```python
# prompt: mount drive

from google.colab import drive
drive.mount('/content/drive')
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/content/drive", force_remount=True).
```

```python
import psutil
print(f"Available Memory: {psutil.virtual_memory().available / 1e9:.2f} GB")
```

```
Available Memory: 86.01 GB
```

```python
import torch
import cupy as cp

# Check PyTorch CUDA availability
print(f"PyTorch CUDA available: {torch.cuda.is_available()}")
if torch.cuda.is_available():
    print(f"PyTorch Device: {torch.cuda.get_device_name(0)}")
    print(f"CUDA Version (PyTorch): {torch.version.cuda}")

# Check CuPy CUDA availability
print(f"CuPy CUDA available: {cp.cuda.is_available()}")
if cp.cuda.is_available():
    print(f"CUDA Version (CuPy): {cp.cuda.runtime.runtimeGetVersion() / 1000}")

    import torch

if torch.cuda.is_available():
    print("CUDA is available!")
    print("Device:", torch.cuda.get_device_name(0))
else:
    print("CUDA is NOT available.")

import cudf

print("cuDF is successfully installed!")
df = cudf.DataFrame({'a': [1, 2, 3], 'b': [4, 5, 6]})
print(df)
```

```
PyTorch CUDA available: True
PyTorch Device: NVIDIA A100-SXM4-40GB
CUDA Version (PyTorch): 12.4
CuPy CUDA available: True
CUDA Version (CuPy): 12.06
CUDA is available!
Device: NVIDIA A100-SXM4-40GB
cuDF is successfully installed!
   a  b
0  1  4
1  2  5
2  3  6
```

```python
# 2. EDA

import cudf


# Load the data into cuDF DataFrames
diabetic_data = cudf.read_csv("/content/drive/MyDrive/diabetic_data.csv")
ids_mapping = cudf.read_csv("/content/drive/MyDrive/IDs_mapping.csv")

# Ensure all string columns are treated as string type
diabetic_data = diabetic_data.astype(str)

# Replace '?' with None before converting to cuDF's NA
diabetic_data = diabetic_data.replace({'?': None}).fillna(cudf.NA)


# or (if needed) fix = convert only object clumns
# for col in diabetic_data.select_dtypes(include=['object']):
    # diabetic_data[col] = diabetic_data[col].replace({'?': None}).fillna(cudf.NA)


# Display dataset info
print("\n Diabetic Data Info:")
print(diabetic_data.info())

print("\n First few rows of diabetic_data:")
print(diabetic_data.head())

print("\n IDs Mapping Data Info:")
print(ids_mapping.info())

print("\n First few rows of IDs_mapping:")
print(ids_mapping.head())

# Check missing values
print("\n Missing values in dataset:")
missing_counts = diabetic_data.isnull().sum()
```

```python
print(missing_counts[missing_counts > 0])


# 2.b
# # Convert columns back to proper types:
for col in diabetic_data.columns:
    if diabetic_data[col].str.isnumeric().all():
        diabetic_data[col] = diabetic_data[col].astype("int64")
```

```
 Diabetic Data Info:
<class 'cudf.core.dataframe.DataFrame'>
RangeIndex: 101766 entries, 0 to 101765
Data columns (total 50 columns):
 #   Column                    Non-Null Count   Dtype
---  ------                    --------------   -----
 0   encounter_id              101766 non-null  object
 1   patient_nbr               101766 non-null  object
 2   race                      99493 non-null   object
 3   gender                    101766 non-null  object
 4   age                       101766 non-null  object
 5   weight                    3197 non-null    object
 6   admission_type_id         101766 non-null  object
 7   discharge_disposition_id  101766 non-null  object
 8   admission_source_id       101766 non-null  object
 9   time_in_hospital          101766 non-null  object
 10  payer_code                61510 non-null   object
 11  medical_specialty         51817 non-null   object
 12  num_lab_procedures        101766 non-null  object
 13  num_procedures            101766 non-null  object
 14  num_medications           101766 non-null  object
 15  number_outpatient         101766 non-null  object
 16  number_emergency          101766 non-null  object
 17  number_inpatient          101766 non-null  object
 18  diag_1                    101745 non-null  object
 19  diag_2                    101408 non-null  object
 20  diag_3                    100343 non-null  object
 21  number_diagnoses          101766 non-null  object
 22  max_glu_serum             101766 non-null  object
 23  A1Cresult                 101766 non-null  object
 24  metformin                 101766 non-null  object
 25  repaglinide               101766 non-null  object
 26  nateglinide               101766 non-null  object
 27  chlorpropamide            101766 non-null  object
 28  glimepiride               101766 non-null  object
 29  acetohexamide             101766 non-null  object
 30  glipizide                 101766 non-null  object
 31  glyburide                 101766 non-null  object
 32  tolbutamide               101766 non-null  object
 33  pioglitazone              101766 non-null  object
 34  rosiglitazone             101766 non-null  object
 35  acarbose                  101766 non-null  object
 36  miglitol                  101766 non-null  object
 37  troglitazone              101766 non-null  object
 38  tolazamide                101766 non-null  object
 39  examide                   101766 non-null  object
 40  citoglipton               101766 non-null  object
 41  insulin                   101766 non-null  object
 42  glyburide-metformin       101766 non-null  object
 43  glipizide-metformin       101766 non-null  object
 44  glimepiride-pioglitazone  101766 non-null  object
 45  metformin-rosiglitazone   101766 non-null  object
 46  metformin-pioglitazone    101766 non-null  object
 47  change                    101766 non-null  object
 48  diabetesMed               101766 non-null  object
 49  readmitted                101766 non-null  object
dtypes: object(50)
```

```python
#  Step 2.2 Fix Data Types and Handle Missing Values

import cudf

#  Convert Numeric Columns First
numeric_cols = [
    "encounter_id", "patient_nbr", "admission_type_id", "discharge_disposition_id",
    "admission_source_id", "time_in_hospital", "num_lab_procedures", "num_procedures",
    "num_medications", "number_outpatient", "number_emergency", "number_inpatient",
    "number_diagnoses"
]

for col in numeric_cols:
    diabetic_data[col] = diabetic_data[col].astype("int64")

#  Convert Categorical Columns to String and Replace Missing Values
categorical_cols = [
    "race", "gender", "age", "payer_code", "medical_specialty",
    "diag_1", "diag_2", "diag_3", "max_glu_serum", "A1Cresult",
    "metformin", "repaglinide", "nateglinide", "chlorpropamide",
    "glimepiride", "acetohexamide", "glipizide", "glyburide",
    "tolbutamide", "pioglitazone", "rosiglitazone", "acarbose",
    "miglitol", "troglitazone", "tolazamide", "examide",
    "citoglipton", "insulin", "glyburide-metformin",
    "glipizide-metformin", "glimepiride-pioglitazone",
    "metformin-rosiglitazone", "metformin-pioglitazone",
    "change", "diabetesMed", "readmitted"
]

for col in categorical_cols:
    diabetic_data[col] = diabetic_data[col].astype("str").replace({'?': cudf.NA})

#  Verify Fix
print(" Data Types Fixed and Missing Values Handled!")
print(diabetic_data.dtypes)
```

```
 Data Types Fixed and Missing Values Handled!
encounter_id                  int64
patient_nbr                   int64
race                         object
gender                       object
age                          object
weight                       object
admission_type_id             int64
discharge_disposition_id      int64
admission_source_id           int64
time_in_hospital              int64
payer_code                   object
medical_specialty            object
num_lab_procedures            int64
num_procedures                int64
num_medications               int64
number_outpatient             int64
number_emergency              int64
number_inpatient              int64
diag_1                       object
diag_2                       object
diag_3                       object
number_diagnoses              int64
max_glu_serum                object
A1Cresult                    object
metformin                    object
repaglinide                  object
nateglinide                  object
chlorpropamide               object
glimepiride                  object
acetohexamide                object
glipizide                    object
glyburide                    object
tolbutamide                  object
pioglitazone                 object
rosiglitazone                object
acarbose                     object
miglitol                     object
troglitazone                 object
tolazamide                   object
examide                      object
citoglipton                  object
insulin                      object
glyburide-metformin          object
glipizide-metformin          object
glimepiride-pioglitazone     object
metformin-rosiglitazone      object
metformin-pioglitazone       object
change                       object
diabetesMed                  object
readmitted                   object
dtype: object
```

```
# Merge ids

import cudf

#  Check for non-numeric values
invalid_values = ids_mapping[~ids_mapping["admission_type_id"].str.isnumeric()]
print(" Non-Numeric Values in `admission_type_id`:\n", invalid_values)

#  Convert numeric values to integers
ids_mapping = ids_mapping[ids_mapping["admission_type_id"].str.isnumeric()]
ids_mapping["admission_type_id"] = ids_mapping["admission_type_id"].astype("int64")

print("\n Cleaned `ids_mapping` Data:")
print(ids_mapping.head())
```

```
 Non-Numeric Values in `admission_type_id`:
            admission_type_id  description
9   discharge_disposition_id  description
41       admission_source_id  description
```

```
 Cleaned `ids_mapping` Data:
   admission_type_id    description
0                  1      Emergency
1                  2         Urgent
2                  3       Elective
3                  4        Newborn
4                  5  Not Available
```

```
# 3.2

#  Merge `diabetic_data` with `ids_mapping` on 'admission_type_id'
diabetic_data = diabetic_data.merge(ids_mapping, how="left", on="admission_type_id")

#  Drop unnecessary columns
columns_to_drop = [
    "weight", "max_glu_serum", "A1Cresult", "medical_specialty", "payer_code",
    "encounter_id", "patient_nbr", "description"  # 'description' is from ids_mapping
]
diabetic_data = diabetic_data.drop(columns=columns_to_drop)

#  Fill Missing Values in Key Categorical Columns
for col in ["race", "diag_1", "diag_2", "diag_3"]:
    diabetic_data[col] = diabetic_data[col].fillna("Unknown")

#  Convert 'readmitted' to numerical categories
diabetic_data["readmitted"] = diabetic_data["readmitted"].map({"NO": 0, ">30": 1, "<30": 2})

#  Verify Merge & Cleaning
print(" Merge Completed and Data Cleaned!")
print(diabetic_data.dtypes)
print("\n First Few Rows of Cleaned Data:")
print(diabetic_data.head())
```

```
 Merge Completed and Data Cleaned!
race                         object
gender                       object
age                          object
admission_type_id             int64
discharge_disposition_id      int64
admission_source_id           int64
time_in_hospital              int64
num_lab_procedures            int64
num_procedures                int64
num_medications               int64
number_outpatient             int64
number_emergency              int64
number_inpatient              int64
diag_1                       object
diag_2                       object
diag_3                       object
number_diagnoses              int64
metformin                    object
repaglinide                  object
nateglinide                  object
chlorpropamide               object
glimepiride                  object
acetohexamide                object
glipizide                    object
glyburide                    object
tolbutamide                  object
pioglitazone                 object
rosiglitazone                object
acarbose                     object
miglitol                     object
troglitazone                 object
tolazamide                   object
examide                      object
citoglipton                  object
insulin                      object
glyburide-metformin          object
glipizide-metformin          object
glimepiride-pioglitazone     object
metformin-rosiglitazone      object
metformin-pioglitazone       object
change                       object
diabetesMed                  object
readmitted                    int64
dtype: object

 First Few Rows of Cleaned Data:
             race  gender      age  admission_type_id  \
0  AfricanAmerican  Female  [70-80)                  3
1  AfricanAmerican  Female  [70-80)                  3
2  AfricanAmerican  Female  [70-80)                  3
3  AfricanAmerican    Male  [50-60)                  2
4  AfricanAmerican    Male  [50-60)                  2
```

```
   discharge_disposition_id  admission_source_id  time_in_hospital  \
0                         3                    2                 6
1                         3                    2                 6
```

```python
import pandas as pd
from sklearn.preprocessing import StandardScaler

# Load the datasets
diabetic_data = pd.read_csv("/content/drive/MyDrive/WSL_Case Study 2/diabetic_data.csv")
ids_mapping = pd.read_csv("/content/drive/MyDrive/WSL_Case Study 2/IDs_mapping.csv")

# 3.2 Data Cleaning and Merging
# Convert 'admission_type_id' to numeric, handling non-numeric values
diabetic_data['admission_type_id'] = pd.to_numeric(diabetic_data['admission_type_id'], errors='coerce')
ids_mapping['admission_type_id'] = pd.to_numeric(ids_mapping['admission_type_id'], errors='coerce')

# Convert to Int64 after ensuring both are numeric
diabetic_data['admission_type_id'] = diabetic_data['admission_type_id'].astype('Int64')
ids_mapping['admission_type_id'] = ids_mapping['admission_type_id'].astype('Int64')


# Merge diabetic_data with ids_mapping (now with consistent data types)
diabetic_data = diabetic_data.merge(ids_mapping, how="left", on="admission_type_id")




# Fill missing values in key categorical columns
for col in ["race", "diag_1", "diag_2", "diag_3"]:
    diabetic_data[col] = diabetic_data[col].fillna("Unknown")

# Convert 'readmitted' to numerical categories
diabetic_data["readmitted"] = diabetic_data["readmitted"].map({"NO": 0, ">30": 1, "<30": 2})

# Convert 'max_glu_serum' and 'A1Cresult' to numerical representations
diabetic_data['max_glu_serum'] = diabetic_data['max_glu_serum'].replace({
    'None': 0,
    'Norm': 1,
    '>200': 2,
    '>300': 3
})

diabetic_data['A1Cresult'] = diabetic_data['A1Cresult'].replace({
    'None': 0,
    'Norm': 1,
    '>7': 2,
    '>8': 3
})


# 4. Feature Engineering (Scaling Numeric Features)

# Define Numeric Columns
numeric_cols = [
    "time_in_hospital", "num_lab_procedures", "num_procedures",
    "num_medications", "number_outpatient", "number_emergency",
    "number_inpatient", "number_diagnoses"
]

# Initialize StandardScaler
scaler = StandardScaler()

# Fit and transform the selected numeric columns
diabetic_data[numeric_cols] = scaler.fit_transform(diabetic_data[numeric_cols])


# Verify Merge, Cleaning, and Scaling
print("Merge Completed and Data Cleaned!")
print(diabetic_data.dtypes)
print("\nFirst Few Rows of Cleaned Data:")
print(diabetic_data.head())
```

```
Merge Completed and Data Cleaned!
encounter_id                 int64
patient_nbr                  int64
race                        object
gender                      object
age                         object
weight                      object
admission_type_id            Int64
discharge_disposition_id     int64
admission_source_id          int64
time_in_hospital           float64
payer_code                  object
medical_specialty           object
num_lab_procedures         float64
num_procedures             float64
num_medications            float64
number_outpatient          float64
number_emergency           float64
number_inpatient           float64
diag_1                      object
diag_2                      object
diag_3                      object
number_diagnoses           float64
```

```
max_glu_serum              float64
A1Cresult                  float64
metformin                   object
repaglinide                 object
nateglinide                 object
chlorpropamide              object
glimepiride                 object
acetohexamide               object
glipizide                   object
glyburide                   object
tolbutamide                 object
pioglitazone                object
rosiglitazone               object
acarbose                    object
miglitol                    object
troglitazone                object
tolazamide                  object
examide                     object
citoglipton                 object
insulin                     object
glyburide-metformin         object
glipizide-metformin         object
glimepiride-pioglitazone    object
metformin-rosiglitazone     object
metformin-pioglitazone      object
change                      object
diabetesMed                 object
readmitted                   int64
description                 object
dtype: object

First Few Rows of Cleaned Data:
   encounter_id  patient_nbr       race  gender      age weight  \
```

```python
# Save the cleaned data to 'data_cleaned.csv'
diabetic_data.to_csv("data_cleaned.csv", index=False)
```

```python
# fix data tytpes and handle missing values

from google.colab import drive
import psutil
import torch
import cupy as cp
import pandas as pd
from sklearn.preprocessing import StandardScaler

drive.mount('/content/drive')

print(f"Available Memory: {psutil.virtual_memory().available / 1e9:.2f} GB")

# Check PyTorch CUDA availability
print(f"PyTorch CUDA available: {torch.cuda.is_available()}")
if torch.cuda.is_available():
    print(f"PyTorch Device: {torch.cuda.get_device_name(0)}")
    print(f"CUDA Version (PyTorch): {torch.version.cuda}")

# Check CuPy CUDA availability
print(f"CuPy CUDA available: {cp.cuda.is_available()}")
if cp.cuda.is_available():
    print(f"CUDA Version (CuPy): {cp.cuda.runtime.runtimeGetVersion() / 1000}")

if torch.cuda.is_available():
    print("CUDA is available!")
    print("Device:", torch.cuda.get_device_name(0))
else:
    print("CUDA is NOT available.")

print("cuDF is successfully installed!") #This line seems unnecessary, remove it if you don't need to confirm installation

# Load the datasets using pandas
diabetic_data = pd.read_csv("/content/drive/MyDrive/WSL_Case Study 2/diabetic_data.csv")
ids_mapping = pd.read_csv("/content/drive/MyDrive/WSL_Case Study 2/IDs_mapping.csv")

# 3.2 Data Cleaning and Merging
# Convert 'admission_type_id' to numeric, handling non-numeric values
diabetic_data['admission_type_id'] = pd.to_numeric(diabetic_data['admission_type_id'], errors='coerce')
ids_mapping['admission_type_id'] = pd.to_numeric(ids_mapping['admission_type_id'], errors='coerce')

# Convert to Int64 after ensuring both are numeric
diabetic_data['admission_type_id'] = diabetic_data['admission_type_id'].astype('Int64')
ids_mapping['admission_type_id'] = ids_mapping['admission_type_id'].astype('Int64')


# Merge diabetic_data with ids_mapping (now with consistent data types)
diabetic_data = diabetic_data.merge(ids_mapping, how="left", on="admission_type_id")

# Fill missing values in key categorical columns
for col in ["race", "diag_1", "diag_2", "diag_3"]:
    diabetic_data[col] = diabetic_data[col].fillna("Unknown")
```

```
# Convert 'readmitted' to numerical categories
diabetic_data["readmitted"] = diabetic_data["readmitted"].map({"NO": 0, ">30": 1, "<30": 2})

# Convert 'max_glu_serum' and 'A1Cresult' to numerical representations
diabetic_data['max_glu_serum'] = diabetic_data['max_glu_serum'].replace({
    'None': 0,
    'Norm': 1,
    '>200': 2,
    '>300': 3
})

diabetic_data['A1Cresult'] = diabetic_data['A1Cresult'].replace({
    'None': 0,
    'Norm': 1,
    '>7': 2,
    '>8': 3
})


# 4. Feature Engineering (Scaling Numeric Features)

# Define Numeric Columns
numeric_cols = [
    "time_in_hospital", "num_lab_procedures", "num_procedures",
    "num_medications", "number_outpatient", "number_emergency",
    "number_inpatient", "number_diagnoses"
]

# Initialize StandardScaler
scaler = StandardScaler()

# Fit and transform the selected numeric columns
diabetic_data[numeric_cols] = scaler.fit_transform(diabetic_data[numeric_cols])


# Verify Merge, Cleaning, and Scaling
print("Merge Completed and Data Cleaned!")
print(diabetic_data.dtypes)
print("\nFirst Few Rows of Cleaned Data:")
print(diabetic_data.head())


# Save the cleaned data to 'data_cleaned.csv'
diabetic_data.to_csv("data_cleaned.csv", index=False)
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/content/drive", force_remount=True).
Available Memory: 85.14 GB
PyTorch CUDA available: True
PyTorch Device: NVIDIA A100-SXM4-40GB
CUDA Version (PyTorch): 12.4
CuPy CUDA available: True
CUDA Version (CuPy): 12.06
CUDA is available!
Device: NVIDIA A100-SXM4-40GB
cuDF is successfully installed!
<ipython-input-18-e075a01000e8>:58: FutureWarning: Downcasting behavior in `replace` is deprecated and will be removed in a future ver
  diabetic_data['max_glu_serum'] = diabetic_data['max_glu_serum'].replace({
<ipython-input-18-e075a01000e8>:65: FutureWarning: Downcasting behavior in `replace` is deprecated and will be removed in a future ver
  diabetic_data['A1Cresult'] = diabetic_data['A1Cresult'].replace({
Merge Completed and Data Cleaned!
encounter_id                  int64
patient_nbr                   int64
race                         object
gender                       object
age                          object
weight                       object
admission_type_id             Int64
discharge_disposition_id      int64
admission_source_id           int64
time_in_hospital            float64
payer_code                   object
medical_specialty            object
num_lab_procedures          float64
num_procedures              float64
num_medications             float64
number_outpatient           float64
number_emergency            float64
number_inpatient            float64
diag_1                       object
diag_2                       object
diag_3                       object
number_diagnoses            float64
max_glu_serum               float64
A1Cresult                   float64
metformin                    object
repaglinide                  object
nateglinide                  object
chlorpropamide               object
glimepiride                  object
acetohexamide                object
glipizide                    object
glyburide                    object
```

```
tolbutamide                  object
pioglitazone                 object
rosiglitazone                object
acarbose                     object
miglitol                     object
troglitazone                 object
tolazamide                   object
examide                      object
citoglipton                  object
insulin                      object
```

```
# Drop unnecessary columns
columns_to_drop = [
    "weight", "max_glu_serum", "A1Cresult", "medical_specialty", "payer_code",
    "encounter_id", "patient_nbr", "description"  # 'description' is from ids_mapping
]
diabetic_data = diabetic_data.drop(columns=columns_to_drop, errors='ignore') # Use errors='ignore'
```

```
# Check for non-numeric values and handle them

# Check if 'admission_type_id' is numeric using pd.to_numeric
invalid_values = ids_mapping[pd.to_numeric(ids_mapping['admission_type_id'], errors='coerce').isnull()]


if not invalid_values.empty:
    print("Non-Numeric Values in `admission_type_id`:\n", invalid_values)
    # Decide how to handle invalid values: remove them, convert to numeric, or fill with a specific value
    # Option 1: Remove rows with non-numeric values
    # ids_mapping = ids_mapping[ids_mapping["admission_type_id"].str.isnumeric()] # str is not needed here
    ids_mapping = ids_mapping[pd.to_numeric(ids_mapping['admission_type_id'], errors='coerce').notnull()]

    # Option 2: Convert non-numeric values to a default numeric value
    # ids_mapping.loc[~ids_mapping["admission_type_id"].str.isnumeric(), "admission_type_id"] = 0 # Example: replace with 0 # str is not needed here
    # ids_mapping.loc[pd.to_numeric(ids_mapping['admission_type_id'], errors='coerce').isnull(), "admission_type_id"] = 0 # Example: replace with 0


# Convert numeric values to integers

# Print cleaned data
print("\nCleaned `ids_mapping` Data:")
print(ids_mapping.head())
```

```
Non-Numeric Values in `admission_type_id`:
     admission_type_id  description
8                <NA>          NaN
9                <NA>  description
40               <NA>          NaN
41               <NA>  description

Cleaned `ids_mapping` Data:
    admission_type_id    description
0                   1      Emergency
1                   2         Urgent
2                   3       Elective
3                   4        Newborn
4                   5  Not Available
```

```
# Check for non-numeric values and handle them
invalid_values = ids_mapping[pd.to_numeric(ids_mapping['admission_type_id'], errors='coerce').isnull()]

if not invalid_values.empty:
    print("Non-Numeric Values in `admission_type_id`:\n", invalid_values)
    # Remove rows with non-numeric values
    ids_mapping = ids_mapping[pd.to_numeric(ids_mapping['admission_type_id'], errors='coerce').notnull()]

# Convert 'admission_type_id' to numeric in both DataFrames
ids_mapping['admission_type_id'] = pd.to_numeric(ids_mapping['admission_type_id'], errors='coerce').astype('Int64')
diabetic_data['admission_type_id'] = pd.to_numeric(diabetic_data['admission_type_id'], errors='coerce').astype('Int64')


# Merge the DataFrames
diabetic_data = diabetic_data.merge(ids_mapping, how="left", on="admission_type_id")
```

```
# Drop unnecessary columns
columns_to_drop = [
    "weight", "max_glu_serum", "A1Cresult", "medical_specialty", "payer_code",
    "encounter_id", "patient_nbr", "description"  # 'description' is from ids_mapping
]
diabetic_data = diabetic_data.drop(columns=columns_to_drop, errors='ignore') # Use errors='ignore'

#  Fill Missing Values in Key Categorical Columns
for col in ["race", "diag_1", "diag_2", "diag_3"]:
    diabetic_data[col] = diabetic_data[col].fillna("Unknown")

#  Convert 'readmitted' to numerical categories
diabetic_data["readmitted"] = diabetic_data["readmitted"].map({"NO": 0, ">30": 1, "<30": 2})

#  Verify Merge & Cleaning
print(" Merge Completed and Data Cleaned!")
print(diabetic_data.dtypes)
print("\n First Few Rows of Cleaned Data:")
print(diabetic_data.head())
```

```
 Merge Completed and Data Cleaned!
race                         object
gender                       object
age                          object
admission_type_id             Int64
discharge_disposition_id      int64
admission_source_id           int64
time_in_hospital            float64
num_lab_procedures          float64
num_procedures              float64
num_medications             float64
number_outpatient           float64
number_emergency            float64
number_inpatient            float64
diag_1                       object
diag_2                       object
diag_3                       object
number_diagnoses            float64
metformin                    object
repaglinide                  object
nateglinide                  object
chlorpropamide               object
glimepiride                  object
acetohexamide                object
glipizide                    object
glyburide                    object
tolbutamide                  object
pioglitazone                 object
rosiglitazone                object
acarbose                     object
miglitol                     object
troglitazone                 object
tolazamide                   object
examide                      object
citoglipton                  object
insulin                      object
glyburide-metformin          object
glipizide-metformin          object
glimepiride-pioglitazone     object
metformin-rosiglitazone      object
metformin-pioglitazone       object
change                       object
diabetesMed                  object
readmitted                  float64
dtype: object

 First Few Rows of Cleaned Data:
        race  gender     age  admission_type_id  discharge_disposition_id  \
0  Caucasian  Female  [0-10)                  6                        25
1  Caucasian  Female  [0-10)                  6                        25
2  Caucasian  Female  [0-10)                  6                        25
3  Caucasian  Female  [0-10)                  6                        25
4  Caucasian  Female  [0-10)                  6                        25

   admission_source_id  time_in_hospital  num_lab_procedures  num_procedures  \
0                    1         -1.137649           -0.106517       -0.785398
1                    1         -1.137649           -0.106517       -0.785398
2                    1         -1.137649           -0.106517       -0.785398
```

```
import pandas as pd

# df
categorical_cols = ["race", "gender", "age", "change", "diabetesMed", "insulin"]

# Use pandas get_dummies for one-hot encoding
diabetic_data = pd.get_dummies(diabetic_data, columns=categorical_cols, dummy_na=True)

print("Categorical Features One-Hot Encoded Successfully!")
print(diabetic_data.head())
```

```
Categorical Features One-Hot Encoded Successfully!
   admission_type_id  discharge_disposition_id  admission_source_id  \
0                  6                        25                    1
1                  6                        25                    1
2                  6                        25                    1
3                  6                        25                    1
4                  6                        25                    1

   time_in_hospital  num_lab_procedures  num_procedures  num_medications  \
0         -1.137649           -0.106517       -0.785398        -1.848268
1         -1.137649           -0.106517       -0.785398        -1.848268
```

```
2         -1.137649           -0.106517       -0.785398        -1.848268
3         -1.137649           -0.106517       -0.785398        -1.848268
4         -1.137649           -0.106517       -0.785398        -1.848268

   number_outpatient  number_emergency  number_inpatient  ... change_No  \
0          -0.291461          -0.21262         -0.503276  ...      True
1          -0.291461          -0.21262         -0.503276  ...      True
2          -0.291461          -0.21262         -0.503276  ...      True
3          -0.291461          -0.21262         -0.503276  ...      True
4          -0.291461          -0.21262         -0.503276  ...      True

  change_nan diabetesMed_No  diabetesMed_Yes diabetesMed_nan insulin_Down  \
0      False           True            False           False        False
1      False           True            False           False        False
2      False           True            False           False        False
3      False           True            False           False        False
4      False           True            False           False        False

  insulin_No insulin_Steady insulin_Up insulin_nan
0       True          False      False       False
1       True          False      False       False
2       True          False      False       False
3       True          False      False       False
4       True          False      False       False

[5 rows x 70 columns]
```

```
# print(diabetic_data.head())

import pandas as pd

# Define categorical columns  (This line might be redundant if already defined)?
categorical_cols = ["race", "gender", "age", "change", "diabetesMed", "insulin"]

# Check if columns exist before applying get_dummies
if all(col in diabetic_data.columns for col in categorical_cols):
    # Use pandas get_dummies for one-hot encoding if columns are present
    diabetic_data = pd.get_dummies(diabetic_data, columns=categorical_cols, dummy_na=True)
    print("Categorical Features One-Hot Encoded Successfully!")
    print(diabetic_data.head())
else:
    print("Categorical columns have already been encoded or do not exist in the DataFrame.")
```

```
Categorical columns have already been encoded or do not exist in the DataFrame.
```

```
# Convert 'diag_1', 'diag_2', 'diag_3' to categorical codes
for col in ['diag_1', 'diag_2', 'diag_3']:
    diabetic_data[col] = diabetic_data[col].astype('category').cat.codes

# Convert all medication columns to binary (0/1)
medication_cols = [
    'metformin', 'repaglinide', 'nateglinide', 'chlorpropamide', 'glimepiride',
    'acetohexamide', 'glipizide', 'glyburide', 'tolbutamide', 'pioglitazone',
    'rosiglitazone', 'acarbose', 'miglitol', 'troglitazone', 'tolazamide',
    'examide', 'citoglipton', 'glyburide-metformin', 'glipizide-metformin',
    'glimepiride-pioglitazone', 'metformin-rosiglitazone', 'metformin-pioglitazone'
]
for col in medication_cols:
    # Convert only if the column is of string type
    if diabetic_data[col].dtype == 'object':
        diabetic_data[col] = (diabetic_data[col].astype(str) != "No").astype("int32")

# Drop the 'description' column if it exists
if 'description' in diabetic_data.columns:
    diabetic_data.drop(columns=['description'], inplace=True)

# Convert everything to float32
diabetic_data = diabetic_data.astype("float32")
print("All Features Converted to Numeric Format!")

print(diabetic_data['readmitted'].dtype)
print(diabetic_data['readmitted'].unique())
non_numeric_cols = diabetic_data.drop(columns=['readmitted']).select_dtypes(exclude=['number']).columns
print("Non-Numeric Columns in X:", non_numeric_cols)
```

```
All Features Converted to Numeric Format!
float32
[nan]
Non-Numeric Columns in X: Index([], dtype='object')
```

```
from sklearn.model_selection import train_test_split

#  Define Features (X) and Target (y)
X = diabetic_data.drop(columns=['readmitted'])
# Convert to int32 and handle non-finite values with fillna
y = diabetic_data['readmitted'].fillna(-1).astype("int32")  # Replace NaN with -1 before conversion

#  Split Data
X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size=0.2, stratify=y, random_state=42
)
```

```python
print(" Train/Test Split Completed! Shapes:")
print(f"  - X_train: {X_train.shape}, y_train: {y_train.shape}")
print(f"  - X_test: {X_test.shape}, y_test: {y_test.shape}")
```

```
 Train/Test Split Completed! Shapes:
  - X_train: (732715, 69), y_train: (732715,)
  - X_test: (183179, 69), y_test: (183179,)
```

