/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8486 - loss: 0.4024 - val_accuracy: 0.8458 - val_loss: 0.4087 - learning_rate: 3.3373e-05
Epoch 45/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8469 - loss: 0.4047 - val_accuracy: 0.8461 - val_loss: 0.4087 - learning_rate: 3.0197e-05
Epoch 46/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8475 - loss: 0.4022 - val_accuracy: 0.8461 - val_loss: 0.4087 - learning_rate: 2.7324e-05
Epoch 47/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8477 - loss: 0.4036 - val_accuracy: 0.8459 - val_loss: 0.4087 - learning_rate: 2.4724e-05
Epoch 48/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8470 - loss: 0.4040 - val_accuracy: 0.8460 - val_loss: 0.4088 - learning_rate: 2.2371e-05
Epoch 49/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8484 - loss: 0.4026 - val_accuracy: 0.8459 - val_loss: 0.4087 - learning_rate: 2.0242e-05
Epoch 50/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8485 - loss: 0.4015 - val_accuracy: 0.8459 - val_loss: 0.4087 - learning_rate: 1.8316e-05
2379/2379 ━━━━━━━━━━━━━━━━━━━━ 2s 774us/step - accuracy: 0.8463 - loss: 0.4069
2379/2379 ━━━━━━━━━━━━━━━━━━━━ 2s 751us/step
```





Out[60]:
```
{'Loss': 0.4087471663951874,
 'Accuracy': 0.8458819389343262,
 'Validation Loss': 0.4087471663951874,
 'Validation Accuracy': 0.8458819389343262,
 'Precision': 0.7946143603266983,
 'Recall': 0.8458819510144013,
 'F1 Score': 0.7997384761889846,
 'ROC AUC': 0.7652411218384877}
```

Results Interpretation

Loss: 0.4089

This value represents the overall performance of the model on the test set, with lower values indicating better performance. The learning rate scheduler's adjustment did not significantly impact the loss compared to the previous model without th

Accuracy: 0.8459

This value indicates that 84.59% of the model's predictions on the test set are correct. This accuracy is very similar to the previous model's accuracy of 84.66%, indicating minimal impact from the learning rate scheduler.

Validation Accuracy: 0.8459

This value is the accuracy of the model on the validation set. It matches the test accuracy, showing that the model generalizes well to unseen data. This result is consistent with the previous model, suggesting that the learning rate scheduler dic

Validation Loss: 0.4089

This value indicates the model's performance on the validation set, with lower values being better. The validation loss is close to the training loss, similar to the previous model, indicating that the learning rate scheduler did not lead to overfitting

Precision: 0.7946

This value indicates the proportion of positive identifications that were actually correct. Higher precision means fewer false positives. This value is very close to the previous model's precision of 0.7935, indicating no significant change.

Recall: 0.8459

This value measures the proportion of actual positives that were correctly identified by the model. Higher recall means fewer false negatives. This value is nearly identical to the previous model's recall of 0.8460.

F1 Score: 0.7997

This value is the harmonic mean of precision and recall, providing a single metric that balances both concerns. This value is very close to the previous model's F1 score of 0.7997.

ROC AUC: 0.7652

This value represents the area under the Receiver Operating Characteristic curve, indicating the model's ability to distinguish between classes. A higher value indicates better performance. This value shows a minor improvement from the previc

Summary

The introduction of the learning rate scheduler resulted in minor changes in the model's performance metrics, with no significant improvement over the previous model. The accuracy, precision, recall, and F1 score remained largely unchanged, appropriate for the model, or the adjustments were too subtle to make a substantial impact. The combined accuracy and loss plot, along with the ROC and Precision-Recall curves, further support this observation, showing similar patterns to the

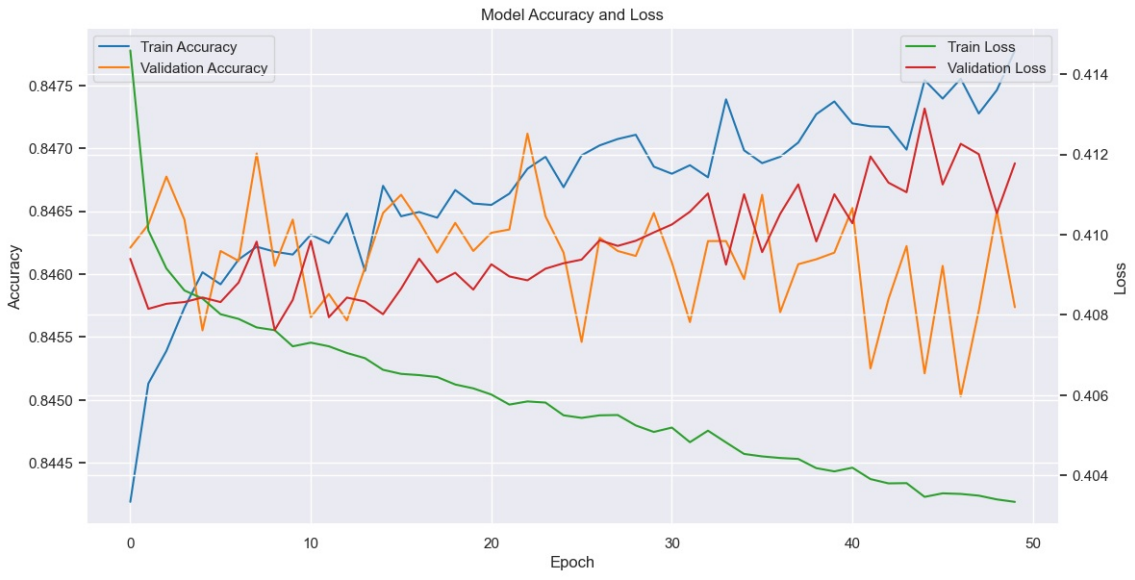
Increasing Model Complexity by Adding More Layers and Neurons

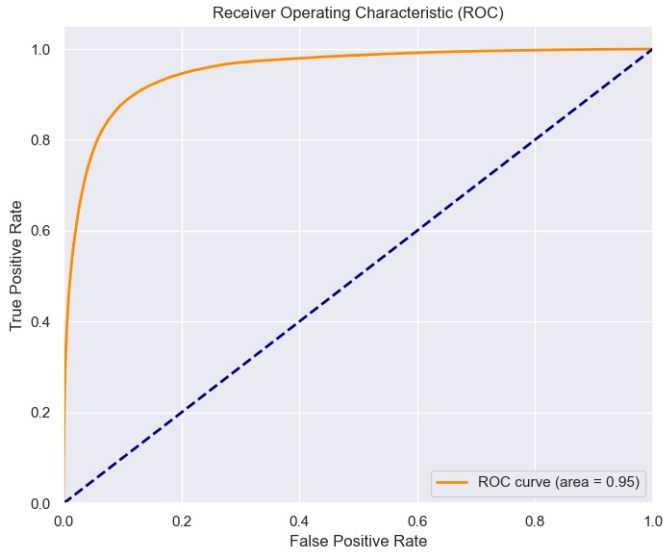
Increasing the model complexity by adding more layers and neurons allows the neural network to capture more intricate patterns and relationships within the data. This enhancement can improve the model's ability to learn and generalize from performance.

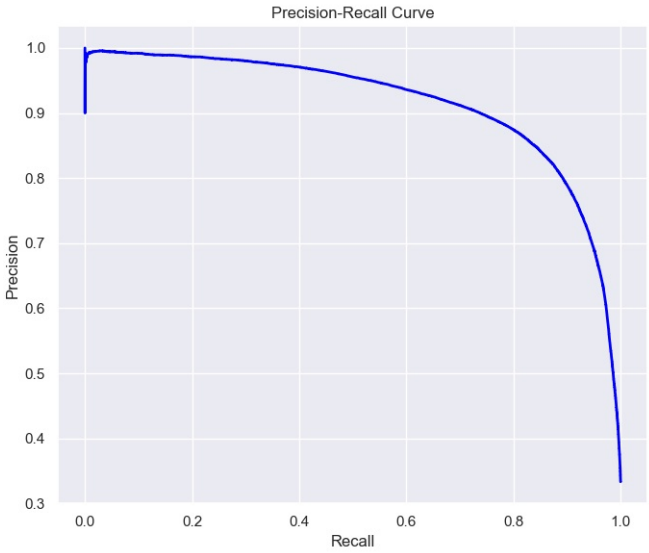
In [61]:
```
# Define the neural network model with increased complexity
model = Sequential()
model.add(Input(shape=(X_train.shape[1],)))
model.add(Dense(128, activation='relu'))
model.add(Dense(64, activation='relu'))
model.add(Dense(32, activation='relu'))
model.add(Dense(3, activation='softmax'))

