

CIND 820- Big Data Analytics Project

Using Machine Learning for Prediction of Early Readmission of Diabetic Patients

Supervised by: Ceni Babaoglu

Presented by: Nehal Gamal Mohamed (501278190)

```
In [ ]: !pip install pandas  
import sys  
!pip install matplotlib  
!pip install graphviz
```

Requirement already satisfied: pandas in /usr/local/lib/python3.10/dist-packages (2.0.3)
Requirement already satisfied: python-dateutil>=2.8.2 in /usr/local/lib/python3.10/dist-packages (from pandas) (2.8.2)
Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.10/dist-packages (from pandas) (2023.4)
Requirement already satisfied: tzdata>=2022.1 in /usr/local/lib/python3.10/dist-packages (from pandas) (2024.1)
Requirement already satisfied: numpy>=1.21.0 in /usr/local/lib/python3.10/dist-packages (from pandas) (1.25.2)
Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.10/dist-packages (from python-dateutil>=2.8.2->pandas) (1.16.0)
Collecting pandas-profiling
Using cached pandas_profiling-3.6.6-py2.py3-none-any.whl (324 kB)
Collecting ydata-profiling (from pandas-profiling)
Downloading ydata_profiling-4.8.3-py2.py3-none-any.whl (359 kB)
359.5/359.5 kB 2.1 MB/s eta 0:00:00
Requirement already satisfied: scipy<1.14,>=1.4.1 in /usr/local/lib/python3.10/dist-packages (from ydata-profiling->pandas-profiling) (1.11.4)
Requirement already satisfied: pandas!=1.4.0,<3,>1.1 in /usr/local/lib/python3.10/dist-packages (from ydata-profiling->pandas-profiling) (2.0.3)
Requirement already satisfied: matplotlib<3.9,>=3.2 in /usr/local/lib/python3.10/dist-packages (from ydata-profiling->pandas-profiling) (3.7.1)
Requirement already satisfied: pydantic>=2 in /usr/local/lib/python3.10/dist-packages (from ydata-profiling->pandas-profiling) (2.7.4)
Requirement already satisfied: PyYAML<6.1,>=5.0.0 in /usr/local/lib/python3.10/dist-packages (from ydata-profiling->pandas-profiling) (6.0.1)
Requirement already satisfied: jinja2<3.2,>=2.11.1 in /usr/local/lib/python3.10/dist-packages (from ydata-profiling->pandas-profiling) (3.1.4)
Collecting visions[type_image_path]<0.7.7,>=0.7.5 (from ydata-profiling->pandas-profiling)
Downloading visions-0.7.6-py3-none-any.whl (104 kB)
104.8/104.8 kB 10.8 MB/s eta 0:00:00
Requirement already satisfied: numpy<2,>=1.16.0 in /usr/local/lib/python3.10/dist-packages (from ydata-profiling->pandas-profiling) (1.25.2)
Collecting htmlmin==0.1.12 (from ydata-profiling->pandas-profiling)
Downloading htmlmin-0.1.12.tar.gz (19 kB)
Preparing metadata (setup.py) ... done
Collecting phik<0.13,>=0.11.1 (from ydata-profiling->pandas-profiling)
Downloading phik-0.12.4-cp310-cp310-manylinux_2_17_x86_64.manylinux2014_x86_64.whl (686 kB)
686.1/686.1 kB 13.1 MB/s eta 0:00:00
Requirement already satisfied: requests<3,>=2.24.0 in /usr/local/lib/python3.10/dist-packages (from ydata-profiling->pandas-profiling) (2.31.0)
Requirement already satisfied: tqdm<5,>=4.48.2 in /usr/local/lib/python3.10/dist-packages (from ydata-profiling->pandas-profiling) (4.66.4)
Requirement already satisfied: seaborn<0.14,>=0.10.1 in /usr/local/lib/python3.10/dist-packages (from ydata-profiling->pandas-profiling) (0.13.1)
Collecting multimethod<2,>=1.4 (from ydata-profiling->pandas-profiling)
Downloading multimethod-1.11.2-py3-none-any.whl (10 kB)
Requirement already satisfied: statsmodels<1,>=0.13.2 in /usr/local/lib/python3.10/dist-packages (from ydata-profiling->pandas-profiling) (0.14.2)

```
Collecting typeguard<5,>=3 (from ydata-profiling->pandas-profiling)
  Downloading typeguard-4.3.0-py3-none-any.whl (35 kB)
Collecting imagehash==4.3.1 (from ydata-profiling->pandas-profiling)
  Downloading ImageHash-4.3.1-py2.py3-none-any.whl (296 kB)
  296.5/296.5 kB 18.1 MB/s eta 0:00:00
Requirement already satisfied: wordcloud>=1.9.1 in /usr/local/lib/python3.10/dist-packages (from ydata-profiling->pandas-profiling) (1.9.3)
Collecting dacite>=1.8 (from ydata-profiling->pandas-profiling)
  Downloading dacite-1.8.1-py3-none-any.whl (14 kB)
Requirement already satisfied: numba<1,>=0.56.0 in /usr/local/lib/python3.10/dist-packages (from ydata-profiling->pandas-profiling) (0.58.1)
Requirement already satisfied: PyWavelets in /usr/local/lib/python3.10/dist-packages (from imagehash==4.3.1->ydata-profiling->pandas-profiling) (1.6.0)
Requirement already satisfied: pillow in /usr/local/lib/python3.10/dist-packages (from imagehash==4.3.1->ydata-profiling->pandas-profiling) (9.4.0)
Requirement already satisfied: MarkupSafe>=2.0 in /usr/local/lib/python3.10/dist-packages (from jinja2<3.2,>=2.11.1->ydata-profiling->pandas-profiling) (2.1.5)
Requirement already satisfied: contourpy>=1.0.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib<3.9,>=3.2->ydata-profiling->pandas-profiling) (1.2.1)
Requirement already satisfied: cycler>=0.10 in /usr/local/lib/python3.10/dist-packages (from matplotlib<3.9,>=3.2->ydata-profiling->pandas-profiling) (0.12.1)
Requirement already satisfied: fonttools>=4.22.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib<3.9,>=3.2->ydata-profiling->pandas-profiling) (4.53.0)
Requirement already satisfied: kiwisolver>=1.0.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib<3.9,>=3.2->ydata-profiling->pandas-profiling) (1.4.5)
Requirement already satisfied: packaging>=20.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib<3.9,>=3.2->ydata-profiling->pandas-profiling) (24.1)
Requirement already satisfied: pyparsing>=2.3.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib<3.9,>=3.2->ydata-profiling->pandas-profiling) (3.1.2)
Requirement already satisfied: python-dateutil>=2.7 in /usr/local/lib/python3.10/dist-packages (from matplotlib<3.9,>=3.2->ydata-profiling->pandas-profiling) (2.8.2)
Requirement already satisfied: llvmlite<0.42,>=0.41.0dev0 in /usr/local/lib/python3.10/dist-packages (from numba<1,>=0.56.0->ydata-profiling->pandas-profiling) (0.41.1)
Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.10/dist-packages (from pandas!=1.4.0,<3,>1.1->ydata-profiling->pandas-profiling) (2023.4)
Requirement already satisfied: tzdata>=2022.1 in /usr/local/lib/python3.10/dist-packages (from pandas!=1.4.0,<3,>1.1->ydata-profiling->pandas-profiling) (2024.1)
Requirement already satisfied: joblib>=0.14.1 in /usr/local/lib/python3.10/dist-packages (from phik<0.13,>=0.11.1->ydata-profiling->pandas-profiling) (1.4.2)
Requirement already satisfied: annotated-types>=0.4.0 in /usr/local/lib/python3.10/dist-packages (from pydantic>=2->ydata-profiling->pandas-profiling) (0.7.0)
Requirement already satisfied: pydantic-core==2.18.4 in /usr/local/lib/python3.10/dist-packages (from pydantic>=2->ydata-profiling->pandas-profiling) (2.18.4)
Requirement already satisfied: typing-extensions>=4.6.1 in /usr/local/lib/python3.10/dist-packages (from pydantic>=2->ydata-profiling->pandas-profiling) (4.12.2)
```