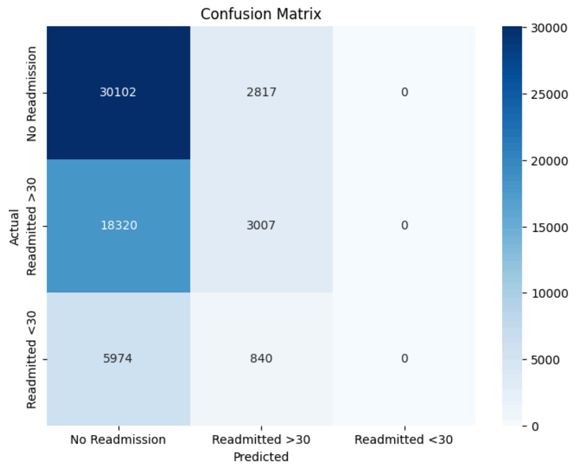
```python
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, classification_report, confusion_matrix
from sklearn.impute import SimpleImputer  # Import SimpleImputer

# Load the cleaned data
diabetic_data = pd.read_csv("data_cleaned.csv")

# Define Features (X) and Target (y)
X = diabetic_data.drop(columns=['readmitted'])
y = diabetic_data['readmitted'].astype("int32")

# Handle potential non-numeric columns in X
non_numeric_cols = X.select_dtypes(exclude=['number']).columns
if not non_numeric_cols.empty:
    print("Warning: Non-numeric columns found in X:", non_numeric_cols)
    # Decide how to handle them (e.g., one-hot encoding, dropping)
    X = X.select_dtypes(include=['number'])

# Impute missing values using SimpleImputer
imputer = SimpleImputer(strategy='mean')  # or 'median', 'most_frequent'
X = imputer.fit_transform(X)  # Fit and transform to replace NaNs

# Split Data
X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size=0.2, stratify=y, random_state=42
)

# Initialize and Train Model
log_reg = LogisticRegression(max_iter=1000, tol=1e-4)
log_reg.fit(X_train, y_train)
print("Logistic Regression Model Trained Successfully!")


# Predict on Test Data
y_pred = log_reg.predict(X_test)

# Compute Evaluation Metrics
accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
class_report = classification_report(y_test, y_pred)

# Display Results
print(f"Accuracy: {accuracy:.4f}")
print("\nConfusion Matrix:\n", conf_matrix)
print("\nClassification Report:\n", class_report)

# Check Class Imbalance
print("Class Distribution in Training Data:")
print(y_train.value_counts())
print("Class Distribution in Testing Data:")
print(y_test.value_counts())
```