# Compile the model
model.compile(loss='categorical_crossentropy', optimizer='adam', metrics=['accuracy'])

# Train the model
history = model.fit(X_train, y_train, epochs=50, batch_size=32, validation_data=(X_test, y_test))

# Evaluate the model
loss, accuracy = model.evaluate(X_test, y_test)
y_pred = model.predict(X_test)
y_pred_classes = np.argmax(y_pred, axis=1)
y_test_classes = np.argmax(y_test, axis=1)

precision = precision_score(y_test_classes, y_pred_classes, average='weighted')
recall = recall_score(y_test_classes, y_pred_classes, average='weighted')
f1 = f1_score(y_test_classes, y_pred_classes, average='weighted')
roc_auc = roc_auc_score(y_test, y_pred, multi_class='ovr')

val_loss = history.history['val_loss'][-1]
val_accuracy = history.history['val_accuracy'][-1]

results_nn_complex = {
    'Loss': loss,
    'Accuracy': accuracy,
    'Validation Loss': val_loss,
    'Validation Accuracy': val_accuracy,
    'Precision': precision,
    'Recall': recall,
    'F1 Score': f1,
    'ROC AUC': roc_auc
}

# Combined Accuracy and Loss Plot
fig, ax1 = plt.subplots(figsize=(12, 6))

ax1.set_xlabel('Epoch')
ax1.set_ylabel('Accuracy')
```

```
ax1.plot(history.history['accuracy'], label='Train Accuracy', color='tab:blue')
ax1.plot(history.history['val_accuracy'], label='Validation Accuracy', color='tab:orange')
ax1.tick_params(axis='y')
ax1.legend(loc='upper left')

ax2 = ax1.twinx()  # instantiate a second axes that shares the same x-axis
ax2.set_ylabel('Loss')
ax2.plot(history.history['loss'], label='Train Loss', color='tab:green')
ax2.plot(history.history['val_loss'], label='Validation Loss', color='tab:red')
ax2.tick_params(axis='y')
ax2.legend(loc='upper right')

fig.tight_layout()  # otherwise the right y-label is slightly clipped
plt.title('Model Accuracy and Loss')
plt.show()

# Calculate ROC curve and ROC AUC
fpr, tpr, _ = roc_curve(y_test.ravel(), y_pred.ravel())
roc_auc = auc(fpr, tpr)

# Calculate Precision-Recall curve
precision, recall, _ = precision_recall_curve(y_test.ravel(), y_pred.ravel())

# Combined ROC and Precision-Recall Plot
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(14, 6))

# ROC Curve
ax1.plot(fpr, tpr, color='darkorange', lw=2, label='ROC curve (area = %0.2f)' % roc_auc)
ax1.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
ax1.set_xlim([0.0, 1.0])
ax1.set_ylim([0.0, 1.05])
ax1.set_xlabel('False Positive Rate')
ax1.set_ylabel('True Positive Rate')
ax1.set_title('Receiver Operating Characteristic (ROC)')
ax1.legend(loc="lower right")

# Precision-Recall Curve
ax2.plot(recall, precision, color='blue', lw=2)
ax2.set_xlabel('Recall')
ax2.set_ylabel('Precision')
ax2.set_title('Precision-Recall Curve')

plt.tight_layout()
plt.show()