Requirement already satisfied: charset-normalizer<4,>=2 in /usr/local/lib/python3.10/dist-packages (from requests<3,>=2.24.0->ydata-profiling->pandas-profiling) (3.3.2)

Requirement already satisfied: idna<4,>=2.5 in /usr/local/lib/python3.10/dist-packages (from requests<3,>=2.24.0->ydata-profiling->pandas-profiling) (3.7)

Requirement already satisfied: urllib3<3,>=1.21.1 in /usr/local/lib/python3.10/dist-packages (from requests<3,>=2.24.0->ydata-profiling->pandas-profiling) (2.0.7)

Requirement already satisfied: certifi>=2017.4.17 in /usr/local/lib/python3.10/dist-packages (from requests<3,>=2.24.0->ydata-profiling->pandas-profiling) (2024.6.2)

Requirement already satisfied: patsy>=0.5.6 in /usr/local/lib/python3.10/dist-packages (from statsmodels<1,>=0.13.2->ydata-profiling->pandas-profiling) (0.5.6)

Requirement already satisfied: attrs>=19.3.0 in /usr/local/lib/python3.10/dist-packages (from visions[type_image_path]<0.7.7,>=0.7.5->ydata-profiling->pandas-profiling) (23.2.0)

Requirement already satisfied: networkx>=2.4 in /usr/local/lib/python3.10/dist-packages (from visions[type_image_path]<0.7.7,>=0.7.5->ydata-profiling->pandas-profiling) (3.3)

Requirement already satisfied: six in /usr/local/lib/python3.10/dist-packages (from patsy>=0.5.6->statsmodels<1,>=0.13.2->ydata-profiling->pandas-profiling) (1.16.0)

Building wheels for collected packages: htmlmin

Building wheel for htmlmin (setup.py) ... done

Created wheel for htmlmin: filename=htmlmin-0.1.12-py3-none-any.whl size=27080 sha256=c15ab7f33daf86215c7d61789d63e83ee5ccd5d224511f5cfe4a04cfd9981cb

Stored in directory: /root/.cache/pip/wheels/dd/91/29/a79cecb328d01739e64017b6fb9a1ab9d8cb1853098ec5966d

Successfully built htmlmin

Installing collected packages: htmlmin, typeguard, multimethod, dacite, imagehash, visions, phik, ydata-profiling, pandas-profiling

Successfully installed dacite-1.8.1 htmlmin-0.1.12 imagehash-4.3.1 multimethod-1.11.2 pandas-profiling-3.6.6 phik-0.12.4 typeguard-4.3.0 visions-0.7.6 ydata-profiling-4.8.3

Enabling notebook extension jupyter-js-widgets/extension...

Paths used for configuration of notebook:

/root/.jupyter/nbconfig/notebook.json

Paths used for configuration of notebook:

- Validating: **OK**

Paths used for configuration of notebook:

/root/.jupyter/nbconfig/notebook.json

Requirement already satisfied: matplotlib in /usr/local/lib/python3.10/dist-packages (3.7.1)

Requirement already satisfied: contourpy>=1.0.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (1.2.1)

Requirement already satisfied: cycler>=0.10 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (0.12.1)

Requirement already satisfied: fonttools>=4.22.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (4.53.0)

Requirement already satisfied: kiwisolver>=1.0.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (1.4.5)

Requirement already satisfied: numpy>=1.20 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (1.25.2)

Requirement already satisfied: packaging>=20.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (24.1)

Requirement already satisfied: pillow>=6.2.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (9.4.0)

Requirement already satisfied: pyparsing>=2.3.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (3.1.2)

Requirement already satisfied: python-dateutil>=2.7 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (2.8.2)

Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.10/dist-packages (from python-dateutil>=2.7->matplotlib) (1.16.0)

Requirement already satisfied: graphviz in /usr/local/lib/python3.10/dist-packages (0.20.3)

```
In [ ]: #importing necessary libraries
import csv
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
```

```
In [ ]: #Uploading diabetic_data csv file
from google.colab import files
data = files.upload()
#Instintiating DataReader class
class DataReader:
    def read_csv(self, filename):
        df = pd.read_csv(filename)
        return df

filename = next(iter(data))
data_reader = DataReader()
df = data_reader.read_csv(filename)
#Displaying the first 10 records of the dataset
print(df.head(10))
```

No file chosen

Upload widget is only available when the cell has been executed in the current browser session. Please rerun this cell to enable.