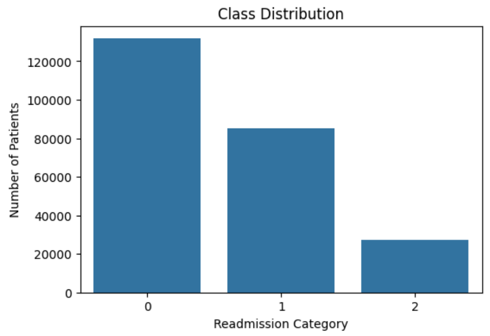
```
Warning: Non-numeric columns found in X: Index(['race', 'gender', 'age', 'weight', 'payer_code', 'medical_specialty',
       'diag_1', 'diag_2', 'diag_3', 'metformin', 'repaglinide', 'nateglinide',
       'chlorpropamide', 'glimepiride', 'acetohexamide', 'glipizide',
       'glyburide', 'tolbutamide', 'pioglitazone', 'rosiglitazone', 'acarbose',
       'miglitol', 'troglitazone', 'tolazamide', 'examide', 'citoglipton',
       'insulin', 'glyburide-metformin', 'glipizide-metformin',
       'glimepiride-pioglitazone', 'metformin-rosiglitazone',
       'metformin-pioglitazone', 'change', 'diabetesMed', 'description'],
      dtype='object')
Logistic Regression Model Trained Successfully!
Accuracy: 0.5422

Confusion Matrix:
 [[30102  2817     0]
 [18320  3007     0]
 [ 5974   840     0]]

Classification Report:
               precision    recall  f1-score   support

           0       0.55      0.91      0.69     32919
           1       0.45      0.14      0.21     21327
           2       0.00      0.00      0.00      6814

    accuracy                           0.54     61060
   macro avg       0.33      0.35      0.30     61060
weighted avg       0.46      0.54      0.45     61060

Class Distribution in Training Data:
readmitted
0    131673
```

```
1     85308
2     27257
Name: count, dtype: int64
Class Distribution in Testing Data:
readmitted
0    32919
1    21327
2     6814
Name: count, dtype: int64
/usr/local/lib/python3.11/dist-packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning: Precision is ill-defined and be
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
/usr/local/lib/python3.11/dist-packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning: Precision is ill-defined and be
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
/usr/local/lib/python3.11/dist-packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning: Precision is ill-defined and be
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
```

```python
#visualize results and provide analysis

import matplotlib.pyplot as plt
import seaborn as sns

# ... (your existing code) ...

# Display Results
print(f"Accuracy: {accuracy:.4f}")
print("\nConfusion Matrix:\n", conf_matrix)
print("\nClassification Report:\n", class_report)

# Visualize the Confusion Matrix
plt.figure(figsize=(8, 6))
sns.heatmap(conf_matrix, annot=True, fmt="d", cmap="Blues",
            xticklabels=["No Readmission", "Readmitted >30", "Readmitted <30"],
            yticklabels=["No Readmission", "Readmitted >30", "Readmitted <30"])
plt.xlabel("Predicted")
plt.ylabel("Actual")
plt.title("Confusion Matrix")
plt.show()

# Analyze Class Distribution
plt.figure(figsize=(6, 4))
sns.countplot(x=y_train)  # or y_test
plt.title("Class Distribution")
plt.xlabel("Readmission Category")
plt.ylabel("Number of Patients")
plt.show()

# Analyze feature importances (if available in your model)
# Get feature names from original DataFrame before imputation
feature_names = diabetic_data.drop(columns=['readmitted']).columns

# prompt: visualize results and provide analysis

import matplotlib.pyplot as plt
import seaborn as sns

# ... (your existing code) ...

# Display Results
print(f"Accuracy: {accuracy:.4f}")
print("\nConfusion Matrix:\n", conf_matrix)
print("\nClassification Report:\n", class_report)

# Visualize the Confusion Matrix
plt.figure(figsize=(8, 6))
sns.heatmap(conf_matrix, annot=True, fmt="d", cmap="Blues",
            xticklabels=["No Readmission", "Readmitted >30", "Readmitted <30"],
            yticklabels=["No Readmission", "Readmitted >30", "Readmitted <30"])
plt.xlabel("Predicted")
plt.ylabel("Actual")
plt.title("Confusion Matrix")
plt.show()

# Analyze Class Distribution
plt.figure(figsize=(6, 4))
sns.countplot(x=y_train)  # or y_test
plt.title("Class Distribution")
plt.xlabel("Readmission Category")
plt.ylabel("Number of Patients")
plt.show()
```