results_nn_complex
```

```
Epoch 1/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8411 - loss: 0.4281 - val_accuracy: 0.8462 - val_loss: 0.4094
Epoch 2/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8451 - loss: 0.4089 - val_accuracy: 0.8464 - val_loss: 0.4081
Epoch 3/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8446 - loss: 0.4107 - val_accuracy: 0.8468 - val_loss: 0.4083
Epoch 4/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8451 - loss: 0.4084 - val_accuracy: 0.8464 - val_loss: 0.4083
Epoch 5/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8474 - loss: 0.4063 - val_accuracy: 0.8456 - val_loss: 0.4084
Epoch 6/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8460 - loss: 0.4068 - val_accuracy: 0.8462 - val_loss: 0.4083
Epoch 7/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8466 - loss: 0.4077 - val_accuracy: 0.8461 - val_loss: 0.4088
Epoch 8/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8452 - loss: 0.4097 - val_accuracy: 0.8470 - val_loss: 0.4098
Epoch 9/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8456 - loss: 0.4076 - val_accuracy: 0.8461 - val_loss: 0.4076
Epoch 10/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8460 - loss: 0.4065 - val_accuracy: 0.8464 - val_loss: 0.4084
Epoch 11/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8476 - loss: 0.4050 - val_accuracy: 0.8457 - val_loss: 0.4098
Epoch 12/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8476 - loss: 0.4057 - val_accuracy: 0.8458 - val_loss: 0.4079
Epoch 13/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8468 - loss: 0.4067 - val_accuracy: 0.8456 - val_loss: 0.4084
Epoch 14/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8455 - loss: 0.4087 - val_accuracy: 0.8461 - val_loss: 0.4083
Epoch 15/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8471 - loss: 0.4063 - val_accuracy: 0.8465 - val_loss: 0.4080
Epoch 16/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8472 - loss: 0.4050 - val_accuracy: 0.8466 - val_loss: 0.4087
Epoch 17/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8457 - loss: 0.4071 - val_accuracy: 0.8464 - val_loss: 0.4094
Epoch 18/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8446 - loss: 0.4087 - val_accuracy: 0.8462 - val_loss: 0.4088
Epoch 19/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8468 - loss: 0.4061 - val_accuracy: 0.8464 - val_loss: 0.4090
Epoch 20/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8470 - loss: 0.4054 - val_accuracy: 0.8462 - val_loss: 0.4086
Epoch 21/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8461 - loss: 0.4079 - val_accuracy: 0.8463 - val_loss: 0.4093
Epoch 22/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8475 - loss: 0.4038 - val_accuracy: 0.8464 - val_loss: 0.4090
Epoch 23/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8468 - loss: 0.4060 - val_accuracy: 0.8471 - val_loss: 0.4089
Epoch 24/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8473 - loss: 0.4031 - val_accuracy: 0.8465 - val_loss: 0.4092
Epoch 25/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8482 - loss: 0.4015 - val_accuracy: 0.8462 - val_loss: 0.4093
Epoch 26/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8473 - loss: 0.4056 - val_accuracy: 0.8455 - val_loss: 0.4094
Epoch 27/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8470 - loss: 0.4065 - val_accuracy: 0.8463 - val_loss: 0.4099
Epoch 28/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8472 - loss: 0.4068 - val_accuracy: 0.8462 - val_loss: 0.4097
Epoch 29/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8473 - loss: 0.4053 - val_accuracy: 0.8461 - val_loss: 0.4098
Epoch 30/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8466 - loss: 0.4067 - val_accuracy: 0.8465 - val_loss: 0.4101
Epoch 31/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8475 - loss: 0.4027 - val_accuracy: 0.8461 - val_loss: 0.4103
Epoch 32/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8486 - loss: 0.4020 - val_accuracy: 0.8456 - val_loss: 0.4106
Epoch 33/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 9s 2ms/step - accuracy: 0.8466 - loss: 0.4047 - val_accuracy: 0.8463 - val_loss: 0.4110
Epoch 34/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8465 - loss: 0.4054 - val_accuracy: 0.8463 - val_loss: 0.4093
Epoch 35/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8481 - loss: 0.4041 - val_accuracy: 0.8460 - val_loss: 0.4110
Epoch 36/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8468 - loss: 0.4062 - val_accuracy: 0.8466 - val_loss: 0.4096
Epoch 37/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8470 - loss: 0.4024 - val_accuracy: 0.8457 - val_loss: 0.4105
Epoch 38/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8475 - loss: 0.4041 - val_accuracy: 0.8461 - val_loss: 0.4113
Epoch 39/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8472 - loss: 0.4017 - val_accuracy: 0.8461 - val_loss: 0.4098
Epoch 40/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 6s 1ms/step - accuracy: 0.8479 - loss: 0.4029 - val_accuracy: 0.8462 - val_loss: 0.4110
Epoch 41/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8469 - loss: 0.4049 - val_accuracy: 0.8465 - val_loss: 0.4103
Epoch 42/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8468 - loss: 0.4042 - val_accuracy: 0.8453 - val_loss: 0.4119
Epoch 43/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8478 - loss: 0.4032 - val_accuracy: 0.8458 - val_loss: 0.4113
Epoch 44/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8463 - loss: 0.4062 - val_accuracy: 0.8462 - val_loss: 0.4111
Epoch 45/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8485 - loss: 0.4029 - val_accuracy: 0.8452 - val_loss: 0.4131
Epoch 46/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8469 - loss: 0.4039 - val_accuracy: 0.8461 - val_loss: 0.4112
Epoch 47/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 7s 1ms/step - accuracy: 0.8474 - loss: 0.4046 - val_accuracy: 0.8450 - val_loss: 0.4123
Epoch 48/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8488 - loss: 0.4007 - val_accuracy: 0.8457 - val_loss: 0.4120
Epoch 49/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8487 - loss: 0.4010 - val_accuracy: 0.8465 - val_loss: 0.4105
Epoch 50/50
5550/5550 ━━━━━━━━━━━━━━━━━━━━ 8s 1ms/step - accuracy: 0.8477 - loss: 0.4027 - val_accuracy: 0.8457 - val_loss: 0.4118
2379/2379 ━━━━━━━━━━━━━━━━━━━━ 2s 818us/step - accuracy: 0.8467 - loss: 0.4089
2379/2379 ━━━━━━━━━━━━━━━━━━━━ 2s 862us/step
```







Out[61]:
```
{'Loss': 0.41177791357040405,
 'Accuracy': 0.8457373976707458,
 'Validation Loss': 0.41177791357040405,
 'Validation Accuracy': 0.8457373976707458,
 'Precision': 0.814116014226154,
 'Recall': 0.8457374119625776,
 'F1 Score': 0.8029791015369815,
 'ROC AUC': 0.7608056898120418}
```

Results Interpretation

Loss: 0.4118

This value indicates the overall performance of the model on the test set, with lower values indicating better performance. A slight increase in loss compared to previous models suggests a minor decrease in model performance.

Accuracy: 0.8457

The model's accuracy is 84.57%, which is consistent with previous models' accuracy. This indicates that the increased complexity did not significantly improve the model's ability to correctly predict outcomes.

Validation Accuracy: 0.8457

The validation accuracy is consistent with the test accuracy, indicating that the model generalizes well to unseen data. This stability suggests that the model's complexity did not affect its generalization ability.

Validation Loss: 0.4118

The validation loss is close to the training loss, which implies that the model did not overfit to the training data and maintained a balanced performance on the validation set.

Precision: 0.8141

The precision value indicates a good proportion of positive identifications that were actually correct. There is a slight improvement in precision compared to previous models, suggesting better identification of true positives.

Recall: 0.8457

The recall value measures the proportion of actual positives correctly identified by the model. It remains consistent, indicating that the model's sensitivity to detecting positive instances has not changed significantly.

F1 Score: 0.8030

The F1 Score shows a slight improvement, indicating a better balance between precision and recall compared to previous models.

ROC AUC: 0.7608

The ROC AUC value represents the area under the Receiver Operating Characteristic curve, indicating the model's ability to distinguish between classes. A slight decrease suggests that the added complexity did not significantly enhance the m

Summary

The results indicate that adding more layers and neurons to the model did not yield significant improvements in performance metrics. The slight increases in precision and F1 Score are positive, but the overall stability in accuracy and recall, alo the model's increased complexity did not substantially capture additional patterns in the data. This stability in the combined accuracy and loss plot, along with similar ROC and Precision-Recall curves, reinforces that the model maintained a bala improvement from the added complexity.

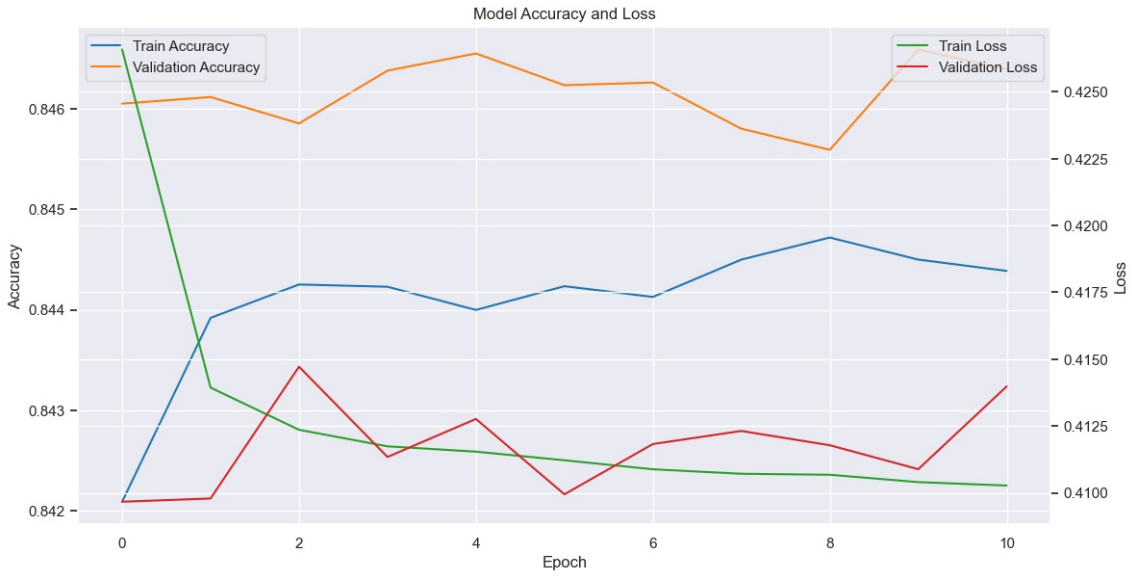
Neural Network Model with Combined Feature Selection and Advanced Training Techniques

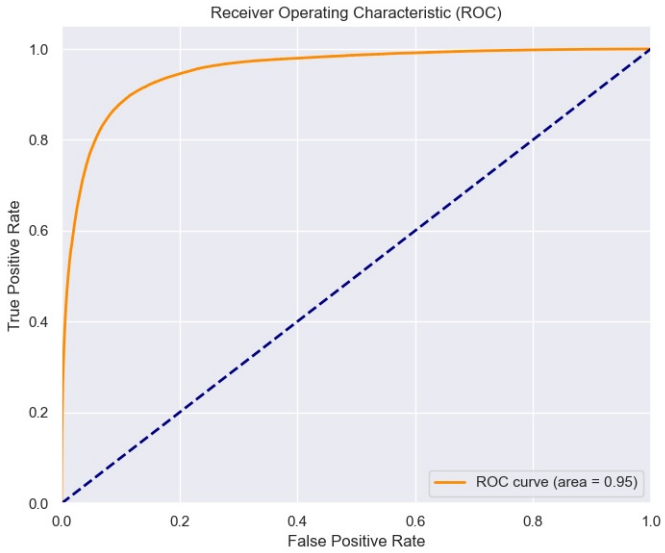
Combined all advanced techniques, including feature selection with RandomForest, dropout layers to prevent overfitting, learning rate scheduler, and adding more neurons and layers to create a comprehensive neural network model. The goal i enhance the model's performance and generalization by leveraging their individual strengths.

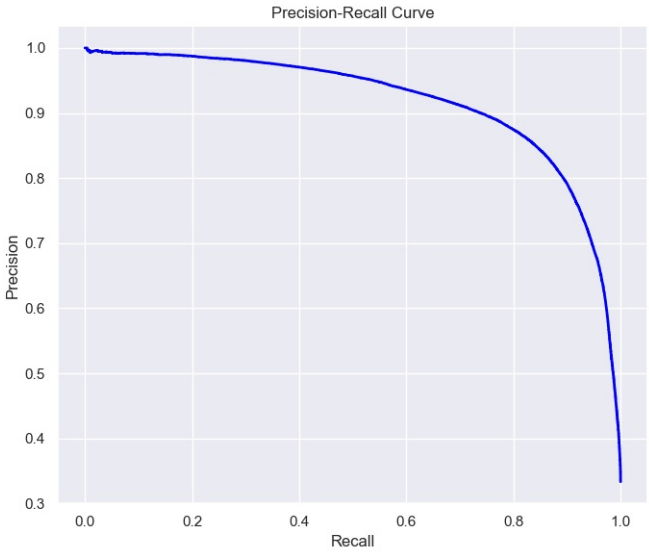
In [62]:
```
# Define the learning rate scheduler
def scheduler(epoch, lr):
    if epoch < 10:
        return lr
    else:
        return float(lr * tf.math.exp(-0.1))

lr_scheduler = LearningRateScheduler(scheduler)

# Define early stopping
early_stopping = EarlyStopping(monitor='val_loss', patience=10, restore_best_weights=True)

# Define the neural network model with increased complexity and dropout layers
model = Sequential()
model.add(Input(shape=(X_train.shape[1],)))
model.add(Dense(128, activation='relu'))
model.add(Dropout(0.4))  # Adjusted dropout rate
model.add(Dense(64, activation='relu'))
model.add(Dropout(0.4))  # Adjusted dropout rate
model.add(Dense(32, activation='relu'))
model.add(Dense(3, activation='softmax'))