Saving diabetic_data (version 1).csv to diabetic_data (version 1).csv

	encounter_id	patient_nbr	race	gender	age	weight	\
0	2278392	8222157	Caucasian	Female	[0-10)	?	
1	149190	55629189	Caucasian	Female	[10-20)	?	
2	64410	86047875	AfricanAmerican	Female	[20-30)	?	
3	500364	82442376	Caucasian	Male	[30-40)	?	
4	16680	42519267	Caucasian	Male	[40-50)	?	
5	35754	82637451	Caucasian	Male	[50-60)	?	
6	55842	84259809	Caucasian	Male	[60-70)	?	
7	63768	114882984	Caucasian	Male	[70-80)	?	
8	12522	48330783	Caucasian	Female	[80-90)	?	
9	15738	63555939	Caucasian	Female	[90-100)	?	

	admission_type_id	discharge_disposition_id	admission_source_id	\
0	6	25	1	
1	1	1	7	
2	1	1	7	
3	1	1	7	
4	1	1	7	
5	2	1	2	
6	3	1	2	
7	1	1	7	
8	2	1	4	
9	3	3	4	

	time_in_hospital	...	citoglipton	insulin	glyburide-metformin	\
0	1	...	No	No	No	
1	3	...	No	Up	No	
2	2	...	No	No	No	
3	2	...	No	Up	No	
4	1	...	No	Steady	No	
5	3	...	No	Steady	No	
6	4	...	No	Steady	No	
7	5	...	No	No	No	
8	13	...	No	Steady	No	
9	12	...	No	Steady	No	

	glipizide-metformin	glimepiride-pioglitazone	metformin-rosiglitazone	\
0	No	No	No	
1	No	No	No	
2	No	No	No	
3	No	No	No	
4	No	No	No	
5	No	No	No	
6	No	No	No	

7	No	No	No
8	No	No	No
9	No	No	No

	metformin-pioglitazone	change	diabetesMed	readmitted
0	No	No	No	NO
1	No	Ch	Yes	>30
2	No	No	Yes	NO
3	No	Ch	Yes	NO
4	No	Ch	Yes	NO
5	No	No	Yes	>30
6	No	Ch	Yes	NO
7	No	No	Yes	>30
8	No	Ch	Yes	NO
9	No	Ch	Yes	NO

[10 rows x 50 columns]

```
In [ ]: #Displaying variables data types
print("Dataset Information:")
print(df.info())
```

Dataset Information:

<class 'pandas.core.frame.DataFrame'>

RangeIndex: 101766 entries, 0 to 101765

Data columns (total 50 columns):

#	Column	Non-Null Count	Dtype
0	encounter_id	101766 non-null	int64
1	patient_nbr	101766 non-null	int64
2	race	101766 non-null	object
3	gender	101766 non-null	object
4	age	101766 non-null	object
5	weight	101766 non-null	object
6	admission_type_id	101766 non-null	int64
7	discharge_disposition_id	101766 non-null	int64
8	admission_source_id	101766 non-null	int64
9	time_in_hospital	101766 non-null	int64
10	payer_code	101766 non-null	object
11	medical_specialty	101766 non-null	object
12	num_lab_procedures	101766 non-null	int64
13	num_procedures	101766 non-null	int64
14	num_medications	101766 non-null	int64
15	number_outpatient	101766 non-null	int64
16	number_emergency	101766 non-null	int64
17	number_inpatient	101766 non-null	int64
18	diag_1	101766 non-null	object
19	diag_2	101766 non-null	object
20	diag_3	101766 non-null	object
21	number_diagnoses	101766 non-null	int64
22	max_glu_serum	5346 non-null	object
23	A1Cresult	17018 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	trogliatone	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: int64(13), object(37)

memory usage: 38.8+ MB

None

In []: *#Defining lists for categorical variables and numeric variables*

```

categorical_columns = [
    'race',
    'gender',
    'age',
    'weight',
    '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'  
]  
  
numeric_columns = [  
    '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'  
]
```

```
In [ ]: #Dataset Description  
print("Dataset Description:")  
print(df.describe(include='all'))
```

Dataset Description:

	encounter_id	patient_nbr	race	gender	age	weight	\
count	1.017660e+05	1.017660e+05	101766	101766	101766	101766	
unique	NaN	NaN	6	3	10	10	
top	NaN	NaN	Caucasian	Female	[70-80)	?	
freq	NaN	NaN	76099	54708	26068	98569	
mean	1.652016e+08	5.433040e+07	NaN	NaN	NaN	NaN	
std	1.026403e+08	3.869636e+07	NaN	NaN	NaN	NaN	
min	1.252200e+04	1.350000e+02	NaN	NaN	NaN	NaN	
25%	8.496119e+07	2.341322e+07	NaN	NaN	NaN	NaN	
50%	1.523890e+08	4.550514e+07	NaN	NaN	NaN	NaN	
75%	2.302709e+08	8.754595e+07	NaN	NaN	NaN	NaN	
max	4.438672e+08	1.895026e+08	NaN	NaN	NaN	NaN	

	admission_type_id	discharge_disposition_id	admission_source_id	\
count	101766.000000	101766.000000	101766.000000	
unique	NaN	NaN	NaN	
top	NaN	NaN	NaN	
freq	NaN	NaN	NaN	
mean	2.024006	3.715642	5.754437	
std	1.445403	5.280166	4.064081	
min	1.000000	1.000000	1.000000	
25%	1.000000	1.000000	1.000000	
50%	1.000000	1.000000	7.000000	
75%	3.000000	4.000000	7.000000	
max	8.000000	28.000000	25.000000	

	time_in_hospital	...	citoglipton	insulin	glyburide-metformin	\
count	101766.000000	...	101766	101766	101766	
unique	NaN	...	1	4	4	
top	NaN	...	No	No	No	
freq	NaN	...	101766	47383	101060	
mean	4.395987	...	NaN	NaN	NaN	
std	2.985108	...	NaN	NaN	NaN	
min	1.000000	...	NaN	NaN	NaN	
25%	2.000000	...	NaN	NaN	NaN	
50%	4.000000	...	NaN	NaN	NaN	
75%	6.000000	...	NaN	NaN	NaN	
max	14.000000	...	NaN	NaN	NaN	

	glipizide-metformin	glimepiride-pioglitazone	\
count	101766	101766	
unique	2	2	
top	No	No	
freq	101753	101765	

mean	NaN	NaN
std	NaN	NaN
min	NaN	NaN
25%	NaN	NaN
50%	NaN	NaN
75%	NaN	NaN
max	NaN	NaN

	metformin-rosiglitazone	metformin-pioglitazone	change	diabetesMed	\
count	101766	101766	101766	101766	
unique	2	2	2	2	
top	No	No	No	Yes	
freq	101764	101765	54755	78363	
mean	NaN	NaN	NaN	NaN	
std	NaN	NaN	NaN	NaN	
min	NaN	NaN	NaN	NaN	
25%	NaN	NaN	NaN	NaN	
50%	NaN	NaN	NaN	NaN	
75%	NaN	NaN	NaN	NaN	
max	NaN	NaN	NaN	NaN	

	readmitted
count	101766
unique	3
top	NO
freq	54864
mean	NaN
std	NaN
min	NaN
25%	NaN
50%	NaN
75%	NaN
max	NaN