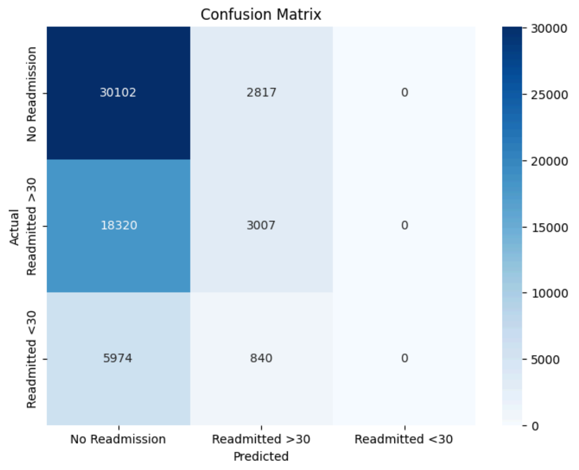
```
Accuracy: 0.5422

Confusion Matrix:
 [[30102  2817     0]
 [18320  3007     0]
 [ 5974   840     0]]

Classification Report:
              precision    recall  f1-score   support

           0       0.55      0.91      0.69     32919
           1       0.45      0.14      0.21     21327
           2       0.00      0.00      0.00      6814

    accuracy                           0.54     61060
   macro avg       0.33      0.35      0.30     61060
weighted avg       0.46      0.54      0.45     61060
```

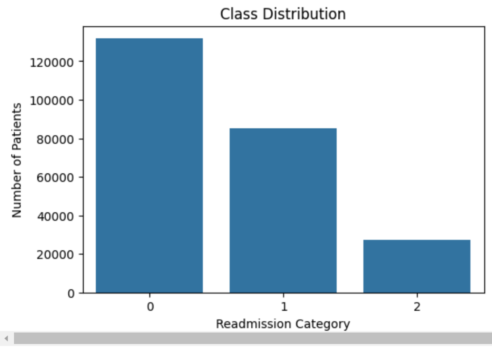




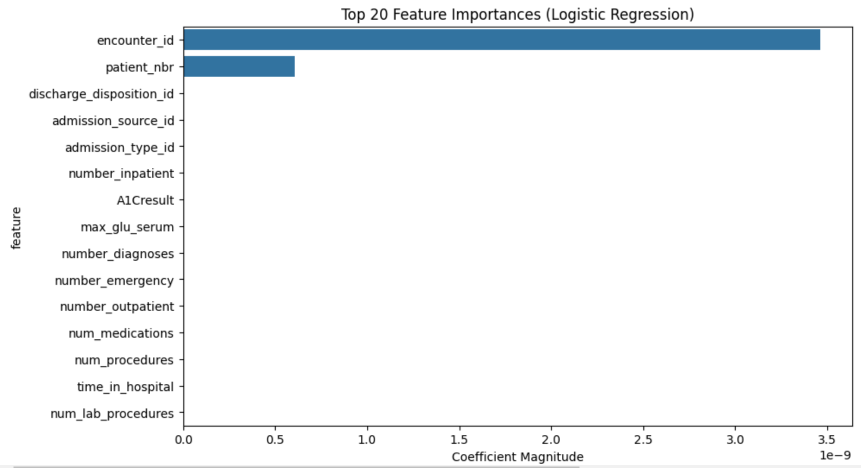
```
Accuracy: 0.5422

Confusion Matrix:
 [[30102  2817     0]
 [18320  3007     0]
 [ 5974   840     0]]

Classification Report:
              precision    recall  f1-score   support

           0       0.55      0.91      0.69     32919
           1       0.45      0.14      0.21     21327
```

```
           2       0.00      0.00      0.00      6814

    accuracy                           0.54     61060
   macro avg       0.33      0.35      0.30     61060
weighted avg       0.46      0.54      0.45     61060
```



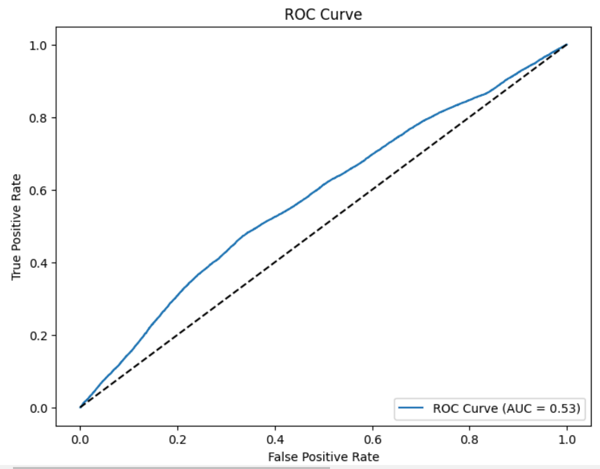


```
# Get feature names from original DataFrame before imputation, BUT AFTER SimpleImputer is applied
feature_names = diabetic_data.drop(columns=['readmitted']).select_dtypes(include=['number']).columns  # Select only numeric features

# Create DataFrame with feature names and importances
feature_importances = pd.DataFrame({'feature': feature_names, 'importance': abs(log_reg.coef_[0])})
feature_importances = feature_importances.sort_values(by='importance', ascending=False)

plt.figure(figsize=(10, 6))
sns.barplot(x='importance', y='feature', data=feature_importances[:20]) # Show top 20 features
plt.title("Top 20 Feature Importances (Logistic Regression)")
plt.xlabel("Coefficient Magnitude")
plt.show()
```