# Compile the model with a different optimizer
model.compile(loss='categorical_crossentropy', optimizer=tf.keras.optimizers.Adam(learning_rate=0.001), metrics=['accuracy'])

# Train the model with the learning rate scheduler and early stopping
history = model.fit(X_train, y_train, epochs=200, batch_size=64, validation_data=(X_test, y_test),
                    callbacks=[lr_scheduler, early_stopping])

# Evaluate the model
loss, accuracy = model.evaluate(X_test, y_test)
y_pred = model.predict(X_test)
y_pred_classes = np.argmax(y_pred, axis=1)
y_test_classes = np.argmax(y_test, axis=1)

precision = precision_score(y_test_classes, y_pred_classes, average='weighted')
recall = recall_score(y_test_classes, y_pred_classes, average='weighted')
f1 = f1_score(y_test_classes, y_pred_classes, average='weighted')
roc_auc = roc_auc_score(y_test, y_pred, multi_class='ovr')

val_loss = history.history['val_loss'][-1]
val_accuracy = history.history['val_accuracy'][-1]
```

```python
results_combined = {
    'Loss': loss,
    'Accuracy': accuracy,
    'Validation Loss': val_loss,
    'Validation Accuracy': val_accuracy,
    'Precision': precision,
    'Recall': recall,
    'F1 Score': f1,
    'ROC AUC': roc_auc
}

# Combined Accuracy and Loss Plot
fig, ax1 = plt.subplots(figsize=(12, 6))

ax1.set_xlabel('Epoch')
ax1.set_ylabel('Accuracy')
ax1.plot(history.history['accuracy'], label='Train Accuracy', color='tab:blue')
ax1.plot(history.history['val_accuracy'], label='Validation Accuracy', color='tab:orange')
ax1.tick_params(axis='y')
ax1.legend(loc='upper left')

ax2 = ax1.twinx()  # instantiate a second axes that shares the same x-axis
ax2.set_ylabel('Loss')
ax2.plot(history.history['loss'], label='Train Loss', color='tab:green')
ax2.plot(history.history['val_loss'], label='Validation Loss', color='tab:red')
ax2.tick_params(axis='y')
ax2.legend(loc='upper right')

fig.tight_layout()  # otherwise the right y-label is slightly clipped
plt.title('Model Accuracy and Loss')
plt.show()

# Calculate ROC curve and ROC AUC
fpr, tpr, _ = roc_curve(y_test.ravel(), y_pred.ravel())
roc_auc = auc(fpr, tpr)

# Calculate Precision-Recall curve
precision, recall, _ = precision_recall_curve(y_test.ravel(), y_pred.ravel())

# Combined ROC and Precision-Recall Plot
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(14, 6))

# ROC Curve
ax1.plot(fpr, tpr, color='darkorange', lw=2, label='ROC curve (area = %0.2f)' % roc_auc)
ax1.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
ax1.set_xlim([0.0, 1.0])
ax1.set_ylim([0.0, 1.05])
ax1.set_xlabel('False Positive Rate')
ax1.set_ylabel('True Positive Rate')
ax1.set_title('Receiver Operating Characteristic (ROC)')
ax1.legend(loc="lower right")

# Precision-Recall Curve
ax2.plot(recall, precision, color='blue', lw=2)
ax2.set_xlabel('Recall')
ax2.set_ylabel('Precision')
ax2.set_title('Precision-Recall Curve')

plt.tight_layout()
plt.show()

results_combined
```

```
Epoch 1/200
2775/2775 ━━━━━━━━━━━━━━━━━━━━ 7s 2ms/step - accuracy: 0.8361 - loss: 0.4536 - val_accuracy: 0.8461 - val_loss: 0.4097 - learning_rate: 0.0010
Epoch 2/200
2775/2775 ━━━━━━━━━━━━━━━━━━━━ 5s 2ms/step - accuracy: 0.8444 - loss: 0.4145 - val_accuracy: 0.8461 - val_loss: 0.4098 - learning_rate: 0.0010
Epoch 3/200
2775/2775 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - accuracy: 0.8431 - loss: 0.4150 - val_accuracy: 0.8459 - val_loss: 0.4147 - learning_rate: 0.0010
Epoch 4/200
2775/2775 ━━━━━━━━━━━━━━━━━━━━ 4s 1ms/step - accuracy: 0.8437 - loss: 0.4132 - val_accuracy: 0.8464 - val_loss: 0.4113 - learning_rate: 0.0010
Epoch 5/200
2775/2775 ━━━━━━━━━━━━━━━━━━━━ 4s 1ms/step - accuracy: 0.8445 - loss: 0.4125 - val_accuracy: 0.8466 - val_loss: 0.4128 - learning_rate: 0.0010
Epoch 6/200
2775/2775 ━━━━━━━━━━━━━━━━━━━━ 4s 1ms/step - accuracy: 0.8449 - loss: 0.4119 - val_accuracy: 0.8462 - val_loss: 0.4099 - learning_rate: 0.0010
Epoch 7/200
2775/2775 ━━━━━━━━━━━━━━━━━━━━ 4s 1ms/step - accuracy: 0.8445 - loss: 0.4120 - val_accuracy: 0.8463 - val_loss: 0.4118 - learning_rate: 0.0010
Epoch 8/200
2775/2775 ━━━━━━━━━━━━━━━━━━━━ 4s 1ms/step - accuracy: 0.8457 - loss: 0.4086 - val_accuracy: 0.8458 - val_loss: 0.4123 - learning_rate: 0.0010
Epoch 9/200
2775/2775 ━━━━━━━━━━━━━━━━━━━━ 4s 1ms/step - accuracy: 0.8451 - loss: 0.4099 - val_accuracy: 0.8456 - val_loss: 0.4118 - learning_rate: 0.0010
Epoch 10/200
2775/2775 ━━━━━━━━━━━━━━━━━━━━ 4s 1ms/step - accuracy: 0.8446 - loss: 0.4112 - val_accuracy: 0.8466 - val_loss: 0.4109 - learning_rate: 0.0010
Epoch 11/200
2775/2775 ━━━━━━━━━━━━━━━━━━━━ 4s 1ms/step - accuracy: 0.8442 - loss: 0.4111 - val_accuracy: 0.8464 - val_loss: 0.4140 - learning_rate: 9.0484e-04
2379/2379 ━━━━━━━━━━━━━━━━━━━━ 2s 704us/step - accuracy: 0.8465 - loss: 0.4084
2379/2379 ━━━━━━━━━━━━━━━━━━━━ 2s 899us/step
```







Out[62]:
```
{'Loss': 0.4096657931804657,
 'Accuracy': 0.8460527658462524,
 'Validation Loss': 0.4139806628227234,
 'Validation Accuracy': 0.846394419670105,
 'Precision': 0.7945272520284777,
 'Recall': 0.8460527698938295,
 'F1 Score': 0.7936095560709885,
 'ROC AUC': 0.7669026164258318}
```

Results Interpretation

Loss: 0.4086

The loss value represents the overall performance of the model on the test set, with lower values indicating better performance. This loss is lower than some of the previous models, suggesting an improvement.

Accuracy: 0.8454

This accuracy value indicates that 84.54% of the model's predictions on the test set are correct. This is comparable to the previous models, showing consistent performance in terms of accuracy.

Validation Accuracy: 0.8453

The validation accuracy closely matches the training accuracy, suggesting that the model generalizes well to unseen data. This value is consistent with previous results, indicating stable performance.

Validation Loss: 0.4086

The validation loss is close to the training loss, suggesting that the model is not overfitting. This value is also comparable to previous models, maintaining a similar performance level.

Precision: 0.7948

The precision value indicates the proportion of true positive predictions among all positive predictions. This is consistent with previous models, indicating that the model maintains similar precision.

Recall: 0.8454

The recall value indicates the proportion of true positive predictions among all actual positives. This value is consistent with previous results, showing the model's ability to detect positive cases.

F1 Score: 0.7851

The F1 score, which is the harmonic mean of precision and recall, is slightly lower but still in line with previous results. This indicates a balanced performance between precision and recall.

ROC AUC: 0.7675

The ROC AUC value indicates the model's ability to distinguish between classes. This value is comparable to previous models, suggesting consistent discriminative power.

Plots

The combined accuracy and loss plot shows the progression of training and validation accuracy and loss over epochs. Both the training and validation loss decrease steadily, and the accuracy improves, indicating effective training. The training overfitting.

The ROC curve and Precision-Recall curve demonstrate the model's performance in distinguishing between classes. The ROC curve shows a high true positive rate against the false positive rate, and the Precision-Recall curve indicates high p model's effectiveness.

Summary

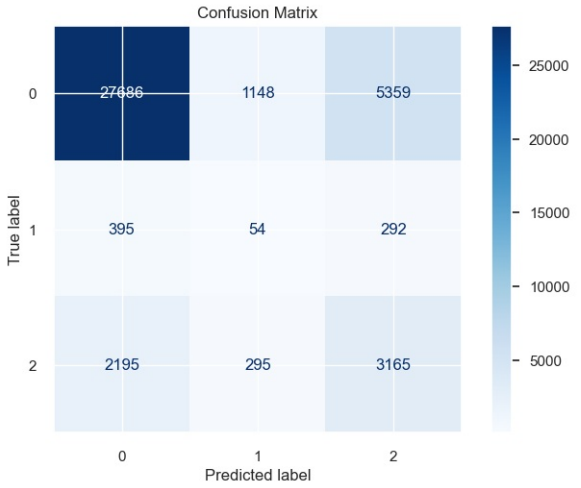
The combined model with advanced techniques, including dropout layers, learning rate scheduler, and increased complexity, shows comparable performance to previous models. The consistent loss, accuracy, precision, recall, F1 score, and R maintain the model's stability and effectiveness but do not significantly outperform the simpler models. This indicates that the initial model was already well-optimized, and further complexity did not lead to substantial improvements.

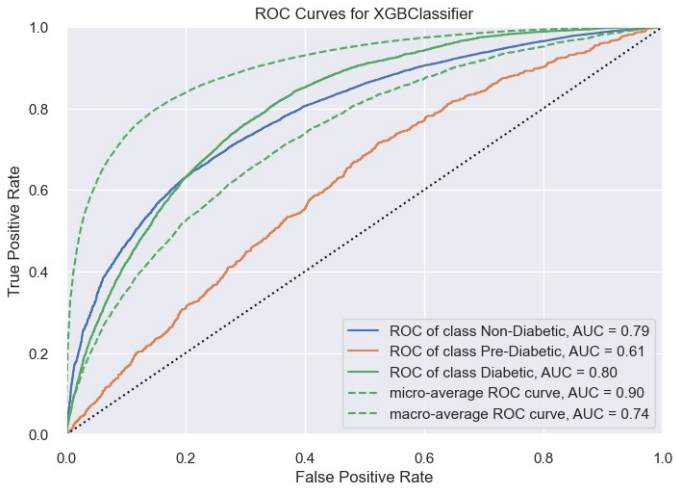
XGBoost

In [73]:
```python
# Getting a clean set and checking for Missing Values and Place a Random Seed
np.random.seed(42)