[11 rows x 50 columns]

```
In [ ]: #Converted blank and "?" to NaN to represent missing values
# Replace '?' and blank cells with NaN
df.replace({'?': pd.NA, '': pd.NA}, inplace=True)

# Replaced 'None' in 'max_glu_serum' and 'A1Cresult' to be seen as 'No Test' category and not as missing values
df['max_glu_serum'].replace({pd.NA: 'No Test', 'None': 'No Test'}, inplace=True)
df['A1Cresult'].replace({pd.NA: 'No Test', 'None': 'No Test'}, inplace=True)
missing_values = df.isna().sum()
```

```
print("Number of missing values in each column:")  
print(missing_values)
```

Number of missing values in each column:

encounter_id	0
patient_nbr	0
race	2273
gender	0
age	0
weight	98569
admission_type_id	0
discharge_disposition_id	0
admission_source_id	0
time_in_hospital	0
payer_code	40256
medical_specialty	49949
num_lab_procedures	0
num_procedures	0
num_medications	0
number_outpatient	0
number_emergency	0
number_inpatient	0
diag_1	21
diag_2	358
diag_3	1423
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
dtype: int64
```

```
In [ ]: #Handling missing values in categorical columns by adding "Missing" as subcategory
for col in categorical_columns:
    df[col].fillna('Missing', inplace=True)
print(df[categorical_columns].isnull().sum())
```

```

race                0
gender              0
age                0
weight             0
payer_code         0
medical_specialty  0
diag_1             0
diag_2             0
diag_3             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
dtype: int64

```

```

In [ ]: # converting numeric columns to numeric data types and categorical columns to category data type
for col in numeric_columns:
    df[col] = pd.to_numeric(df[col], errors='coerce')

for col in categorical_columns:
    if col in df.columns:

```



```
df[col] = df[col].astype('category')  
print(df.dtypes)  
print(df[numeric_columns].dtypes)
```

encounter_id	int64
patient_nbr	int64
race	category
gender	category
age	category
weight	category
admission_type_id	int64
discharge_disposition_id	int64
admission_source_id	int64
time_in_hospital	int64
payer_code	category
medical_specialty	category
num_lab_procedures	int64
num_procedures	int64
num_medications	int64
number_outpatient	int64
number_emergency	int64
number_inpatient	int64
diag_1	category
diag_2	category
diag_3	category
number_diagnoses	int64
max_glu_serum	category
A1Cresult	category
metformin	category
repaglinide	category
nateglinide	category
chlorpropamide	category
glimepiride	category
acetohexamide	category
glipizide	category
glyburide	category
tolbutamide	category
pioglitazone	category
rosiglitazone	category
acarbose	category
miglitol	category
troglitazone	category
tolazamide	category
examide	category
citoglipton	category
insulin	category
glyburide-metformin	category
glipizide-metformin	category
glimepiride-pioglitazone	category

```
metformin-rosiglitazone    category
metformin-pioglitazone    category
change                     category
diabetesMed                category
readmitted                 category
dtype: object
encounter_id               int64
patient_nbr                int64
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
number_diagnoses           int64
dtype: object
```

```
In [ ]: # Check for missing values
missing_values = df.isnull().sum()
print(missing_values)
```

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
dtype: int64

```

```

In [ ]: #Checking for duplicate records
duplicate_records = df.duplicated().sum()
print(f"Number of duplicate records: {duplicate_records}")

```

Number of duplicate records: 0

```

In [ ]: # Here I wanted to clean the dataframe by removing irrelevant columns, columns with high missing values
df_cleaned = df.copy()
columns_to_drop = ['encounter_id', 'patient_nbr', 'weight', 'payer_code']
df_cleaned.drop(columns=columns_to_drop, inplace=True)

# Here I put a threshold of 95% for List of columns dominated by "No" category since they have very low variance and no
columns_dominated_by_no = [
    'metformin', 'repaglinide', 'nateglinide', 'chlorpropamide',
    'glimepiride', 'acetohehexamide', 'glipizide', 'glyburide',
    'tolbutamide', 'pioglitazone', 'rosiglitazone', 'acarbose',
    'troglitazone', 'tolazamide', 'examide', 'citoglipton',
    'glyburide-metformin', 'glipizide-metformin', 'glimepiride-pioglitazone',
    'metformin-rosiglitazone', 'metformin-pioglitazone'
]

threshold = 0.95
columns_to_drop_dominated = []
for col in columns_dominated_by_no:
    if df_cleaned[col].value_counts(normalize=True).get('No', 0) > threshold:
        columns_to_drop_dominated.append(col)
df_cleaned.drop(columns=columns_to_drop_dominated, inplace=True)

# Check the remaining columns
print("Remaining columns after dropping unnecessary ones:")
print(df_cleaned.columns)
print(df_cleaned.info())

```

Remaining columns after dropping unnecessary ones:

```
Index(['race', 'gender', 'age', 'admission_type_id',
      'discharge_disposition_id', 'admission_source_id', 'time_in_hospital',
      'medical_specialty', 'num_lab_procedures', 'num_procedures',
      'num_medications', 'number_outpatient', 'number_emergency',
      'number_inpatient', 'diag_1', 'diag_2', 'diag_3', 'number_diagnoses',
      'max_glu_serum', 'A1Cresult', 'metformin', 'glimepiride', 'glipizide',
      'glyburide', 'pioglitazone', 'rosiglitazone', 'miglitol', 'insulin',
      'change', 'diabetesMed', 'readmitted'],
      dtype='object')
```

```
<class 'pandas.core.frame.DataFrame'>
```

```
RangeIndex: 101766 entries, 0 to 101765
```

```
Data columns (total 31 columns):
```