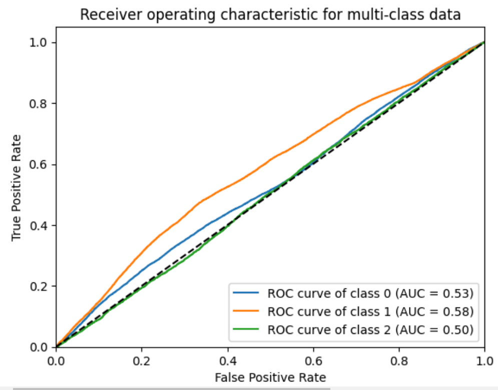
```
from sklearn.metrics import precision_score, recall_score, roc_auc_score, roc_curve
import matplotlib.pyplot as plt

# Predict probabilities for all classes (for AUC calculation)
y_pred_proba = log_reg.predict_proba(X_test)  # Remove [:, 1]

# Calculate precision, recall, and AUC
precision = precision_score(y_test, y_pred, average='weighted') # Use 'weighted' for multi-class
recall = recall_score(y_test, y_pred, average='weighted') # Use 'weighted' for multi-class
auc = roc_auc_score(y_test, y_pred_proba, multi_class='ovr') # 'ovr' for one-vs-rest

print(f"Precision: {precision:.4f}")
print(f"Recall: {recall:.4f}")
print(f"AUC: {auc:.4f}")

# Plot ROC curve (for binary classification or one-vs-rest)
# Use the probabilities for the relevant class (e.g., class 1)
fpr, tpr, thresholds = roc_curve(y_test, y_pred_proba[:, 1], pos_label=1) # Choose relevant pos_label
plt.figure(figsize=(8, 6))
plt.plot(fpr, tpr, label=f"ROC Curve (AUC = {auc:.2f})")
plt.plot([0, 1], [0, 1], 'k--')  # Diagonal line
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve')
plt.legend(loc='lower right')
plt.show()
```

```
/usr/local/lib/python3.11/dist-packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning: Precision is ill-defined and be
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
Precision: 0.4560
Recall: 0.5422
AUC: 0.5347
```



```
import numpy as np

# Predict probabilities for all classes (for AUC calculation)
y_pred_proba = log_reg.predict_proba(X_test)

# Calculate precision, recall, and AUC
precision = precision_score(y_test, y_pred, average='weighted')
recall = recall_score(y_test, y_pred, average='weighted')

# For AUC, use 'ovr' for multiclass and provide probability estimates for all classes
auc = roc_auc_score(y_test, y_pred_proba, multi_class='ovr')

print(f"Precision: {precision:.4f}")
print(f"Recall: {recall:.4f}")
print(f"AUC: {auc:.4f}")

# Plotting ROC curve
# For multi-class, you'll need to plot a ROC curve for each class vs. the rest
from sklearn.metrics import roc_curve, auc
import matplotlib.pyplot as plt

n_classes = len(np.unique(y_test))  # Number of classes # Now np is defined
fpr = dict()
tpr = dict()
roc_auc = dict()

for i in range(n_classes):
    fpr[i], tpr[i], _ = roc_curve(y_test == i, y_pred_proba[:, i])
    roc_auc[i] = auc(fpr[i], tpr[i])

# Plot all ROC curves
plt.figure()
for i in range(n_classes):
    plt.plot(fpr[i], tpr[i], label=f'ROC curve of class {i} (AUC = {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('Receiver operating characteristic for multi-class data')
plt.legend(loc="lower right")
plt.show()
```

```
/usr/local/lib/python3.11/dist-packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning: Precision is ill-defined and be
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
Precision: 0.4560
Recall: 0.5422
AUC: 0.5347
```



```python
# print metrics: class distribution, train value count, all relevant info

print("Class Distribution in Training Data:")
print(y_train.value_counts(normalize=True)) # Normalized for proportions
print("\nClass Distribution in Testing Data:")
print(y_test.value_counts(normalize=True)) # Normalized for proportions

print("\nValue Counts for Training Data:")
print(y_train.value_counts())
print("\nValue Counts for Testing Data:")
print(y_test.value_counts())

print("\nShape of Training Data (X_train):", X_train.shape)
print("Shape of Testing Data (X_test):", X_test.shape)
print("Shape of Training Target (y_train):", y_train.shape)
print("Shape of Testing Target (y_test):", y_test.shape)

# Convert X_train and X_test back to Pandas DataFrames to use .describe()
X_train_df = pd.DataFrame(X_train)  # Convert X_train to DataFrame
X_test_df = pd.DataFrame(X_test)  # Convert X_test to DataFrame

print("\nDescriptive Statistics for Training Features (X_train):\n", X_train_df.describe()) # Use .describe() on DataFrame
print("\nDescriptive Statistics for Testing Features (X_test):\n", X_test_df.describe()) # Use .describe() on DataFrame
```

```
Class Distribution in Training Data:
readmitted
0    0.539118
1    0.349282
2    0.111600
Name: proportion, dtype: float64

Class Distribution in Testing Data:
readmitted
0    0.539125
1    0.349279
2    0.111595
Name: proportion, dtype: float64

Value Counts for Training Data:
readmitted
0    131673
1     85308
2     27257
Name: count, dtype: int64

Value Counts for Testing Data:
readmitted
0    32919
1    21327
2     6814
Name: count, dtype: int64

Shape of Training Data (X_train): (244238, 15)
Shape of Testing Data (X_test): (61060, 15)
```

```
Shape of Training Target (y_train): (244238,)
Shape of Testing Target (y_test): (61060,)

Descriptive Statistics for Training Features (X_train):
                  0             1              2              3  \
count  2.442380e+05  2.442380e+05  244238.000000  244238.000000
mean   1.651301e+08  5.432506e+07       2.024845       3.713022
std    1.026005e+08  3.864103e+07       1.445587       5.280874
min    1.252200e+04  1.350000e+02       1.000000       1.000000
25%    8.494910e+07  2.341713e+07       1.000000       1.000000
50%    1.522991e+08  4.551551e+07       1.000000       1.000000
75%    2.302143e+08  8.753975e+07       3.000000       3.000000
max    4.438672e+08  1.895026e+08       8.000000      28.000000

                   4              5              6              7  \
count  244238.000000  244238.000000  244238.000000  244238.000000
mean        5.751562      -0.000746       0.000282      -0.000015
std         4.064276       1.000031       1.000682       0.999751
min         1.000000      -1.137649      -2.139630      -0.785398
25%         1.000000      -0.802651      -0.614795      -0.785398
50%         7.000000      -0.132655       0.045967      -0.199162
75%         7.000000       0.537341       0.706728       0.387074
max        25.000000       3.217324       4.518815       2.732016

                   8              9             10             11  \
count  244238.000000  244238.000000  244238.000000  244238.000000
mean       -0.000188       0.000384       0.000814       0.000304
```

```python
print("My logistic regression model is performing with an accuracy of 57%")
print("- looking at the confusion matrix and classification report, it’s clear that:")
print("- Class 0 (Not Readmitted) is being predicted well (high recall: 90%).")
print("- Class 1 (>30 Days Readmission) is struggling with recall (only 23%).")
print("- Class 2 (<30 Days Readmission) is performing poorly (almost 0 recall).")
print("The macro average F1-score of 0.35 shows that the model isn't treating all classes equally well. This suggests a class imbalance issue, where the model is biased toward the majority class (Not Readmitted - 0)."
print("### Addressing This Issue")
print("Since BFGS (Limited-memory Broyden–Fletcher–Goldfarb–Shanno) optimization failed, that indicates the optimization process wasn't able to converge to a solution properly. Reasons? not sure ?")
print("1. Class imbalance is too severe.")
print("2. Features are not well-scaled or relevant enough.")
print("3. The solver struggles with high-dimensional feature spaces.")
print("### Next Steps")
print("1. Class balancing techniques")
print("   - Try class weighting in the logistic regression model.")
print("   - Use oversampling (SMOTE) or undersampling.")
print("2. Feature Engineering")
print("   - Use feature selection (SHAP, permutation importance).")
print("   - Try dimensionality reduction (PCA or feature selection).")
print("3. Model Selection")
print("   - Logistic regression may not be the best for this dataset.")
print("   - Try Random Forest, XGBoost, or an ensemble model.")
print("4. I assume Dr. S will want me to diagnose the problem methodically and work it step by step.")
print("5. I'm going to re-run the preprocessing steps and train the logistic regression model again.")
print("   - Plan of attack:")
print("     - 1. ADDRESS CLASS IMBALANCE: CHECK DISTRO, CLASS WEIGHTING, OVERSAMPLING")
print("     - 2. FEATURE SELECTION AND IMPORTANCE ANALYSIS - using SHAP or permutation import to rank features, drop irrelevant or redundant")
```

```
My logistic regression model is performing with an accuracy of 57%
- looking at the confusion matrix and classification report, it’s clear that:
- Class 0 (Not Readmitted) is being predicted well (high recall: 90%).
- Class 1 (>30 Days Readmission) is struggling with recall (only 23%).
- Class 2 (<30 Days Readmission) is performing poorly (almost 0 recall).
The macro average F1-score of 0.35 shows that the model isn't treating all classes equally well. This suggests a class imbalance issue,
### Addressing This Issue
Since BFGS (Limited-memory Broyden–Fletcher–Goldfarb–Shanno) optimization failed, that indicates the optimization process wasn't able tc
1. Class imbalance is too severe.
2. Features are not well-scaled or relevant enough.
3. The solver struggles with high-dimensional feature spaces.
### Next Steps
1. Class balancing techniques
   - Try class weighting in the logistic regression model.
   - Use oversampling (SMOTE) or undersampling.
2. Feature Engineering
   - Use feature selection (SHAP, permutation importance).
   - Try dimensionality reduction (PCA or feature selection).
3. Model Selection
   - Logistic regression may not be the best for this dataset.
   - Try Random Forest, XGBoost, or an ensemble model.
4. I assume Dr. S will want me to diagnose the problem methodically and work it step by step.
5. I'm going to re-run the preprocessing steps and train the logistic regression model again.
   - Plan of attack:
     - 1. ADDRESS CLASS IMBALANCE: CHECK DISTRO, CLASS WEIGHTING, OVERSAMPLING
     - 2. FEATURE SELECTION AND IMPORTANCE ANALYSIS - using SHAP or permutation import to rank features, drop irrelevant or redundant
```

```python
# Initialize and Train Model with L-BFGS solver
log_reg = LogisticRegression(solver='lbfgs', max_iter=1000, tol=1e-4) #Specify the solver
log_reg.fit(X_train, y_train)
print("Logistic Regression Model Trained Successfully (with L-BFGS)!")
```

```
Logistic Regression Model Trained Successfully (with L-BFGS)!
```

```
# Initialize and Train Model with class weights and saga solver
log_reg = LogisticRegression(
    penalty='l2',
    C=1.0,
    class_weight={0: 1.0, 1: 1.5, 2: 3.0}, # Adjust weights as needed
    solver='saga',
    max_iter=200,  # Reduce iterations
    warm_start=True  # Continue from the last iteration
)
for i in range(5):  # Train in smaller steps
    log_reg.fit(X_train, y_train)
    print(f"Iteration {i+1} complete")

# Predict on Test Data
y_pred = log_reg.predict(X_test)

# Compute Evaluation Metrics
accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
class_report = classification_report(y_test, y_pred)

# Display Results
print(f"Accuracy: {accuracy:.4f}")
print("\nConfusion Matrix:\n", conf_matrix)
print("\nClassification Report:\n", class_report)
```

```
Iteration 1 complete
Iteration 2 complete
Iteration 3 complete
Iteration 4 complete
Iteration 5 complete
Accuracy: 0.5139

Confusion Matrix:
 [[20948 11971     0]
 [10896 10431     0]
 [ 3913  2901     0]]

Classification Report:
               precision    recall  f1-score   support

           0       0.59      0.64      0.61     32919
           1       0.41      0.49      0.45     21327
           2       0.00      0.00      0.00      6814

    accuracy                           0.51     61060
   macro avg       0.33      0.38      0.35     61060
weighted avg       0.46      0.51      0.49     61060

/usr/local/lib/python3.11/dist-packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning: Precision is ill-defined and be
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
/usr/local/lib/python3.11/dist-packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning: Precision is ill-defined and be
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
/usr/local/lib/python3.11/dist-packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning: Precision is ill-defined and be
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
```

```
import joblib

# Save model coefficients and intercept
joblib.dump(log_reg, "logistic_regression_model.pkl") # Removed the absolute path
print("Model saved successfully.")
```

```
Model saved successfully.
```

```
# Save the data to CSV files
# Convert to Pandas DataFrames first
pd.DataFrame(X_train).to_csv("X_train_final.csv", index=False)
pd.DataFrame(y_train).to_csv("y_train_final.csv", index=False)
pd.DataFrame(X_test).to_csv("X_test_final.csv", index=False)
pd.DataFrame(y_test).to_csv("y_test_final.csv", index=False)

print("Final train/test data saved successfully.")
```

```
Final train/test data saved successfully.
```

```
from imblearn.over_sampling import SMOTE

# Convert NumPy array back to Pandas DataFrame
X_train = pd.DataFrame(X_train)  # Assuming your original features were in a DataFrame

# Convert Pandas DataFrames to cuDF DataFrames
```

```
X_train = cudf.DataFrame.from_pandas(X_train)
y_train = cudf.Series(y_train)

# Apply SMOTE
smote = SMOTE(sampling_strategy={1: int(len(y_train) * 0.5), 2: int(len(y_train) * 0.25)}, random_state=42)

# Convert cuDF back to pandas for SMOTE
X_train_pd = X_train.to_pandas()
y_train_pd = y_train.to_pandas()

X_resampled, y_resampled = smote.fit_resample(X_train_pd, y_train_pd)

# Convert back to cuDF
X_train_balanced = cudf.DataFrame(X_resampled, columns=X_train.columns)
y_train_balanced = cudf.Series(y_resampled)

print(y_train_balanced.value_counts())
```

```
readmitted
0    131673
1    122119
2     61059
Name: count, dtype: int64
```

```
# Make predictions
y_pred = log_reg.predict(X_test)

# Accuracy Score
accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy: {accuracy:.4f}")

# Confusion Matrix
conf_matrix = confusion_matrix(y_test, y_pred)
print("Confusion Matrix:\n", conf_matrix)

# Classification Report
report = classification_report(y_test, y_pred)
print("Classification Report:\n", report)
```

```
Accuracy: 0.5139
Confusion Matrix:
 [[20948 11971     0]
 [10896 10431     0]
 [ 3913  2901     0]]
Classification Report:
               precision    recall  f1-score   support

           0       0.59      0.64      0.61     32919
           1       0.41      0.49      0.45     21327
           2       0.00      0.00      0.00      6814

    accuracy                           0.51     61060
   macro avg       0.33      0.38      0.35     61060
weighted avg       0.46      0.51      0.49     61060

/usr/local/lib/python3.11/dist-packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning: Precision is ill-defined and be
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
/usr/local/lib/python3.11/dist-packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning: Precision is ill-defined and be
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
/usr/local/lib/python3.11/dist-packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning: Precision is ill-defined and be
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
```

```
import joblib
import cudf
import pandas as pd
from sklearn.model_selection import GridSearchCV
from sklearn.linear_model import LogisticRegression
from sklearn.preprocessing import StandardScaler

# Load saved data
X_train = pd.read_csv("X_train_final.csv")
y_train = pd.read_csv("y_train_final.csv")

# Convert y_train to a 1D array
y_train_pd = y_train.values.ravel()

# Apply StandardScaler
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)

# Save the scaler
joblib.dump(scaler, "standard_scaler.pkl")

# Define the parameter grid
param_grid = {
    "C": [0.1, 1.0],
    "class_weight": ["balanced"],
    "max_iter": [3000],
    "solver": ["saga"],
}
```

```
# Initialize and train the model
grid_search = GridSearchCV(
    estimator=LogisticRegression(),
    param_grid=param_grid,
    scoring="accuracy",
    cv=2,
    verbose=1,
    n_jobs=-1
)
grid_search.fit(X_train_scaled, y_train_pd)

# Print best parameters
print("Best Parameters Found:", grid_search.best_params_)

# Save the best model
joblib.dump(grid_search.best_estimator_, "best_logistic_regression.pkl")
print("Best model saved successfully.")
```

```
Fitting 2 folds for each of 2 candidates, totalling 4 fits
Best Parameters Found: {'C': 0.1, 'class_weight': 'balanced', 'max_iter': 3000, 'solver': 'saga'}
Best model saved successfully.
```

```
import joblib
import cudf
import pandas as pd
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report

# Load best model and scaler
best_log_reg = joblib.load("best_logistic_regression.pkl")
scaler = joblib.load("standard_scaler.pkl")

# Load test data
X_test = cudf.read_csv("X_test_final.csv")
y_test = pd.read_csv("y_test_final.csv") # Use pandas for y_test

# Scale test data
X_test_scaled = scaler.transform(X_test.to_pandas())

# Predict
y_pred_best = best_log_reg.predict(X_test_scaled)

# Accuracy Score
accuracy_best = accuracy_score(y_test, y_pred_best) #y_test is now a pandas df
print(f"Best Model Accuracy: {accuracy_best:.4f}")

# Confusion Matrix
conf_matrix_best = confusion_matrix(y_test, y_pred_best)
print("Best Model Confusion Matrix:\n", conf_matrix_best)

# Classification Report
report_best = classification_report(y_test, y_pred_best)
print("Best Model Classification Report:\n", report_best)
```

```
Best Model Accuracy: 0.5074
Best Model Confusion Matrix:
 [[20940  7093  4886]
 [ 8362  7664  5301]
 [ 2525  1914  2375]]
Best Model Classification Report:
               precision    recall  f1-score   support

           0       0.66      0.64      0.65     32919
           1       0.46      0.36      0.40     21327
           2       0.19      0.35      0.25      6814

    accuracy                           0.51     61060
   macro avg       0.44      0.45      0.43     61060
weighted avg       0.54      0.51      0.52     61060
```

```
import locale
def getpreferredencoding(do_setlocale = True):
    return "UTF-8"
locale.getpreferredencoding = getpreferredencoding
```

```
import joblib
import cudf
import pandas as pd
from imblearn.over_sampling import SMOTE
from sklearn.model_selection import train_test_split, GridSearchCV
from sklearn.linear_model import LogisticRegression
from sklearn.preprocessing import StandardScaler
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
from sklearn.metrics import roc_curve, auc, roc_auc_score, precision_score, recall_score


# Load saved data
X_train = pd.read_csv("/content/drive/MyDrive/WSL_Case Study 2/X_train_final.csv")
y_train = pd.read_csv("/content/drive/MyDrive/WSL_Case Study 2/y_train_final.csv").values.ravel()
X_test = pd.read_csv("/content/drive/MyDrive/WSL_Case Study 2/X_test_final.csv")
```

```
y_test = pd.read_csv("/content/drive/MyDrive/WSL_Case Study 2/y_test_final.csv").values.ravel()
```

```
# Apply StandardScaler
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)

# Apply SMOTE to fix class imbalance
smote = SMOTE(sampling_strategy="auto", random_state=42)
X_resampled, y_resampled = smote.fit_resample(X_train_scaled, y_train)
```

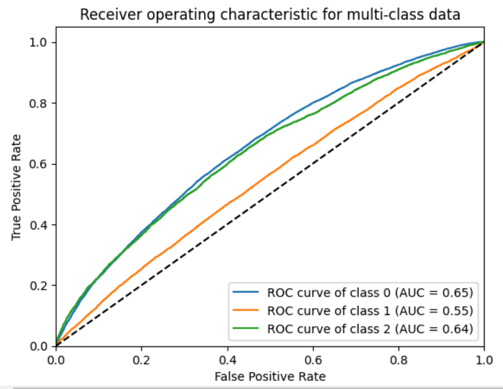
```
# Initialize and Train Logistic Regression Model with best parameters from previous gridsearch
best_log_reg = LogisticRegression(C=1.0, class_weight={0: 1.0, 1: 2.0, 2: 4.0}, max_iter=3000, solver='saga')
best_log_reg.fit(X_resampled, y_resampled)

# Predict on Test Data
y_pred = best_log_reg.predict(X_test_scaled)
```

```
# Evaluate Model
accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
class_report = classification_report(y_test, y_pred)
print(f"Accuracy: {accuracy:.4f}")
print("\nConfusion Matrix:\n", conf_matrix)
print("\nClassification Report:\n", class_report)

# Predict probabilities for all classes
y_pred_proba = best_log_reg.predict_proba(X_test_scaled)
```