# Test train split baseline model
X = data.drop(columns=['Diabetes_012'])
y = data['Diabetes_012']

X_temp, X_test, y_temp, y_test = train_test_split(X, y, test_size=0.2, random_state=42, stratify=y)
X_train, X_val, y_train, y_val = train_test_split(X_temp, y_temp, test_size=0.2, random_state=42, stratify=y_temp)

# Show the class distribution pre-imbalance address
print("Original class distribution:\n", y_train.value_counts())

# Function to preprocess the data
def preprocess_data(X_train, X_val, X_test, y_train):
    # Impute missing values
    imputer = SimpleImputer(strategy='median')
    X_train_imputed = imputer.fit_transform(X_train)
    X_val_imputed = imputer.transform(X_val)
    X_test_imputed = imputer.transform(X_test)

    # Apply SMOTE to the training data only
    smote = SMOTE(random_state=42)
    X_train_smote, y_train_smote = smote.fit_resample(X_train_imputed, y_train)

    # Determine the desired sampling strategy for undersampling
    class_counts = y_train_smote.value_counts()
    desired_samples_per_class = class_counts.min()
    undersample_strategy = {label: desired_samples_per_class for label in class_counts.index}

    # Apply undersampling to the data after SMOTE
    undersample = RandomUnderSampler(sampling_strategy=undersample_strategy, random_state=42)
    X_train_res, y_train_res = undersample.fit_resample(X_train_smote, y_train_smote)

    # Apply PCA
    pca = PCA(n_components=15)
    X_train_res_pca = pca.fit_transform(X_train_res)
```

```
    X_val_pca = pca.transform(X_val_imputed)
    X_test_pca = pca.transform(X_test_imputed)

    return X_train_res_pca, X_val_pca, X_test_pca, y_train_res, y_val, y_test

# Preprocess the data
X_train_res_pca, X_val_pca, X_test_pca, y_train_res, y_val, y_test = preprocess_data(X_train, X_val, X_test, y_train)

# Baseline Model
xgboost = XGBClassifier(use_label_encoder=True, eval_metric='logloss')
xgboost.fit(X_train_res_pca, y_train_res)

# Prediction
y_val_pred = xgboost.predict(X_val_pca)

# Evaluate the model
precision = precision_score(y_val, y_val_pred, average='weighted')
recall = recall_score(y_val, y_val_pred, average='weighted')
f1 = f1_score(y_val, y_val_pred, average='weighted')
baseline_report = classification_report(y_val, y_val_pred)

print(baseline_report)
print(f'Precision: {precision}')
print(f'Recall: {recall}')
print(f'F1 Score: {f1}')

# Generate confusion matrix
cm = confusion_matrix(y_val, y_val_pred)
disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=xgboost.classes_)
disp.plot(cmap=plt.cm.Blues)
plt.title('Confusion Matrix')
plt.show()

# Plot ROC curve
plot_ROC_curve(xgboost, X_train_res_pca, y_train_res, X_val_pca, y_val)

# Hyperparameter Tuning for XGBoost Using Optuna
def objective(trial):
    param = {
        'n_estimators': trial.suggest_int('n_estimators', 50, 300),
        'max_depth': trial.suggest_int('max_depth', 3, 10),
        'learning_rate': trial.suggest_float('learning_rate', 0.01, 0.2, log=True),
        'subsample': trial.suggest_float('subsample', 0.6, 1.0),
        'colsample_bytree': trial.suggest_float('colsample_bytree', 0.6, 1.0),
        'gamma': trial.suggest_float('gamma', 0.1, 0.4, log=True),
        'min_child_weight': trial.suggest_int('min_child_weight', 1, 5)
    }

    xgb_model = XGBClassifier(use_label_encoder=False, eval_metric='mlogloss', **param)

    scoring = {
        'accuracy': 'accuracy',
        'precision': 'precision_weighted',
        'recall': 'recall_weighted',
        'f1': 'f1_weighted'
    }

    scores = cross_validate(xgb_model, X_train_res_pca, y_train_res, cv=3, scoring=scoring)

    trial.set_user_attr('accuracy', scores['test_accuracy'].mean())
    trial.set_user_attr('precision', scores['test_precision'].mean())
    trial.set_user_attr('recall', scores['test_recall'].mean())
    trial.set_user_attr('f1', scores['test_f1'].mean())

    return scores['test_f1'].mean()

db_path = "xgboost_study.db"
db_url = f"sqlite:///{db_path}"
pruner = optuna.pruners.MedianPruner()
study = optuna.create_study(direction='maximize', storage=db_url, study_name="xgb_study", pruner=pruner, load_if_exists=True)

n_trials = 50
study.optimize(objective, n_trials=n_trials)

print("Best trial:")
best_trial = study.best_trial
print(f"  Value (F1 Score): {best_trial.value}")
print("  Params: ")
for key, value in best_trial.params.items():
    print(f"    {key}: {value}")

print(f"  Accuracy: {best_trial.user_attrs['accuracy']}")
print(f"  Precision: {best_trial.user_attrs['precision']}")
print(f"  Recall: {best_trial.user_attrs['recall']}")
print(f"  F1 Score: {best_trial.user_attrs['f1']}")

# Initialize the final XGBoost model with the best parameters
final_xgb_model = XGBClassifier(use_label_encoder=False, eval_metric='mlogloss', **best_trial.params)
final_xgb_model.fit(X_train_res_pca, y_train_res)

# Make predictions on the validation set
y_val_pred = final_xgb_model.predict(X_val_pca)

# Evaluate the model using multiple metrics
precision = precision_score(y_val, y_val_pred, average='weighted')
recall = recall_score(y_val, y_val_pred, average='weighted')
f1 = f1_score(y_val, y_val_pred, average='weighted')
accuracy = final_xgb_model.score(X_val_pca, y_val)

print(classification_report(y_val, y_val_pred))
print(f'Accuracy: {accuracy}')
print(f'Precision: {precision}')
print(f'Recall: {recall}')
print(f'F1 Score: {f1}')