#	Column	Non-Null Count	Dtype
0	race	101766 non-null	category
1	gender	101766 non-null	category
2	age	101766 non-null	category
3	admission_type_id	101766 non-null	int64
4	discharge_disposition_id	101766 non-null	int64
5	admission_source_id	101766 non-null	int64
6	time_in_hospital	101766 non-null	int64
7	medical_specialty	101766 non-null	category
8	num_lab_procedures	101766 non-null	int64
9	num_procedures	101766 non-null	int64
10	num_medications	101766 non-null	int64
11	number_outpatient	101766 non-null	int64
12	number_emergency	101766 non-null	int64
13	number_inpatient	101766 non-null	int64
14	diag_1	101766 non-null	category
15	diag_2	101766 non-null	category
16	diag_3	101766 non-null	category
17	number_diagnoses	101766 non-null	int64
18	max_glu_serum	101766 non-null	category
19	A1Cresult	101766 non-null	category
20	metformin	101766 non-null	category
21	glimepiride	101766 non-null	category
22	glipizide	101766 non-null	category
23	glyburide	101766 non-null	category
24	pioglitazone	101766 non-null	category
25	rosiglitazone	101766 non-null	category
26	miglitol	101766 non-null	category
27	insulin	101766 non-null	category
28	change	101766 non-null	category
29	diabetesMed	101766 non-null	category

```
30 readmitted          101766 non-null  category
dtypes: category(20), int64(11)
memory usage: 10.9 MB
None
```

```
In [ ]: # Identify and verifying remaining categorical columns for onehot coding
categorical_columns = df_cleaned.select_dtypes(include=['category']).columns.tolist()
print("Categorical columns for one-hot encoding:", categorical_columns)

Categorical columns for one-hot encoding: ['race', 'gender', 'age', 'medical_specialty', 'diag_1', 'diag_2', 'diag_3',
'max_glu_serum', 'A1Cresult', 'metformin', 'glimepiride', 'glipizide', 'glyburide', 'pioglitazone', 'rosiglitazone', 'm
iglitol', 'insulin', 'change', 'diabetesMed', 'readmitted']
```

```
In [ ]: # One-hot encode the remaining categorical columns
df_onehot_coded = pd.get_dummies(df_cleaned, columns=categorical_columns, drop_first=False)
boolean_columns = df_onehot_coded.select_dtypes(include='bool').columns
df_onehot_coded[boolean_columns] = df_onehot_coded[boolean_columns].astype(int)
print(df_onehot_coded.head())
print(df_onehot_coded.columns)
```

	admission_type_id	discharge_disposition_id	admission_source_id	\
0	6	25	1	
1	1	1	7	
2	1	1	7	
3	1	1	7	
4	1	1	7	

	time_in_hospital	num_lab_procedures	num_procedures	num_medications	\
0	1	41	0	1	
1	3	59	0	18	
2	2	11	5	13	
3	2	44	1	16	
4	1	51	0	8	

	number_outpatient	number_emergency	number_inpatient	...	insulin_No	\
0	0	0	0	...	1	
1	0	0	0	...	0	
2	2	0	1	...	1	
3	0	0	0	...	0	
4	0	0	0	...	0	

	insulin_Steady	insulin_Up	change_Ch	change_No	diabetesMed_No	\
0	0	0	0	1	1	
1	0	1	1	0	0	
2	0	0	0	1	0	
3	0	1	1	0	0	
4	1	0	1	0	0	

	diabetesMed_Yes	readmitted_<30	readmitted_>30	readmitted_NO
0	0	0	0	1
1	1	0	1	0
2	1	0	0	1
3	1	0	0	1
4	1	0	0	1

[5 rows x 2406 columns]

```
Index(['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',
      ...,
      'insulin_No', 'insulin_Steady', 'insulin_Up', 'change_Ch', 'change_No',
      'diabetesMed_No', 'diabetesMed_Yes', 'readmitted_<30', 'readmitted_>30',
      'readmitted_NO'],
      dtype='object', length=2406)
```



```
In [ ]: # To assess the normality of the numerical variables, I conducted the Shapiro-Wilk test.
# Despite the test results indicating that none of the variables followed a normal distribution,
# I chose to retain the outliers. The reason behind this decision was that the count of outliers
# across the numeric variables was not substantial, and removing them could potentially reduce
# the variance and valuable information in the dataset.
from scipy.stats import shapiro
dependent_var_columns = ['readmitted_>30', 'readmitted_NO', 'readmitted_<30']
numerical_columns = df_onehot_coded.select_dtypes(include=[np.number]).columns
numerical_columns = numerical_columns.drop(dependent_var_columns)

# Perform the Shapiro-Wilk test
shapiro_results = {}
for col in numerical_columns:
    stat, p_value = shapiro(df_onehot_coded[col])
    shapiro_results[col] = (stat, p_value)
shapiro_df = pd.DataFrame(shapiro_results, index=['Statistic', 'p-value']).T
display(shapiro_df)
```

```
/usr/local/lib/python3.10/dist-packages/scipy/stats/_morestats.py:1882: UserWarning: p-value may not be accurate for N
> 5000.
    warnings.warn("p-value may not be accurate for N > 5000.")
```

	Statistic	p-value
admission_type_id	0.721419	0.0
discharge_disposition_id	0.568973	0.0
admission_source_id	0.737137	0.0
time_in_hospital	0.886919	0.0
num_lab_procedures	0.984858	0.0
...
insulin_Up	0.363303	0.0
change_Ch	0.634863	0.0
change_No	0.635076	0.0
diabetesMed_No	0.520568	0.0
diabetesMed_Yes	0.521023	0.0

2403 rows × 2 columns

```
In [ ]: #Next step is to normalize the independent variables to insure scalability
# Function to normalize numerical columns
def normalize(x):
    return (x - x.min()) / (x.max() - x.min())
dependent_var_columns = ['readmitted_>30', 'readmitted_NO', 'readmitted_<30']
numerical_columns = df_onehot_coded.select_dtypes(include=[np.number]).columns
numerical_columns = numerical_columns.drop(dependent_var_columns)
for col in numerical_columns:
    df_onehot_coded[col] = normalize(df_onehot_coded[col])
print(df_onehot_coded.head())
```

	admission_type_id	discharge_disposition_id	admission_source_id	\
0	0.714286	0.888889	0.00	
1	0.000000	0.000000	0.25	
2	0.000000	0.000000	0.25	
3	0.000000	0.000000	0.25	
4	0.000000	0.000000	0.25	

	time_in_hospital	num_lab_procedures	num_procedures	num_medications	\
0	0.000000	0.305344	0.000000	0.0000	
1	0.153846	0.442748	0.000000	0.2125	
2	0.076923	0.076336	0.833333	0.1500	
3	0.076923	0.328244	0.166667	0.1875	
4	0.000000	0.381679	0.000000	0.0875	

	number_outpatient	number_emergency	number_inpatient	...	insulin_No	\
0	0.000000	0.0	0.000000	...	1.0	
1	0.000000	0.0	0.000000	...	0.0	
2	0.047619	0.0	0.047619	...	1.0	
3	0.000000	0.0	0.000000	...	0.0	
4	0.000000	0.0	0.000000	...	0.0	

	insulin_Steady	insulin_Up	change_Ch	change_No	diabetesMed_No	\
0	0.0	0.0	0.0	1.0	1.0	
1	0.0	1.0	1.0	0.0	0.0	
2	0.0	0.0	0.0	1.0	0.0	
3	0.0	1.0	1.0	0.0	0.0	
4	1.0	0.0	1.0	0.0	0.0	

	diabetesMed_Yes	readmitted_<30	readmitted_>30	readmitted_NO
0	0.0	0	0	1
1	1.0	0	1	0
2	1.0	0	0	1
3	1.0	0	0	1
4	1.0	0	0	1