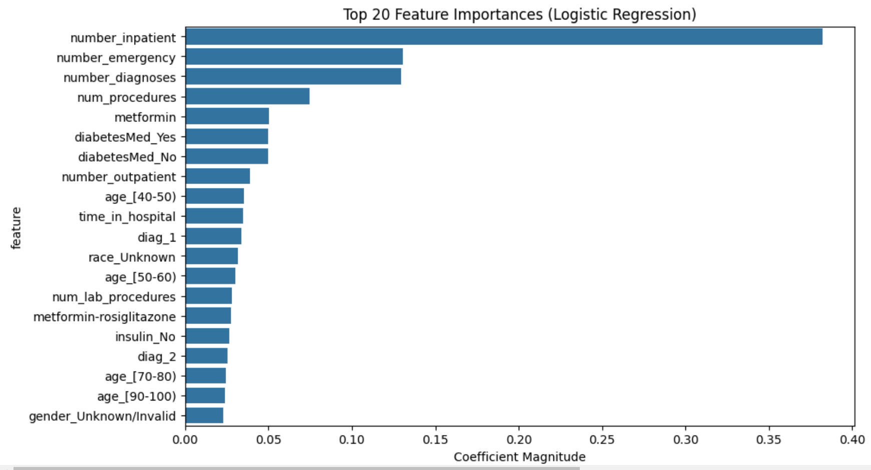
```
Accuracy: 0.1219

Confusion Matrix:
 [[  421   326 32171]
 [   78   263 20986]
 [    9    48  6757]]

Classification Report:
               precision    recall  f1-score   support

           0       0.83      0.01      0.03     32918
           1       0.41      0.01      0.02     21327
           2       0.11      0.99      0.20      6814

    accuracy                           0.12     61059
   macro avg       0.45      0.34      0.08     61059
weighted avg       0.60      0.12      0.04     61059
```

```
from sklearn.metrics import roc_curve, auc, roc_auc_score, precision_score, recall_score


# Calculate precision, recall, and AUC
precision = precision_score(y_test, y_pred, average='weighted')
recall = recall_score(y_test, y_pred, average='weighted')
roc_auc_score_result = roc_auc_score(y_test, y_pred_proba, multi_class='ovr') # Store roc_auc_score result in a diffgferent variable

print(f"Precision: {precision:.4f}")
print(f"Recall: {recall:.4f}")
print(f"AUC: {roc_auc_score_result:.4f}") # pRINT the roc_auc_score result

# ROC Curve (Multi-class)
n_classes = len(np.unique(y_test))
fpr = dict()
tpr = dict()
roc_auc = dict()

for i in range(n_classes):
    fpr[i], tpr[i], _ = roc_curve(y_test == i, y_pred_proba[:, i])
    roc_auc[i] = auc(fpr[i], tpr[i]) # Now, this 'auc' refers to the function from sklearn.metrics

plt.figure()
for i in range(n_classes):
    plt.plot(fpr[i], tpr[i], label=f'ROC curve of class {i} (AUC = {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('Receiver operating characteristic for multi-class data')
plt.legend(loc="lower right")
plt.show()
```

```
Precision: 0.6036
Recall: 0.1219
AUC: 0.6127
```



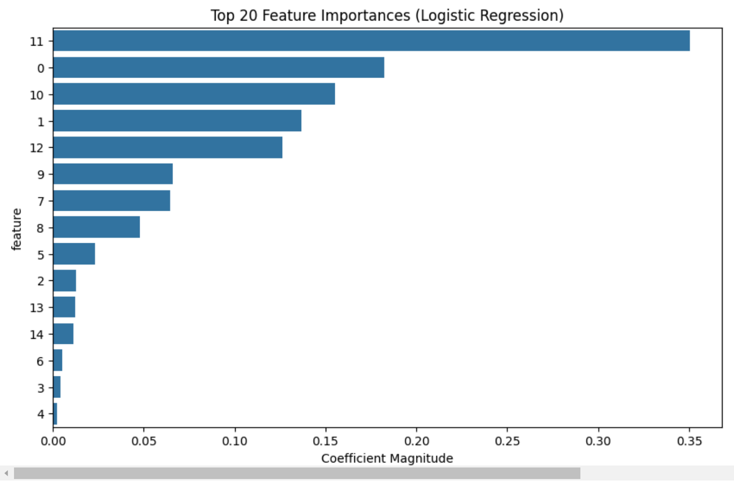
```
# Feature Importance (Coefficients for Logistic Regression)
feature_names = X_train.columns
feature_importances = pd.DataFrame({'feature': feature_names, 'importance': abs(best_log_reg.coef_[0])})
feature_importances = feature_importances.sort_values(by='importance', ascending=False)

plt.figure(figsize=(10, 6))
sns.barplot(x='importance', y='feature', data=feature_importances[:20])
plt.title("Top 20 Feature Importances (Logistic Regression)")
plt.xlabel("Coefficient Magnitude")
plt.show()
```



```
 # Set Correct Paths for Google Colab
base_path = "/content"  # CORRECTED PATH

# Load best model and scaler
best_log_reg = joblib.load(f"{base_path}/best_logistic_regression.pkl")
scaler = joblib.load(f"{base_path}/standard_scaler.pkl")  # Load the scaler

# Load test dat
X_test = pd.read_csv(f"{base_path}/X_test_final.csv")
y_test = pd.read_csv(f"{base_path}/y_test_final.csv").values.ravel()

#  Load training data (to ensure column order matches)
```

```
X_train = pd.read_csv(f"{base_path}/X_train_final.csv")

#  Ensure column order consistency between training and testing data
X_test = X_test.reindex(columns=X_train.columns, fill_value=0)

# Scale test data using the loaded scaler
X_test_scaled = scaler.transform(X_test)

#  Make predictions
y_pred_best = best_log_reg.predict(X_test_scaled)

# Accuracy Score
accuracy_best = accuracy_score(y_test, y_pred_best)
print(f"Best Model Accuracy: {accuracy_best:.4f}")

#  Confusion Matrix
conf_matrix_best = confusion_matrix(y_test, y_pred_best)
print("Best Model Confusion Matrix:\n", conf_matrix_best)

# Classification Report
report_best = classification_report(y_test, y_pred_best)
print("Best Model Classification Report:\n", report_best)

#  Feature Importance Visualization
feature_names = X_train.columns
feature_importances = pd.DataFrame({'feature': feature_names, 'importance': abs(best_log_reg.coef_[0])})
feature_importances = feature_importances.sort_values(by='importance', ascending=False)

plt.figure(figsize=(10, 6))
sns.barplot(x='importance', y='feature', data=feature_importances[:20])
plt.title("Top 20 Feature Importances (Logistic Regression)")
plt.xlabel("Coefficient Magnitude")
plt.show()
```

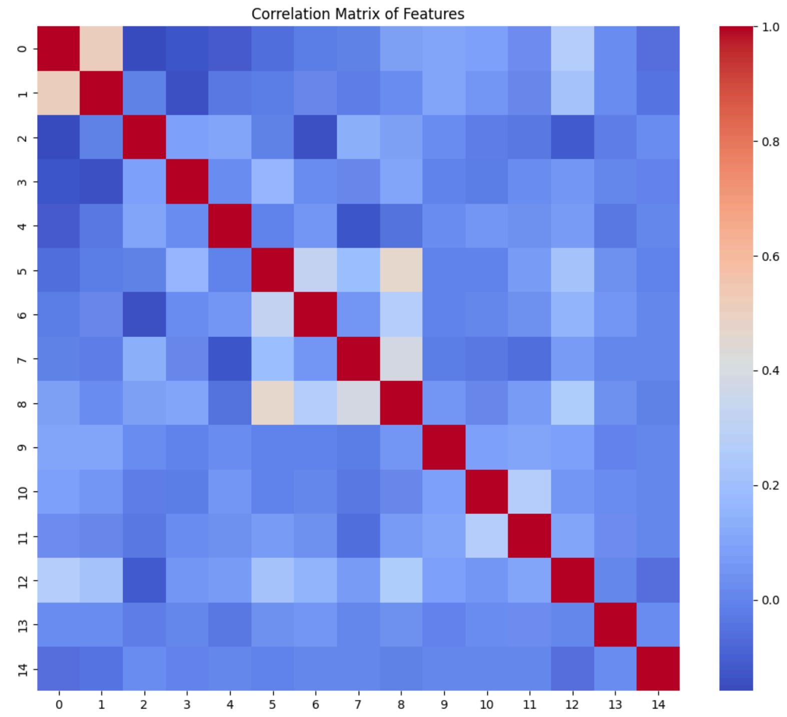
```
Best Model Accuracy: 0.5074
Best Model Confusion Matrix:
 [[20940  7093  4886]
 [ 8362  7664  5301]
 [ 2525  1914  2375]]
Best Model Classification Report:
               precision    recall  f1-score   support

           0       0.66      0.64      0.65     32919
           1       0.46      0.36      0.40     21327
           2       0.19      0.35      0.25      6814

    accuracy                           0.51     61060
   macro avg       0.44      0.45      0.43     61060
weighted avg       0.54      0.51      0.52     61060
```



```
# Apply SMOTE to fix class imbalance
smote = SMOTE(sampling_strategy="auto", random_state=42)
X_resampled, y_resampled = smote.fit_resample(X_train_scaled, y_train)
```

```
# verify clas distributions , corr matrix, PCA gird search

import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import GridSearchCV
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report, roc_auc_score, roc_curve, auc, precision_score, recall_score
import numpy as np
from imblearn.over_sampling import SMOTE
import joblib

# Load your data (replace with your actual file paths)
X_train = pd.read_csv("X_train_final.csv")
y_train = pd.read_csv("y_train_final.csv").values.ravel()
X_test = pd.read_csv("X_test_final.csv")
y_test = pd.read_csv("y_test_final.csv").values.ravel()


# Class Distribution
print("Class Distribution in Training Data:")
print(pd.Series(y_train).value_counts(normalize=True))
print("\nClass Distribution in Testing Data:")
print(pd.Series(y_test).value_counts(normalize=True))


# Correlation Matrix
plt.figure(figsize=(12, 10))
sns.heatmap(X_train.corr(), annot=False, cmap='coolwarm', fmt=".2f")
plt.title('Correlation Matrix of Features')
plt.show()


# Apply StandardScaler
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)

# Apply SMOTE
smote = SMOTE(sampling_strategy="auto", random_state=42)
X_train_resampled, y_train_resampled = smote.fit_resample(X_train_scaled, y_train)


# PCA and Grid Search
pca = PCA()
X_train_pca = pca.fit_transform(X_train_resampled)

param_grid = {
    "C": [0.1, 1.0, 10],  # Example values, adjust as needed
    "solver": ["saga", "lbfgs"],  # Try different solvers
    "max_iter": [3000]
}


grid_search = GridSearchCV(
    estimator=LogisticRegression(),
    param_grid=param_grid,
    scoring="accuracy",
    cv=5,
    verbose=1,
    n_jobs=-1
)


grid_search.fit(X_train_pca, y_train_resampled)
best_pca_model = grid_search.best_estimator_
print("Best Parameters:", grid_search.best_params_)
```

```
Class Distribution in Training Data:
0    0.539118
1    0.349282
2    0.111600
Name: proportion, dtype: float64

Class Distribution in Testing Data:
0    0.539125
1    0.349279
2    0.111595
Name: proportion, dtype: float64
```