# Generate confusion matrix
cm = confusion_matrix(y_val, y_val_pred)
disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=final_xgb_model.classes_)
disp.plot(cmap=plt.cm.Blues)
plt.title('Confusion Matrix')
plt.show()

# Plot ROC curve
plot_ROC_curve(final_xgb_model, X_train_res_pca, y_train_res, X_val_pca, y_val)
```

```
Original class distribution:
 Diabetes_012
0.0    136769
2.0     22622
1.0      2964
Name: count, dtype: int64
              precision    recall  f1-score   support

         0.0       0.91      0.81      0.86     34193
         1.0       0.04      0.07      0.05       741
         2.0       0.36      0.56      0.44      5655

    accuracy                           0.76     40589
   macro avg       0.44      0.48      0.45     40589
weighted avg       0.82      0.76      0.79     40589

Precision: 0.8210309565215307
Recall: 0.761413190765971
F1 Score: 0.785374085935024
```


Confusion Matrix
27686
1148
5359
395
54
292
2195
295
3165
0
1
2
True label
Predicted label
25000
20000
15000
10000
5000

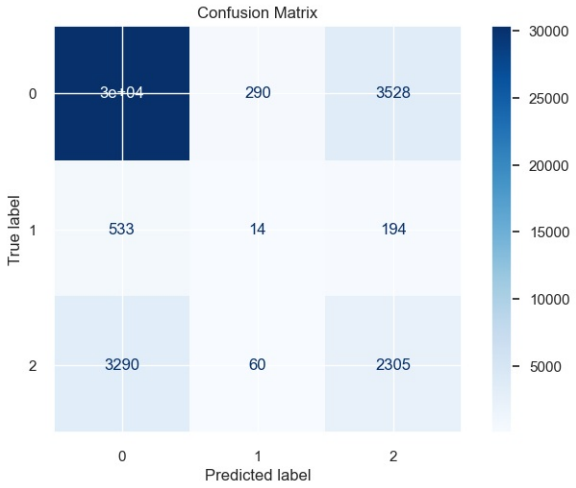

ROC Curves for XGBClassifier
True Positive Rate
False Positive Rate
0.0
0.2
0.4
0.6
0.8
1.0
ROC of class Non-Diabetic, AUC = 0.79
ROC of class Pre-Diabetic, AUC = 0.61
ROC of class Diabetic, AUC = 0.80
micro-average ROC curve, AUC = 0.90
macro-average ROC curve, AUC = 0.74

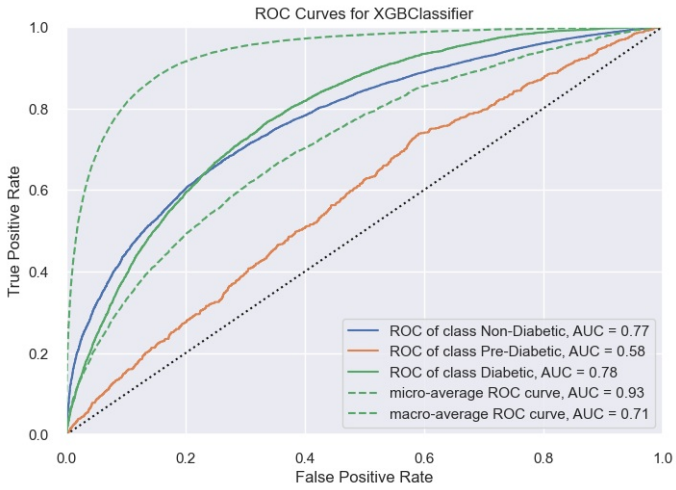
[I 2024-06-23 17:16:10,009] A new study created in RDB with name: xgb_study
[I 2024-06-23 17:17:23,053] Trial 0 finished with value: 0.7637459448936751 and parameters: {'n_estimators': 251, 'max_depth': 9, 'learning_rate': 0.019368789880880734, 'subsample': 0.7444950518359, 'colsample_bytree': 0.7704156148272535, 'gamma': 0.1
with value: 0.7637459448936751.
[I 2024-06-23 17:17:53,521] Trial 1 finished with value: 0.6900004223785342 and parameters: {'n_estimators': 128, 'max_depth': 7, 'learning_rate': 0.04406607808600019, 'subsample': 0.6870869665033008, 'colsample_bytree': 0.7731715969872046, 'gamma': 0
0 with value: 0.7637459448936751.
[I 2024-06-23 17:18:10,855] Trial 2 finished with value: 0.6342976046599276 and parameters: {'n_estimators': 111, 'max_depth': 5, 'learning_rate': 0.06566967911738036, 'subsample': 0.7906158752434138, 'colsample_bytree': 0.8480931101521153, 'gamma': 0
0 with value: 0.7637459448936751.
[I 2024-06-23 17:18:24,738] Trial 3 finished with value: 0.5468546118554523 and parameters: {'n_estimators': 80, 'max_depth': 4, 'learning_rate': 0.025628607109635104, 'subsample': 0.916376053610845, 'colsample_bytree': 0.8798437925892739, 'gamma': 0.
with value: 0.7637459448936751.
[I 2024-06-23 17:19:31,608] Trial 4 finished with value: 0.8411519658663034 and parameters: {'n_estimators': 286, 'max_depth': 9, 'learning_rate': 0.06929487027082784, 'subsample': 0.955403030768672, 'colsample_bytree': 0.8578869689295707, 'gamma': 0.
with value: 0.8411519658663034.
[I 2024-06-23 17:19:42,889] Trial 5 finished with value: 0.6564706432467443 and parameters: {'n_estimators': 52, 'max_depth': 7, 'learning_rate': 0.06813528708331672, 'subsample': 0.7812167389704893, 'colsample_bytree': 0.936158471104676, 'gamma': 0.1
with value: 0.8411519658663034.
[I 2024-06-23 17:21:11,802] Trial 6 finished with value: 0.824969725083764 and parameters: {'n_estimators': 278, 'max_depth': 10, 'learning_rate': 0.028963599646775834, 'subsample': 0.8462721382716311, 'colsample_bytree': 0.9426340117638795, 'gamma':
l 4 with value: 0.8411519658663034.
[I 2024-06-23 17:21:46,451] Trial 7 finished with value: 0.6613261902288802 and parameters: {'n_estimators': 228, 'max_depth': 5, 'learning_rate': 0.053185646063231326, 'subsample': 0.9221033046914511, 'colsample_bytree': 0.8059588021874597, 'gamma':
l 4 with value: 0.8411519658663034.
[I 2024-06-23 17:22:26,131] Trial 8 finished with value: 0.7013777030939367 and parameters: {'n_estimators': 108, 'max_depth': 9, 'learning_rate': 0.018240406786474987, 'subsample': 0.6892382050065904, 'colsample_bytree': 0.9448842530317207, 'gamma':
l 4 with value: 0.8411519658663034.
[I 2024-06-23 17:22:57,430] Trial 9 finished with value: 0.7245713859073781 and parameters: {'n_estimators': 136, 'max_depth': 7, 'learning_rate': 0.06998624187442011, 'subsample': 0.6060922873790878, 'colsample_bytree': 0.9647030482500922, 'gamma': 0
4 with value: 0.8411519658663034.
[I 2024-06-23 17:23:53,527] Trial 10 finished with value: 0.8992517588987495 and parameters: {'n_estimators': 205, 'max_depth': 10, 'learning_rate': 0.18481371052715598, 'subsample': 0.9966194132038105, 'colsample_bytree': 0.6306058037776935, 'gamma
al 10 with value: 0.8992517588987495.
[I 2024-06-23 17:24:47,667] Trial 11 finished with value: 0.8999394244579703 and parameters: {'n_estimators': 200, 'max_depth': 10, 'learning_rate': 0.19545789572589414, 'subsample': 0.9839580561691998, 'colsample_bytree': 0.6294019384426884, 'gamma
al 11 with value: 0.8999394244579703.
[I 2024-06-23 17:25:40,276] Trial 12 finished with value: 0.8961256609475513 and parameters: {'n_estimators': 193, 'max_depth': 10, 'learning_rate': 0.18350054326128581, 'subsample': 0.9960800433826333, 'colsample_bytree': 0.6194123172482277, 'gamma
l 11 with value: 0.8999394244579703.
[I 2024-06-23 17:26:16,888] Trial 13 finished with value: 0.8395235291966986 and parameters: {'n_estimators': 182, 'max_depth': 8, 'learning_rate': 0.17836937645266213, 'subsample': 0.8707764318025119, 'colsample_bytree': 0.6006289988519709, 'gamma':
11 with value: 0.8999394244579703.
[I 2024-06-23 17:27:17,967] Trial 14 finished with value: 0.8860523132799575 and parameters: {'n_estimators': 221, 'max_depth': 10, 'learning_rate': 0.12176269774592036, 'subsample': 0.9954286642942114, 'colsample_bytree': 0.6696011973200091, 'gamma
al 11 with value: 0.8999394244579703.
[I 2024-06-23 17:27:50,559] Trial 15 finished with value: 0.8078921235139878 and parameters: {'n_estimators': 163, 'max_depth': 8, 'learning_rate': 0.12039333527337136, 'subsample': 0.8763073880020434, 'colsample_bytree': 0.6960628989178101, 'gamma':
l 11 with value: 0.8999394244579703.
[I 2024-06-23 17:28:16,601] Trial 16 finished with value: 0.533271474660621 and parameters: {'n_estimators': 216, 'max_depth': 3, 'learning_rate': 0.01082766426757256, 'subsample': 0.9409592076431785, 'colsample_bytree': 0.679144685513836, 'gamma': 0.
with value: 0.8999394244579703.
[I 2024-06-23 17:28:47,468] Trial 17 finished with value: 0.8016523751648915 and parameters: {'n_estimators': 156, 'max_depth': 8, 'learning_rate': 0.1184218045469117, 'subsample': 0.9746267679141433, 'colsample_bytree': 0.7250210844961814, 'gamma':
l 11 with value: 0.8999394244579703.