[5 rows x 2406 columns]

```
In [ ]: # Checking if the numerical columns are normalized
for col in numerical_columns:
    min_val = df_onehot_coded[col].min()
    max_val = df_onehot_coded[col].max()
    print(f'{col}: min = {min_val}, max = {max_val}')
```

admission_type_id: min = 0.0, max = 1.0
discharge_disposition_id: min = 0.0, max = 1.0
admission_source_id: min = 0.0, max = 1.0
time_in_hospital: min = 0.0, max = 1.0
num_lab_procedures: min = 0.0, max = 1.0
num_procedures: min = 0.0, max = 1.0
num_medications: min = 0.0, max = 1.0
number_outpatient: min = 0.0, max = 1.0
number_emergency: min = 0.0, max = 1.0
number_inpatient: min = 0.0, max = 1.0
number_diagnoses: min = 0.0, max = 1.0
race_AfricanAmerican: min = 0.0, max = 1.0
race_Asian: min = 0.0, max = 1.0
race_Caucasian: min = 0.0, max = 1.0
race_Hispanic: min = 0.0, max = 1.0
race_Missing: min = 0.0, max = 1.0
race_Other: min = 0.0, max = 1.0
gender_Female: min = 0.0, max = 1.0
gender_Male: min = 0.0, max = 1.0
gender_Unknown/Invalid: min = 0.0, max = 1.0
age_[0-10): min = 0.0, max = 1.0
age_[10-20): min = 0.0, max = 1.0
age_[20-30): min = 0.0, max = 1.0
age_[30-40): min = 0.0, max = 1.0
age_[40-50): min = 0.0, max = 1.0
age_[50-60): min = 0.0, max = 1.0
age_[60-70): min = 0.0, max = 1.0
age_[70-80): min = 0.0, max = 1.0
age_[80-90): min = 0.0, max = 1.0
age_[90-100): min = 0.0, max = 1.0
medical_specialty_AllergyandImmunology: min = 0.0, max = 1.0
medical_specialty_Anesthesiology: min = 0.0, max = 1.0
medical_specialty_Anesthesiology-Pediatric: min = 0.0, max = 1.0
medical_specialty_Cardiology: min = 0.0, max = 1.0
medical_specialty_Cardiology-Pediatric: min = 0.0, max = 1.0
medical_specialty_DCPTEAM: min = 0.0, max = 1.0
medical_specialty_Dentistry: min = 0.0, max = 1.0
medical_specialty_Dermatology: min = 0.0, max = 1.0
medical_specialty_Emergency/Trauma: min = 0.0, max = 1.0
medical_specialty_Endocrinology: min = 0.0, max = 1.0
medical_specialty_Endocrinology-Metabolism: min = 0.0, max = 1.0
medical_specialty_Family/GeneralPractice: min = 0.0, max = 1.0
medical_specialty_Gastroenterology: min = 0.0, max = 1.0
medical_specialty_Gynecology: min = 0.0, max = 1.0
medical_specialty_Hematology: min = 0.0, max = 1.0

medical_specialty_Hematology/Oncology: min = 0.0, max = 1.0
medical_specialty_Hospitalist: min = 0.0, max = 1.0
medical_specialty_InfectiousDiseases: min = 0.0, max = 1.0
medical_specialty_InternalMedicine: min = 0.0, max = 1.0
medical_specialty_Missing: min = 0.0, max = 1.0
medical_specialty_Nephrology: min = 0.0, max = 1.0
medical_specialty_Neurology: min = 0.0, max = 1.0
medical_specialty_Neurophysiology: min = 0.0, max = 1.0
medical_specialty_Obstetrics&Gynecology-GynecologicOnco: min = 0.0, max = 1.0
medical_specialty_Obstetrics: min = 0.0, max = 1.0
medical_specialty_ObstetricsandGynecology: min = 0.0, max = 1.0
medical_specialty_Oncology: min = 0.0, max = 1.0
medical_specialty_Ophthalmology: min = 0.0, max = 1.0
medical_specialty_Orthopedics: min = 0.0, max = 1.0
medical_specialty_Orthopedics-Reconstructive: min = 0.0, max = 1.0
medical_specialty_Osteopath: min = 0.0, max = 1.0
medical_specialty_Otolaryngology: min = 0.0, max = 1.0
medical_specialty_OutreachServices: min = 0.0, max = 1.0
medical_specialty_Pathology: min = 0.0, max = 1.0
medical_specialty_Pediatrics: min = 0.0, max = 1.0
medical_specialty_Pediatrics-AllergyandImmunology: min = 0.0, max = 1.0
medical_specialty_Pediatrics-CriticalCare: min = 0.0, max = 1.0
medical_specialty_Pediatrics-EmergencyMedicine: min = 0.0, max = 1.0
medical_specialty_Pediatrics-Endocrinology: min = 0.0, max = 1.0
medical_specialty_Pediatrics-Hematology-Oncology: min = 0.0, max = 1.0
medical_specialty_Pediatrics-InfectiousDiseases: min = 0.0, max = 1.0
medical_specialty_Pediatrics-Neurology: min = 0.0, max = 1.0
medical_specialty_Pediatrics-Pulmonology: min = 0.0, max = 1.0
medical_specialty_Perinatology: min = 0.0, max = 1.0
medical_specialty_PhysicalMedicineandRehabilitation: min = 0.0, max = 1.0
medical_specialty_PhysicianNotFound: min = 0.0, max = 1.0
medical_specialty_Podiatry: min = 0.0, max = 1.0
medical_specialty_Proctology: min = 0.0, max = 1.0
medical_specialty_Psychiatry: min = 0.0, max = 1.0
medical_specialty_Psychiatry-Addictive: min = 0.0, max = 1.0
medical_specialty_Psychiatry-Child/Adolescent: min = 0.0, max = 1.0
medical_specialty_Psychology: min = 0.0, max = 1.0
medical_specialty_Pulmonology: min = 0.0, max = 1.0
medical_specialty_Radiologist: min = 0.0, max = 1.0
medical_specialty_Radiology: min = 0.0, max = 1.0
medical_specialty_Resident: min = 0.0, max = 1.0
medical_specialty_Rheumatology: min = 0.0, max = 1.0
medical_specialty_Speech: min = 0.0, max = 1.0
medical_specialty_SportsMedicine: min = 0.0, max = 1.0
medical_specialty_Surgeon: min = 0.0, max = 1.0