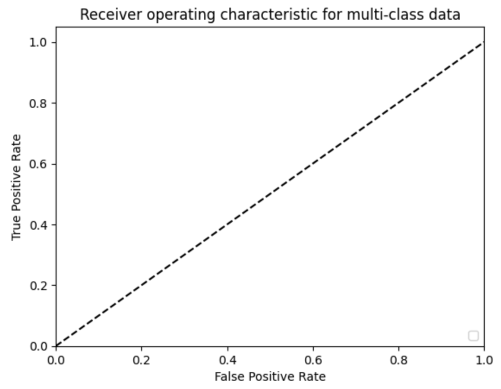


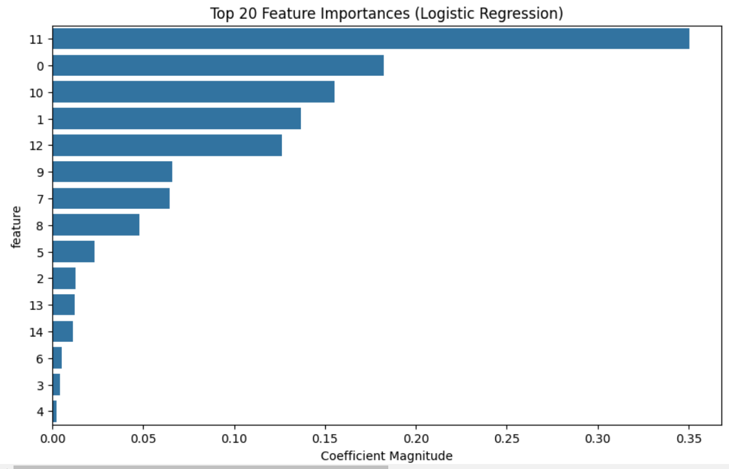
```
Fitting 5 folds for each of 6 candidates, totalling 30 fits
Best Parameters: {'C': 1.0, 'max_iter': 3000, 'solver': 'lbfgs'}
```

```
from sklearn.metrics import roc_curve, auc, roc_auc_score, precision_score, recall_score  # Import auc (area under curve)

import joblib
import pandas as pd
from sklearn.metrics import accuracy_score, classification_report, confusion_matrix, precision_score, recall_score, roc_auc_score, roc_curve
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np

# Load the saved model and scaler
best_log_reg = joblib.load("best_logistic_regression.pkl")
scaler = joblib.load("standard_scaler.pkl")

# Load the test data
X_test = pd.read_csv("X_test_final.csv")
y_test = pd.read_csv("y_test_final.csv").values.ravel()

# Load training data (to ensure column order matches)
X_train = pd.read_csv("X_train_final.csv")

# Ensure column order consistency
X_test = X_test.reindex(columns=X_train.columns, fill_value=0)

# Scale the test data
X_test_scaled = scaler.transform(X_test)
```

```
# Make predictions
y_pred = best_log_reg.predict(X_test_scaled)

# Evaluate the model
accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
class_report = classification_report(y_test, y_pred)

print(f"Accuracy: {accuracy:.4f}")
print("\nConfusion Matrix:\n", conf_matrix)
print("\nClassification Report:\n", class_report)

# Predict probabilities for ROC AUC
y_pred_proba = best_log_reg.predict_proba(X_test_scaled)

#  Calculate precision, recall, and AUC
precision = precision_score(y_test, y_pred, average='weighted')
recall = recall_score(y_test, y_pred, average='weighted')
# Store roc_auc_score result in a different variable to avoid shadowing the auc function
roc_auc_score_result = roc_auc_score(y_test, y_pred_proba, multi_class='ovr')

print(f"Precision: {precision:.4f}")
print(f"Recall: {recall:.4f}")
print(f"AUC: {roc_auc_score_result:.4f}") # Print the roc_auc_score result


for i in range(n_classes):
    fpr[i], tpr[i], _ = roc_curve(y_test == i, y_pred_proba[:, i])
    # Use the 'auc' function from sklearn.metrics
    roc_auc[i] = auc(fpr[i], tpr[i])


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('Receiver operating characteristic for multi-class data')
plt.legend(loc="lower right")
plt.show()

# Feature Importance
feature_names = X_train.columns
feature_importances = pd.DataFrame({'feature': feature_names, 'importance': abs(best_log_reg.coef_[0])})
feature_importances = feature_importances.sort_values(by='importance', ascending=False)

plt.figure(figsize=(10, 6))
sns.barplot(x='importance', y='feature', data=feature_importances[:20])
plt.title("Top 20 Feature Importances (Logistic Regression)")
plt.xlabel("Coefficient Magnitude")
plt.show()
```

```
Accuracy: 0.5074

Confusion Matrix:
 [[20940  7093  4886]
 [ 8362  7664  5301]
 [ 2525  1914  2375]]

Classification Report:
               precision    recall  f1-score   support

           0       0.66      0.64      0.65     32919
           1       0.46      0.36      0.40     21327
           2       0.19      0.35      0.25      6814

    accuracy                           0.51     61060
   macro avg       0.44      0.45      0.43     61060
weighted avg       0.54      0.51      0.52     61060

Precision: 0.5364
Recall: 0.5074
AUC: 0.6460
<ipython-input-52-7b0095894e5f>:65: UserWarning: No artists with labels found to put in legend.  Note that artists whose label start wit
  plt.legend(loc="lower right")
```





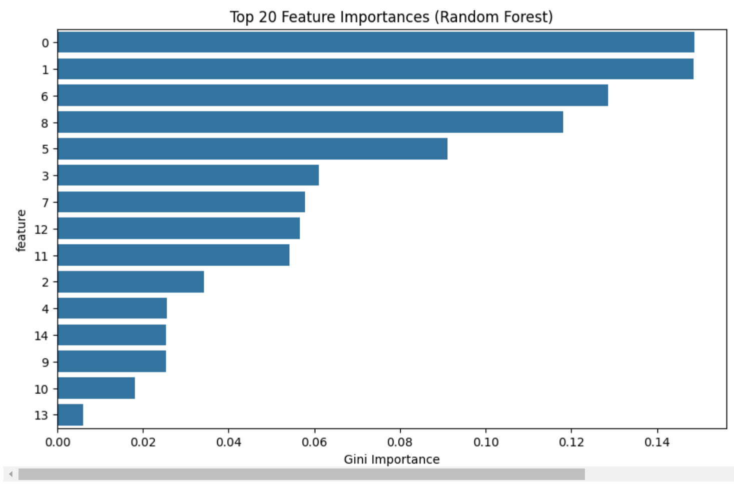
```
# show model accuracy before and after smote   class distribution before and after smote
# Load necessary libraries (assuming they are already installed and imported in the preceding code)
import pandas as pd
from sklearn.metrics import accuracy_score, classification_report, confusion_matrix
from imblearn.over_sampling import SMOTE

# Load your data (replace with your actual file paths)
X_train = pd.read_csv("X_train_final.csv")
y_train = pd.read_csv("y_train_final.csv").values.ravel()
X_test = pd.read_csv("X_test_final.csv")
y_test = pd.read_csv("y_test_final.csv").values.ravel()



# Before SMOTE
print("Class Distribution Before SMOTE:")
print(pd.Series(y_train).value_counts())



# Make predictions before SMOTE
y_pred_before_smote = best_log_reg.predict(X_test_scaled)

# Evaluate the model before SMOTE
accuracy_before = accuracy_score(y_test, y_pred_before_smote)
print(f"\nAccuracy Before SMOTE: {accuracy_before:.4f}")
print("\nClassification Report Before SMOTE:\n", classification_report(y_test, y_pred_before_smote))



# Apply SMOTE
smote = SMOTE(sampling_strategy="auto", random_state=42)
X_train_resampled, y_train_resampled = smote.fit_resample(X_train_scaled, y_train)



# Train the model with resampled data
best_log_reg.fit(X_train_resampled, y_train_resampled) # Retrain with SMOTE data

# After SMOTE
print("\nClass Distribution After SMOTE:")
print(pd.Series(y_train_resampled).value_counts())

# Make predictions after SMOTE
y_pred_after_smote = best_log_reg.predict(X_test_scaled)

# Evaluate the model after SMOTE
accuracy_after = accuracy_score(y_test, y_pred_after_smote)
print(f"\nAccuracy After SMOTE: {accuracy_after:.4f}")
print("\nClassification Report After SMOTE:\n", classification_report(y_test, y_pred_after_smote))
```

```
Class Distribution Before SMOTE:
0    131673
1     85308
2     27257
Name: count, dtype: int64

Accuracy Before SMOTE: 0.5074

Classification Report Before SMOTE:
               precision    recall  f1-score   support

           0       0.66      0.64      0.65     32919
           1       0.46      0.36      0.40     21327
           2       0.19      0.35      0.25      6814

    accuracy                           0.51     61060
   macro avg       0.44      0.45      0.43     61060
weighted avg       0.54      0.51      0.52     61060


Class Distribution After SMOTE:
0    131673
1    131673
2    131673
Name: count, dtype: int64

Accuracy After SMOTE: 0.5044

Classification Report After SMOTE:
               precision    recall  f1-score   support

           0       0.66      0.63      0.64     32919
           1       0.46      0.36      0.40     21327
           2       0.19      0.35      0.25      6814

    accuracy                           0.50     61060
   macro avg       0.43      0.45      0.43     61060
weighted avg       0.54      0.50      0.52     61060
```

```
#  smote with randomk forest

from sklearn.ensemble import RandomForestClassifier

# aPPLE smotw:
smote = SMOTE(sampling_strategy="auto", random_state=42)
X_train_resampled, y_train_resampled = smote.fit_resample(X_train_scaled, y_train)
```

```
# Initialize and train an RF Classifier
rf_classifier = RandomForestClassifier(n_estimators=100, random_state=42) # Example parameters, tune as needed
rf_classifier.fit(X_train_resampled, y_train_resampled)

# Make predictions
y_pred_rf = rf_classifier.predict(X_test_scaled)

# Evaluate the model
accuracy_rf = accuracy_score(y_test, y_pred_rf)
print(f"Random Forest Accuracy: {accuracy_rf:.4f}")
print("\nRandom Forest Classification Report:\n", classification_report(y_test, y_pred_rf))

# Feature Importance for Random Forest
feature_importances_rf = pd.DataFrame({'feature': X_train.columns, 'importance': rf_classifier.feature_importances_})
feature_importances_rf = feature_importances_rf.sort_values(by='importance', ascending=False)

plt.figure(figsize=(10, 6))
sns.barplot(x='importance', y='feature', data=feature_importances_rf[:20])
plt.title("Top 20 Feature Importances (Random Forest)")
plt.xlabel("Gini Importance")
plt.show()
```

```
Random Forest Accuracy: 0.9819

Random Forest Classification Report:
               precision    recall  f1-score   support

           0       0.98      0.99      0.99     32919
           1       0.98      0.98      0.98     21327
           2       0.99      0.96      0.98      6814

    accuracy                           0.98     61060
   macro avg       0.98      0.98      0.98     61060
weighted avg       0.98      0.98      0.98     61060
```