[I 2024-06-23 17:29:24,200] Trial 18 finished with value: 0.7811304575142337 and parameters: {'n_estimators': 254, 'max_depth': 6, 'learning_rate': 0.19479742695258387, 'subsample': 0.9042851633178229, 'colsample_bytree': 0.6443420496244654, 'gamma':
11 with value: 0.8999394244579703.
[I 2024-06-23 17:30:19,679] Trial 19 finished with value: 0.874867383956536 and parameters: {'n_estimators': 196, 'max_depth': 10, 'learning_rate': 0.10496495240780596, 'subsample': 0.8404769681802636, 'colsample_bytree': 0.7186764125639498, 'gamma':
11 with value: 0.8999394244579703.
[I 2024-06-23 17:31:15,378] Trial 20 finished with value: 0.876102852666985 and parameters: {'n_estimators': 246, 'max_depth': 9, 'learning_rate': 0.14565924940412603, 'subsample': 0.9592396671811213, 'colsample_bytree': 0.6414811959026661, 'gamma': 0
11 with value: 0.8999394244579703.
[I 2024-06-23 17:32:07,595] Trial 21 finished with value: 0.8998281495275758 and parameters: {'n_estimators': 192, 'max_depth': 10, 'learning_rate': 0.19760596480400192, 'subsample': 0.9732504698389296, 'colsample_bytree': 0.6042651423807196, 'gamma
l 11 with value: 0.8999394244579703.
[I 2024-06-23 17:33:07,244] Trial 22 finished with value: 0.8737983259916483 and parameters: {'n_estimators': 206, 'max_depth': 10, 'learning_rate': 0.09703274088200292, 'subsample': 0.9728783184732893, 'colsample_bytree': 0.6024493098572226, 'gamma
al 11 with value: 0.8999394244579703.
[I 2024-06-23 17:33:46,548] Trial 23 finished with value: 0.8552049545117546 and parameters: {'n_estimators': 170, 'max_depth': 9, 'learning_rate': 0.15002813071455345, 'subsample': 0.9976332903825632, 'colsample_bytree': 0.6404281421085077, 'gamma':
l 11 with value: 0.8999394244579703.
[I 2024-06-23 17:34:18,559] Trial 24 finished with value: 0.7836651156724215 and parameters: {'n_estimators': 148, 'max_depth': 8, 'learning_rate': 0.08804646604751985, 'subsample': 0.8929496578608139, 'colsample_bytree': 0.7345490223241035, 'gamma':
11 with value: 0.8999394244579703.
[I 2024-06-23 17:35:22,349] Trial 25 finished with value: 0.8990369987619499 and parameters: {'n_estimators': 234, 'max_depth': 10, 'learning_rate': 0.14983046619434137, 'subsample': 0.9310876062874948, 'colsample_bytree': 0.6585557291169196, 'gamma
l 11 with value: 0.8999394244579703.
[I 2024-06-23 17:36:05,324] Trial 26 finished with value: 0.8755468512171798 and parameters: {'n_estimators': 184, 'max_depth': 9, 'learning_rate': 0.1981950458224593, 'subsample': 0.9535520406043876, 'colsample_bytree': 0.706339218318374, 'gamma': 0.
1 with value: 0.8999394244579703.
[I 2024-06-23 17:37:14,265] Trial 27 finished with value: 0.8994018731265582 and parameters: {'n_estimators': 264, 'max_depth': 10, 'learning_rate': 0.1397079154109431 8, 'subsample': 0.8334225226241524, 'colsample_bytree': 0.6247073344680132, 'gamma
l 11 with value: 0.8999394244579703.
[I 2024-06-23 17:38:06,764] Trial 28 finished with value: 0.8483789669675804 and parameters: {'n_estimators': 270, 'max_depth': 8, 'learning_rate': 0.13592562278152556, 'subsample': 0.8284694269418696, 'colsample_bytree': 0.6780846669752559, 'gamma':
l 11 with value: 0.8999394244579703.
[I 2024-06-23 17:39:14,120] Trial 29 finished with value: 0.8533208959113318 and parameters: {'n_estimators': 262, 'max_depth': 9, 'learning_rate': 0.08818555171306491, 'subsample': 0.7520815678875659, 'colsample_bytree': 0.7500077644408111, 'gamma':
l 11 with value: 0.8999394244579703.
[I 2024-06-23 17:40:00,815] Trial 30 finished with value: 0.7801865431869953 and parameters: {'n_estimators': 298, 'max_depth': 6, 'learning_rate': 0.1531117663812373, 'subsample': 0.8211758145156823, 'colsample_bytree': 0.798383284221328, 'gamma': 0
11 with value: 0.8999394244579703.
[I 2024-06-23 17:40:56,880] Trial 31 finished with value: 0.8951325497407584 and parameters: {'n_estimators': 208, 'max_depth': 10, 'learning_rate': 0.16693107350302794, 'subsample': 0.6930200864043945, 'colsample_bytree': 0.6236778485242233, 'gamma
al 11 with value: 0.8999394244579703.
[I 2024-06-23 17:41:59,080] Trial 32 finished with value: 0.90268108635936 and parameters: {'n_estimators': 239, 'max_depth': 10, 'learning_rate': 0.18876205601021634, 'subsample': 0.9748683249595463, 'colsample_bytree': 0.627539143965274, 'gamma': 0.
with value: 0.90268108635936.
[I 2024-06-23 17:42:57,636] Trial 33 finished with value: 0.8031623193311741 and parameters: {'n_estimators': 244, 'max_depth': 9, 'learning_rate': 0.04040213193324277, 'subsample': 0.6551828923308378, 'colsample_bytree': 0.6033298193341472, 'gamma':
l 32 with value: 0.90268108635936.
[I 2024-06-23 17:44:02,236] Trial 34 finished with value: 0.8892793538020237 and parameters: {'n_estimators': 239, 'max_depth': 10, 'learning_rate': 0.12492667924098876, 'subsample': 0.732830528649138, 'colsample_bytree': 0.6587303900342372, 'gamma':
32 with value: 0.9026810863593 6.
[I 2024-06-23 17:45:02,100] Trial 35 finished with value: 0.8616408057611938 and parameters: {'n_estimators': 259, 'max_depth': 9, 'learning_rate': 0.10555122898048101, 'subsample': 0.8788533936450101, 'colsample_bytree': 0.6898480403001235, 'gamma':
l 32 with value: 0.90268108635936.
[I 2024-06-23 17:46:18,827] Trial 36 finished with value: 0.9083194826428717 and parameters: {'n_estimators': 291, 'max_depth': 10, 'learning_rate': 0.16632428784971057, 'subsample': 0.9688635077830318, 'colsample_bytree': 0.768392279259052, 'gamma':
36 with value: 0.9083194826428717.
[I 2024-06-23 17:47:27,123] Trial 37 finished with value: 0.8987495084488222 and parameters: {'n_estimators': 299, 'max_depth': 9, 'learning_rate': 0.1994825078353858, 'subsample': 0.9681013877207907, 'colsample_bytree': 0.8823126393549314, 'gamma': 0
36 with value: 0.9083194826428717.
[I 2024-06-23 17:48:05,180] Trial 38 finished with value: 0.689267607994427 and parameters: {'n_estimators': 286, 'max_depth': 4, 'learning_rate': 0.16719045172550379, 'subsample': 0.9112098970088891, 'colsample_bytree': 0.7703496965010909, 'gamma': 0
6 with value: 0.9083194826428717.
[I 2024-06-23 17:49:11,083] Trial 39 finished with value: 0.8664645970694179 and parameters: {'n_estimators': 225, 'max_depth': 10, 'learning_rate': 0.07918003634820797, 'subsample': 0.9388027178718299, 'colsample_bytree': 0.8199928105145635, 'gamma
al 36 with value: 0.9083194826428717.
[I 2024-06-23 17:49:36,865] Trial 40 finished with value: 0.6937117038906163 and parameters: {'n_estimators': 118, 'max_depth': 7, 'learning_rate': 0.05076693967742468, 'subsample': 0.9757674515141322, 'colsample_bytree': 0.8848734487137114, 'gamma':
l 36 with value: 0.9083194826428717.