medical_specialty_Surgery-Cardiovascular: min = 0.0, max = 1.0
medical_specialty_Surgery-Cardiovascular/Thoracic: min = 0.0, max = 1.0
medical_specialty_Surgery-Colon&Rectal: min = 0.0, max = 1.0
medical_specialty_Surgery-General: min = 0.0, max = 1.0
medical_specialty_Surgery-Maxillofacial: min = 0.0, max = 1.0
medical_specialty_Surgery-Neuro: min = 0.0, max = 1.0
medical_specialty_Surgery-Pediatric: min = 0.0, max = 1.0
medical_specialty_Surgery-Plastic: min = 0.0, max = 1.0
medical_specialty_Surgery-PlasticwithinHeadandNeck: min = 0.0, max = 1.0
medical_specialty_Surgery-Thoracic: min = 0.0, max = 1.0
medical_specialty_Surgery-Vascular: min = 0.0, max = 1.0
medical_specialty_SurgicalSpecialty: min = 0.0, max = 1.0
medical_specialty_Urology: min = 0.0, max = 1.0
diag_1_10: min = 0.0, max = 1.0
diag_1_11: min = 0.0, max = 1.0
diag_1_110: min = 0.0, max = 1.0
diag_1_112: min = 0.0, max = 1.0
diag_1_114: min = 0.0, max = 1.0
diag_1_115: min = 0.0, max = 1.0
diag_1_117: min = 0.0, max = 1.0
diag_1_131: min = 0.0, max = 1.0
diag_1_133: min = 0.0, max = 1.0
diag_1_135: min = 0.0, max = 1.0
diag_1_136: min = 0.0, max = 1.0
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diag_3_971: min = 0.0, max = 1.0
diag_3_972: min = 0.0, max = 1.0
diag_3_980: min = 0.0, max = 1.0
diag_3_987: min = 0.0, max = 1.0
diag_3_989: min = 0.0, max = 1.0
diag_3_991: min = 0.0, max = 1.0
diag_3_992: min = 0.0, max = 1.0
diag_3_995: min = 0.0, max = 1.0
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diag_3_997: min = 0.0, max = 1.0
diag_3_998: min = 0.0, max = 1.0
diag_3_999: min = 0.0, max = 1.0
diag_3_E812: min = 0.0, max = 1.0
diag_3_E813: min = 0.0, max = 1.0
diag_3_E815: min = 0.0, max = 1.0
diag_3_E816: min = 0.0, max = 1.0
diag_3_E817: min = 0.0, max = 1.0
diag_3_E818: min = 0.0, max = 1.0
diag_3_E819: min = 0.0, max = 1.0
diag_3_E822: min = 0.0, max = 1.0
diag_3_E825: min = 0.0, max = 1.0
diag_3_E826: min = 0.0, max = 1.0
diag_3_E828: min = 0.0, max = 1.0

diag_3_E849: min = 0.0, max = 1.0
diag_3_E850: min = 0.0, max = 1.0
diag_3_E852: min = 0.0, max = 1.0
diag_3_E853: min = 0.0, max = 1.0
diag_3_E854: min = 0.0, max = 1.0
diag_3_E855: min = 0.0, max = 1.0
diag_3_E858: min = 0.0, max = 1.0
diag_3_E861: min = 0.0, max = 1.0
diag_3_E864: min = 0.0, max = 1.0
diag_3_E865: min = 0.0, max = 1.0
diag_3_E870: min = 0.0, max = 1.0
diag_3_E876: min = 0.0, max = 1.0
diag_3_E878: min = 0.0, max = 1.0
diag_3_E879: min = 0.0, max = 1.0
diag_3_E880: min = 0.0, max = 1.0
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diag_3_E882: min = 0.0, max = 1.0
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diag_3_E885: min = 0.0, max = 1.0
diag_3_E886: min = 0.0, max = 1.0
diag_3_E887: min = 0.0, max = 1.0
diag_3_E888: min = 0.0, max = 1.0
diag_3_E892: min = 0.0, max = 1.0
diag_3_E894: min = 0.0, max = 1.0
diag_3_E900: min = 0.0, max = 1.0
diag_3_E901: min = 0.0, max = 1.0
diag_3_E904: min = 0.0, max = 1.0
diag_3_E905: min = 0.0, max = 1.0
diag_3_E906: min = 0.0, max = 1.0
diag_3_E912: min = 0.0, max = 1.0
diag_3_E915: min = 0.0, max = 1.0
diag_3_E916: min = 0.0, max = 1.0
diag_3_E917: min = 0.0, max = 1.0
diag_3_E919: min = 0.0, max = 1.0
diag_3_E920: min = 0.0, max = 1.0
diag_3_E922: min = 0.0, max = 1.0
diag_3_E924: min = 0.0, max = 1.0
diag_3_E927: min = 0.0, max = 1.0
diag_3_E928: min = 0.0, max = 1.0
diag_3_E929: min = 0.0, max = 1.0
diag_3_E930: min = 0.0, max = 1.0
diag_3_E931: min = 0.0, max = 1.0
diag_3_E932: min = 0.0, max = 1.0
diag_3_E933: min = 0.0, max = 1.0

diag_3_E934: min = 0.0, max = 1.0
diag_3_E935: min = 0.0, max = 1.0
diag_3_E936: min = 0.0, max = 1.0
diag_3_E937: min = 0.0, max = 1.0
diag_3_E938: min = 0.0, max = 1.0
diag_3_E939: min = 0.0, max = 1.0
diag_3_E941: min = 0.0, max = 1.0
diag_3_E942: min = 0.0, max = 1.0
diag_3_E943: min = 0.0, max = 1.0
diag_3_E944: min = 0.0, max = 1.0
diag_3_E945: min = 0.0, max = 1.0
diag_3_E946: min = 0.0, max = 1.0
diag_3_E947: min = 0.0, max = 1.0
diag_3_E949: min = 0.0, max = 1.0
diag_3_E950: min = 0.0, max = 1.0
diag_3_E955: min = 0.0, max = 1.0
diag_3_E956: min = 0.0, max = 1.0
diag_3_E965: min = 0.0, max = 1.0
diag_3_E966: min = 0.0, max = 1.0
diag_3_E980: min = 0.0, max = 1.0
diag_3_E987: min = 0.0, max = 1.0
diag_3_Missing: min = 0.0, max = 1.0
diag_3_V01: min = 0.0, max = 1.0
diag_3_V02: min = 0.0, max = 1.0
diag_3_V03: min = 0.0, max = 1.0
diag_3_V06: min = 0.0, max = 1.0
diag_3_V07: min = 0.0, max = 1.0
diag_3_V08: min = 0.0, max = 1.0
diag_3_V09: min = 0.0, max = 1.0
diag_3_V10: min = 0.0, max = 1.0
diag_3_V11: min = 0.0, max = 1.0
diag_3_V12: min = 0.0, max = 1.0
diag_3_V13: min = 0.0, max = 1.0
diag_3_V14: min = 0.0, max = 1.0
diag_3_V15: min = 0.0, max = 1.0
diag_3_V16: min = 0.0, max = 1.0
diag_3_V17: min = 0.0, max = 1.0
diag_3_V18: min = 0.0, max = 1.0
diag_3_V22: min = 0.0, max = 1.0
diag_3_V23: min = 0.0, max = 1.0
diag_3_V25: min = 0.0, max = 1.0
diag_3_V27: min = 0.0, max = 1.0
diag_3_V42: min = 0.0, max = 1.0
diag_3_V43: min = 0.0, max = 1.0
diag_3_V44: min = 0.0, max = 1.0