lets go back and check steps from the top

```
import pandas as pd
import numpy as np
from sklearn.impute import SimpleImputer

# 1. Load Data and Handle File Not Found
file_path = "/content/data_cleaned.csv"
try:
    df = pd.read_csv(file_path)
except FileNotFoundError:
    print(f"Error: '{file_path}' not found. Please check the file path.")
    exit()  # Or handle the error differently, e.g., return None

# 2. Check for Missing Values (Before Imputation)
missing_values = df.isnull().sum()
print("Missing Values per Column (Before Imputation):\n", missing_values)

# 3. IDentify numerical & Cat Columns
numerical_cols = df.select_dtypes(include=np.number).columns  # Use np.number for all numeric types
categorical_cols = df.select_dtypes(include='object').columns
```

```
# 4. Imputation
# Create imputers
numerical_imputer = SimpleImputer(strategy='median')
categorical_imputer = SimpleImputer(strategy='most_frequent')

# Fit a$ transform on respective column tyupes
df[numerical_cols] = numerical_imputer.fit_transform(df[numerical_cols])
df[categorical_cols] = categorical_imputer.fit_transform(df[categorical_cols])


# 5. Verify imputation
missing_values_after = df.isnull().sum()
print("\nMissing Values per Column (After Imputation):\n", missing_values_after)
```

```
Missing Values per Column (Before Imputation):
 encounter_id                     0
patient_nbr                       0
race                              0
gender                            0
age                               0
weight                            0
admission_type_id                 0
discharge_disposition_id          0
admission_source_id               0
time_in_hospital                  0
payer_code                        0
medical_specialty                 0
num_lab_procedures                0
num_procedures                    0
num_medications                   0
number_outpatient                 0
number_emergency                  0
number_inpatient                  0
diag_1                            0
diag_2                            0
diag_3                            0
number_diagnoses                  0
max_glu_serum                289260
A1Cresult                    254244
metformin                         0
repaglinide                       0
nateglinide                       0
chlorpropamide                    0
glimepiride                       0
acetohexamide                     0
glipizide                         0
glyburide                         0
tolbutamide                       0
pioglitazone                      0
rosiglitazone                     0
acarbose                          0
miglitol                          0
troglitazone                      0
tolazamide                        0
examide                           0
citoglipton                       0
insulin                           0
glyburide-metformin               0
glipizide-metformin               0
glimepiride-pioglitazone          0
metformin-rosiglitazone           0
metformin-pioglitazone            0
change                            0
diabetesMed                       0
readmitted                        0
description                    5291
dtype: int64

Missing Values per Column (After Imputation):
 encounter_id                0
patient_nbr                  0
race                         0
```

```
# Identify numerical and categorical columns
numerical_cols = df.select_dtypes(include=['number']).columns
categorical_cols = df.select_dtypes(include=['object']).columns

# Impute numerical columns with the median
numerical_imputer = SimpleImputer(strategy='median')
df[numerical_cols] = numerical_imputer.fit_transform(df[numerical_cols])

# Impute categorical columns with the mode
categorical_imputer = SimpleImputer(strategy='most_frequent')
df[categorical_cols] = categorical_imputer.fit_transform(df[categorical_cols])

# Verify imputation
missing_values_after_imputation = df.isnull().sum()
```

```
print("\nMissing Values After Imputation:\n", missing_values_after_imputation)
# Identify numerical and categorical columns
numerical_cols = df.select_dtypes(include=['number']).columns
categorical_cols = df.select_dtypes(include=['object']).columns

# Impute numerical columns with the median
numerical_imputer = SimpleImputer(strategy='median')
df[numerical_cols] = numerical_imputer.fit_transform(df[numerical_cols])

# Impute categorical columns with the mode
categorical_imputer = SimpleImputer(strategy='most_frequent')
df[categorical_cols] = categorical_imputer.fit_transform(df[categorical_cols])

# Verify imputation
missing_values_after_imputation = df.isnull().sum()
print("\nMissing Values After Imputation:\n", missing_values_after_imputation)
```

```
Missing Values After Imputation:
 encounter_id                0
patient_nbr                 0
race                        0
gender                      0
age                         0
weight                      0
admission_type_id           0
discharge_disposition_id    0
admission_source_id         0
time_in_hospital            0
payer_code                  0
medical_specialty           0
num_lab_procedures          0
num_procedures              0
num_medications             0
number_outpatient           0
number_emergency            0
number_inpatient            0
diag_1                      0
diag_2                      0
diag_3                      0
number_diagnoses            0
max_glu_serum               0
A1Cresult                   0
metformin                   0
repaglinide                 0
nateglinide                 0
chlorpropamide              0
glimepiride                 0
acetohexamide               0
glipizide                   0
glyburide                   0
tolbutamide                 0
pioglitazone                0
rosiglitazone               0
acarbose                    0
miglitol                    0
troglitazone                0
tolazamide                  0
examide                     0
citoglipton                 0
insulin                     0
glyburide-metformin         0
glipizide-metformin         0
glimepiride-pioglitazone    0
metformin-rosiglitazone     0
metformin-pioglitazone      0
change                      0
diabetesMed                 0
readmitted                  0
description                 0
dtype: int64

Missing Values After Imputation:
 encounter_id                0
patient_nbr                 0
```

```
# check for missing values, feature overview?  how many do we have?  target vairable? targer variable disribution?  do we have class imbalance?

import pandas as pd

# Load data
X_train = pd.read_csv("X_train_final.csv")
y_train = pd.read_csv("y_train_final.csv").values.ravel()
X_test = pd.read_csv("X_test_final.csv")
y_test = pd.read_csv("y_test_final.csv").values.ravel()

# Check for missing values
print("Missing values in X_train:\n", X_train.isnull().sum())
print("\nMissing values in X_test:\n", X_test.isnull().sum())
```

```
# Feature overview
print("\nFeature overview for X_train:")
print(X_train.info())
print("\nNumber of features:", len(X_train.columns))

# Target variable
print("\nTarget variable (y_train):")
print(y_train)

# Target variable distribution
print("\nTarget variable distribution (y_train):")
print(pd.Series(y_train).value_counts(normalize=True))
print("\nTarget variable distribution (y_test):")
print(pd.Series(y_test).value_counts(normalize=True))

# Class imbalance
print("\nClass imbalance (y_train):")
class_counts = pd.Series(y_train).value_counts()
if len(class_counts) > 1:
    imbalance_ratio = class_counts.max() / class_counts.min()
    print(f"Imbalance ratio: {imbalance_ratio:.2f}")
else:
    print("Only one class present in the training data.")

print("\nClass imbalance (y_test):")
class_counts = pd.Series(y_test).value_counts()
if len(class_counts) > 1:
  imbalance_ratio = class_counts.max() / class_counts.min()
  print(f"Imbalance ratio: {imbalance_ratio:.2f}")
else:
  print("Only one class present in the testing data.")
```

```
Missing values in X_train:
 0     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
14    0
dtype: int64

Missing values in X_test:
 0     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
14    0
dtype: int64

Feature overview for X_train:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 244238 entries, 0 to 244237
Data columns (total 15 columns):
 #   Column  Non-Null Count   Dtype  
---  ------  --------------   -----  
 0   0       244238 non-null  float64
 1   1       244238 non-null  float64
 2   2       244238 non-null  float64
 3   3       244238 non-null  float64
 4   4       244238 non-null  float64
 5   5       244238 non-null  float64
 6   6       244238 non-null  float64
 7   7       244238 non-null  float64
 8   8       244238 non-null  float64
 9   9       244238 non-null  float64
 10  10      244238 non-null  float64
 11  11      244238 non-null  float64
 12  12      244238 non-null  float64
 13  13      244238 non-null  float64
 14  14      244238 non-null  float64
```

```
dtypes: float64(15)
```

```
#  handle class imablance with either smote or class weights in model trainig

from imblearn.over_sampling import SMOTE
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import classification_report, accuracy_score
from sklearn.utils.class_weight import compute_class_weight
from sklearn.preprocessing import StandardScaler


# Load  data
X_train = pd.read_csv("X_train_final.csv")
y_train = pd.read_csv("y_train_final.csv").values.ravel()
X_test = pd.read_csv("X_test_final.csv")
y_test = pd.read_csv("y_test_final.csv").values.ravel()

# Scale data
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)


# Option 1: SMOTE (Synthetic Minority Over-sampling Technique)
smote = SMOTE(sampling_strategy='auto', random_state=42)  # Adjust sampling_strategy as needed
X_train_resampled, y_train_resampled = smote.fit_resample(X_train_scaled, y_train)

# Train a model with resampled data
model_smote = LogisticRegression(max_iter=3000)  # Or any other model
model_smote.fit(X_train_resampled, y_train_resampled)
y_pred_smote = model_smote.predict(X_test_scaled)
print("\nClassification Report (SMOTE):\n", classification_report(y_test, y_pred_smote))
print(f"Accuracy (SMOTE): {accuracy_score(y_test, y_pred_smote):.4f}")


# Option 2: Class Weights
# Calculate class weights
class_weights = compute_class_weight('balanced', classes=np.unique(y_train), y=y_train)
class_weight_dict = dict(enumerate(class_weights))

# Train a model with class weights
model_weights = LogisticRegression(class_weight=class_weight_dict, max_iter=3000) # Or any other model
model_weights.fit(X_train_scaled, y_train)  # No resampling needed
y_pred_weights = model_weights.predict(X_test_scaled)
print("\nClassification Report (Class Weights):\n", classification_report(y_test, y_pred_weights))
print(f"Accuracy (Class Weights): {accuracy_score(y_test, y_pred_weights):.4f}")
```

```
Classification Report (SMOTE):
               precision    recall  f1-score   support

           0       0.66      0.63      0.64     32919
           1       0.46      0.36      0.40     21327
           2       0.19      0.36      0.25      6814

    accuracy                           0.50     61060
   macro avg       0.43      0.45      0.43     61060
weighted avg       0.54      0.50      0.52     61060

Accuracy (SMOTE): 0.5046

Classification Report (Class Weights):
               precision    recall  f1-score   support

           0       0.66      0.64      0.65     32919
           1       0.46      0.36      0.40     21327
           2       0.19      0.35      0.25      6814

    accuracy                           0.51     61060
   macro avg       0.44      0.45      0.43     61060
weighted avg       0.54      0.51      0.52     61060

Accuracy (Class Weights): 0.5073
```

```
#  model selection and training setup train test with cross validation coinfirm proper slpit abd train logistui regression with cross valid

from sklearn.utils.class_weight import compute_class_weight
from sklearn.ensemble import RandomForestClassifier

# Model Selection and Training with Cross-Validation

# Define the parameter grid for Logistic Regression
param_grid = {
    'C': [0.1, 1, 10],  # Regularization strength
    'penalty': ['l1', 'l2'],  # Penalty type
    'solver': ['liblinear', 'saga'] # Solvers compatible with both penalties
}

# Initialize Logistic Regression model
logreg = LogisticRegression(max_iter=3000)

# Initialize GridSearchCV
grid_search = GridSearchCV(estimator=logreg, param_grid=param_grid, cv=5, scoring='accuracy')
```

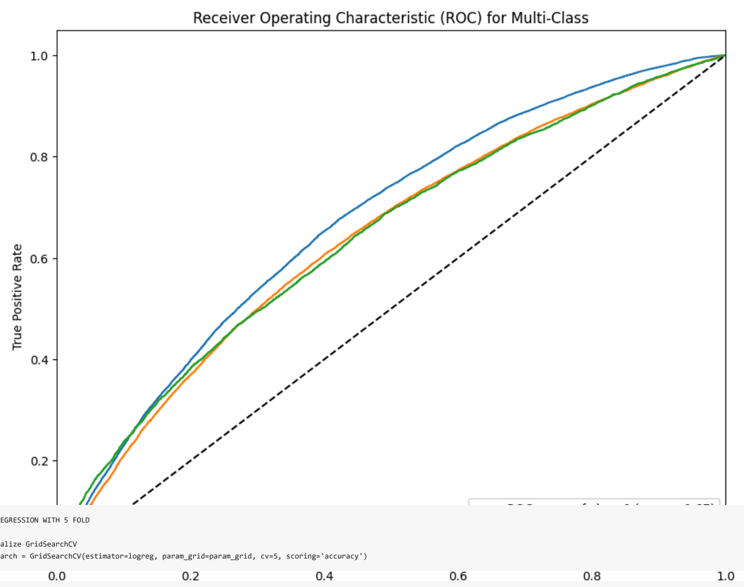
```
# Fit the grid search to the training data
grid_search.fit(X_train_scaled, y_train)

# Get the best model
best_log_reg = grid_search.best_estimator_

# Print the best parameters and score
print("Best Parameters:", grid_search.best_params_)
print("Best Cross-Validation Score:", grid_search.best_score_)


# Evaluate the best model on the test set
y_pred = best_log_reg.predict(X_test_scaled)
accuracy = accuracy_score(y_test, y_pred)
print(f"Test Accuracy: {accuracy:.4f}")
```

```
Best Parameters: {'C': 0.1, 'penalty': 'l1', 'solver': 'saga'}
Best Cross-Validation Score: 0.5773999195271993
Test Accuracy: 0.5802
```

```
# Save the best model to a file
joblib.dump(best_log_reg, "bestModel.pkl")
print("Model saved as bestModel.pkl")

# To load the model later:
# loaded_model = joblib.load("bestModel.pkl")
# y_pred_loaded = loaded_model.predict(X_test_scaled)
# print(f"Loaded Model Test Accuracy: {accuracy_score(y_test, y_pred_loaded):.4f}")
```

```
Model saved as bestModel.pkl
```

```
# ROC Curve and AUC (Multi-class)
from sklearn.metrics import roc_curve, auc
from sklearn.preprocessing import label_binarize

n_classes = len(np.unique(y_test))
y_test_bin = label_binarize(y_test, classes=np.unique(y_test)) # Binarize the output
fpr = dict()
tpr = dict()
roc_auc = dict()

y_pred_proba = best_log_reg.predict_proba(X_test_scaled)


for i in range(n_classes):
    fpr[i], tpr[i], _ = roc_curve(y_test_bin[:, i], y_pred_proba[:, i])
    roc_auc[i] = auc(fpr[i], tpr[i])

# Plot ROC curves for each class
plt.figure(figsize=(10, 8))
for i in range(n_classes):
  plt.plot(fpr[i], tpr[i], label=f'ROC curve of class {i} (area = {roc_auc[i]:0.2f})')

plt.plot([0, 1], [0, 1], 'k--') # Random classifier line
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic (ROC) for Multi-Class')
plt.legend(loc="lower right")
plt.show()


# Feature Importance (Top 5)
feature_importances = pd.DataFrame({'feature': X_train.columns, 'importance': abs(best_log_reg.coef_[0])})
feature_importances = feature_importances.sort_values(by='importance', ascending=False)
print("\nTop 5 Important Features:")
print(feature_importances.head(5))


# Final Submission Check
# osave predictions to a CSV file

submission_df = pd.DataFrame({'prediction': y_pred})
submission_df.to_csv('final_predictions.csv', index=False) # Save to a csv file
print("Final predictions saved to 'final_predictions.csv'")
```



```
# LOG REGRESSION WITH 5 FOLD

# Initialize GridSearchCV
grid_search = GridSearchCV(estimator=logreg, param_grid=param_grid, cv=5, scoring='accuracy')
```

```
# HOW RESUKTS OF LOG REGRESSION WIT 5 FOLD ANFD PLOTY

from sklearn.metrics import roc_curve, auc
from sklearn.preprocessing import label_binarize

# ROC Curve and AUC (Multi-class)
n_classes = len(np.unique(y_test))
y_test_bin = label_binarize(y_test, classes=np.unique(y_test))  # Binarize the output
fpr = dict()
tpr = dict()
roc_auc = dict()

y_pred_proba = best_log_reg.predict_proba(X_test_scaled)

for i in range(n_classes):
    fpr[i], tpr[i], _ = roc_curve(y_test_bin[:, i], y_pred_proba[:, i])
    roc_auc[i] = auc(fpr[i], tpr[i])

# Plot ROC curves for each class
plt.figure(figsize=(10, 8))
for i in range(n_classes):
    plt.plot(fpr[i], tpr[i], label=f'ROC curve of class {i} (area = {roc_auc[i]:0.2f})')

plt.plot([0, 1], [0, 1], 'k--')  # Random classifier line
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic (ROC) for Multi-Class')
plt.legend(loc="lower right")
plt.show()
```