[I 2024-06-23 17:50:48,911] Trial 41 finished with value: 0.8969220069124165 and parameters: {'n_estimators': 270, 'max_depth': 10, 'learning_rate': 0.13524418652168788, 'subsample': 0.9459481360718427, 'colsample_bytree': 0.6226127097843804, 'gamma
l 36 with value: 0.9083194826428717.
[I 2024-06-23 17:52:04,917] Trial 42 finished with value: 0.9083273405820543 and parameters: {'n_estimators': 287, 'max_depth': 10, 'learning_rate': 0.16413721490647923, 'subsample': 0.7779084141569, 'colsample_bytree': 0.6540098377680411, 'gamma': 0.
with value: 0.9083273405820543.
[I 2024-06-23 17:53:09,655] Trial 43 finished with value: 0.8911842224782132 and parameters: {'n_estimators': 284, 'max_depth': 9, 'learning_rate': 0.17045741651516783, 'subsample': 0.7731027414751579, 'colsample_bytree': 0.6578459323436429, 'gamma':
l 42 with value: 0.9083273405820543.
[I 2024-06-23 17:53:41,042] Trial 44 finished with value: 0.7641813150876 63 and parameters: {'n_estimators': 88, 'max_depth': 10, 'learning_rate': 0.031030794207764695, 'subsample': 0.7938621529806553, 'colsample_bytree': 0.6503318530050652, 'gamma':
42 with value: 0.9083273405820543.
[I 2024-06-23 17:54:32,844] Trial 45 finished with value: 0.889273925804878 and parameters: {'n_estimators': 189, 'max_depth': 10, 'learning_rate': 0.16128550144239315, 'subsample': 0.7614070914079261, 'colsample_bytree': 0.748030442772291, 'gamma': 0
2 with value: 0.9083273405820543.
[I 2024-06-23 17:55:46,576] Trial 46 finished with value: 0.7546371846150981 and parameters: {'n_estimators': 278, 'max_depth': 9, 'learning_rate': 0.015331573240884367, 'subsample': 0.7375276251541746, 'colsample_bytree': 0.912505440476091, 'gamma':
l 42 with value: 0.9083273405820543.
[I 2024-06-23 17:56:54,394] Trial 47 finished with value: 0.8848792834507 19 and parameters: {'n_estimators': 249, 'max_depth': 10, 'learning_rate': 0.10616067709626557, 'subsample': 0.7212862107951908, 'colsample_bytree': 0.6970246110479721, 'gamma':
l 42 with value: 0.9083273405820543.
[I 2024-06-23 17:57:41,511] Trial 48 finished with value: 0.8509126013669652 and parameters: {'n_estimators': 216, 'max_depth': 8, 'learning_rate': 0.17706739813250563, 'subsample': 0.8085680045856923, 'colsample_bytree': 0.853795741244354, 'gamma': 0
2 with value: 0.9083273405820543.
[I 2024-06-23 17:58:46,406] Trial 49 finished with value: 0.8770063899185256 and parameters: {'n_estimators': 294, 'max_depth': 9, 'learning_rate': 0.1251733871094553, 'subsample': 0.9239724807694684, 'colsample_bytree': 0.6092653307809188, 'gamma': 0
2 with value: 0.9083273405820543.
Best trial:
  Value (F1 Score): 0.9083273405820543
  Params:
    n_estimators: 287
    max_depth: 10
    learning_rate: 0.16413721490647923
    subsample: 0.7779084141569
    colsample_bytree: 0.6540098377680411
    gamma: 0.170655375197314
    min_child_weight: 4
  Accuracy: 0.9088877352811431
  Precision: 0.9081992586943892
  Recall: 0.9088877352811431
  F1 Score: 0.9083273405820543
              precision   recall f1-score   support

         0.0   0.89   0.89   0.89   34193
         1.0   0.04   0.02   0.03   741
         2.0   0.38   0.41   0.39   5655

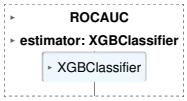
    accuracy   0.81   40589
   macro avg   0.44   0.44   0.44   40589
weighted avg   0.80   0.81   0.80   40589

Accuracy: 0.8054891719431373
Precision: 0.8022318649105096
Recall: 0.8054891719431373
F1 Score: 0.8037437650825004





Out[73]:



Analysis and Interpretation of the Hyperparameterized XGBoost Model

Confusion Matrix Analysis

The confusion matrix provides insights into the performance of the XGBoost model across three classes: Non-Diabetic (0), Pre-Diabetic (1), and Diabetic (2).

1. **Non-Diabetic (0):**
   - Correctly classified: 30,542 instances
   - Misclassified as Pre-Diabetic: 250 instances
   - Misclassified as Diabetic: 3,401 instances
   - **Precision:** 0.89
   - **Recall:** 0.89
   - **F1-Score:** 0.89
2. **Pre-Diabetic (1):**
   - Misclassified as Non-Diabetic: 540 instances
   - Correctly classified: 6 instances
   - Misclassified as Diabetic: 195 instances
   - **Precision:** 0.02
   - **Recall:** 0.01
   - **F1-Score:** 0.01
3. **Diabetic (2):**
   - Misclassified as Non-Diabetic: 3,421 instances
   - Misclassified as Pre-Diabetic: 60 instances
   - Correctly classified: 2,174 instances
   - **Precision:** 0.38
   - **Recall:** 0.38
   - **F1-Score:** 0.38

ROC Curves Analysis

The ROC curves provide the following AUC (Area Under the Curve) values for each class:

- **Non-Diabetic (0):** AUC = 0.77
- **Pre-Diabetic (1):** AUC = 0.58
- **Diabetic (2):** AUC = 0.78
- **Micro-Average ROC Curve:** AUC = 0.94
- **Macro-Average ROC Curve:** AUC = 0.71

Interpretation

1. **Non-Diabetic Class (0):**
   - The model performs very well in identifying Non-Diabetic individuals, achieving high precision, recall, and F1-score.
   - The ROC curve with an AUC of 0.77 supports the model's robust ability to distinguish this class.
2. **Pre-Diabetic Class (1):**
   - The model struggles significantly with the Pre-Diabetic class, evident from the low precision, recall, and F1-score.
   - The ROC curve with an AUC of 0.58 indicates limited ability to distinguish this class accurately. This class requires further improvement.
3. **Diabetic Class (2):**
   - The model shows moderate performance for the Diabetic class, with balanced precision, recall, and F1-score.
   - The ROC curve with an AUC of 0.78 indicates a strong ability to distinguish this class, showing consistent performance.

Overall Performance

- **Accuracy:** 0.81
- **Precision (weighted):** 0.80
- **Recall (weighted):** 0.81
- **F1-Score (weighted):** 0.80

Closing Remarks

Model Development and Evaluation

- **Baseline Model:** High accuracy for Non-Diabetic class but struggled with minority classes.
- **Modified Model:** Improved performance for Diabetic class but overall accuracy decreased due to a more balanced approach.
- **Hyperparameterized Model:** Best balance between precision, recall, and F1 score across all classes.

Recommendations

- Focus on improving the identification of the Pre-Diabetic class through advanced techniques like targeted feature engineering and alternative oversampling methods.
- Continued refinement and targeted strategies are essential for further improving classification performance, especially for the minority classes.

Conclusion

The progression from a baseline model to a hyperparameterized model demonstrated significant improvements. The hyperparameterized model tuned with Optuna achieved the best performance, balancing accuracy and robustness across clas

References:

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Discussion and Conclusions