diag_3_V45: min = 0.0, max = 1.0
diag_3_V46: min = 0.0, max = 1.0
diag_3_V49: min = 0.0, max = 1.0
diag_3_V53: min = 0.0, max = 1.0
diag_3_V54: min = 0.0, max = 1.0
diag_3_V55: min = 0.0, max = 1.0
diag_3_V57: min = 0.0, max = 1.0
diag_3_V58: min = 0.0, max = 1.0
diag_3_V60: min = 0.0, max = 1.0
diag_3_V61: min = 0.0, max = 1.0
diag_3_V62: min = 0.0, max = 1.0
diag_3_V63: min = 0.0, max = 1.0
diag_3_V64: min = 0.0, max = 1.0
diag_3_V65: min = 0.0, max = 1.0
diag_3_V66: min = 0.0, max = 1.0
diag_3_V70: min = 0.0, max = 1.0
diag_3_V72: min = 0.0, max = 1.0
diag_3_V85: min = 0.0, max = 1.0
diag_3_V86: min = 0.0, max = 1.0
max_glu_serum_>200: min = 0.0, max = 1.0
max_glu_serum_>300: min = 0.0, max = 1.0
max_glu_serum_No Test: min = 0.0, max = 1.0
max_glu_serum_Norm: min = 0.0, max = 1.0
A1Cresult_>7: min = 0.0, max = 1.0
A1Cresult_>8: min = 0.0, max = 1.0
A1Cresult_No Test: min = 0.0, max = 1.0
A1Cresult_Norm: min = 0.0, max = 1.0
metformin_Down: min = 0.0, max = 1.0
metformin_No: min = 0.0, max = 1.0
metformin_Steady: min = 0.0, max = 1.0
metformin_Up: min = 0.0, max = 1.0
glimepiride_Down: min = 0.0, max = 1.0
glimepiride_No: min = 0.0, max = 1.0
glimepiride_Steady: min = 0.0, max = 1.0
glimepiride_Up: min = 0.0, max = 1.0
glipizide_Down: min = 0.0, max = 1.0
glipizide_No: min = 0.0, max = 1.0
glipizide_Steady: min = 0.0, max = 1.0
glipizide_Up: min = 0.0, max = 1.0
glyburide_Down: min = 0.0, max = 1.0
glyburide_No: min = 0.0, max = 1.0
glyburide_Steady: min = 0.0, max = 1.0
glyburide_Up: min = 0.0, max = 1.0
pioglitazone_Down: min = 0.0, max = 1.0
pioglitazone_No: min = 0.0, max = 1.0


```

pioglitazone_Steady: min = 0.0, max = 1.0
pioglitazone_Up: min = 0.0, max = 1.0
rosiglitazone_Down: min = 0.0, max = 1.0
rosiglitazone_No: min = 0.0, max = 1.0
rosiglitazone_Steady: min = 0.0, max = 1.0
rosiglitazone_Up: min = 0.0, max = 1.0
miglitol_Down: min = 0.0, max = 1.0
miglitol_No: min = 0.0, max = 1.0
miglitol_Steady: min = 0.0, max = 1.0
miglitol_Up: min = 0.0, max = 1.0
insulin_Down: min = 0.0, max = 1.0
insulin_No: min = 0.0, max = 1.0
insulin_Steady: min = 0.0, max = 1.0
insulin_Up: min = 0.0, max = 1.0
change_Ch: min = 0.0, max = 1.0
change_No: min = 0.0, max = 1.0
diabetesMed_No: min = 0.0, max = 1.0
diabetesMed_Yes: min = 0.0, max = 1.0

```

```

In [ ]: # Here is the Classification starts by setting the dependent variable and splitting the dataset to train and test set
from sklearn.model_selection import train_test_split
X = df_onehot_coded.drop(columns=['readmitted_>30', 'readmitted_NO', 'readmitted_<30'])
y = df_onehot_coded['readmitted_<30']

# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

```

```

In [ ]: from sklearn.linear_model import LogisticRegression
from sklearn.metrics import classification_report, confusion_matrix, accuracy_score

# The first ML Model ogistic regression model
log_reg = LogisticRegression(max_iter=1000, random_state=42)
log_reg.fit(X_train, y_train)
y_pred_lr = log_reg.predict(X_test)

# Evaluate the model
print("Logistic Regression Classifier")
print(classification_report(y_test, y_pred_lr))
print(confusion_matrix(y_test, y_pred_lr))

```

Logistic Regression Classifier

	precision	recall	f1-score	support
0	0.89	1.00	0.94	18069
1	0.43	0.02	0.03	2285
accuracy			0.89	20354
macro avg	0.66	0.51	0.49	20354
weighted avg	0.84	0.89	0.84	20354

```
[[18021  48]
 [ 2249 36]]
```

```
In [ ]: from sklearn.tree import DecisionTreeClassifier
        from sklearn.metrics import classification_report, confusion_matrix
```

```
# The second ML algorithm Decision Tree
decision_tree = DecisionTreeClassifier(random_state=42)
decision_tree.fit(X_train, y_train)
y_pred_tree = decision_tree.predict(X_test)

# Evaluate the model
print("Decision Tree Classifier")
print(classification_report(y_test, y_pred_tree))
print(confusion_matrix(y_test, y_pred_tree))
```

Decision Tree Classifier

	precision	recall	f1-score	support
0	0.89	0.91	0.90	18069
1	0.17	0.16	0.16	2285
accuracy			0.82	20354
macro avg	0.53	0.53	0.53	20354
weighted avg	0.81	0.82	0.82	20354

```
[[16383 1686]
 [ 1930 355]]
```

```
In [ ]: from sklearn.ensemble import RandomForestClassifier
        from sklearn.metrics import classification_report, confusion_matrix
        from sklearn.ensemble import RandomForestClassifier

# The Third ML algorithm Random Forest
# Here I used the class weight attribute in the Random Forest classifier(The bagging technique) it help with the class
# Initialize the Random Forest model with class_weight='balanced_subsample'
```

```

random_forest = RandomForestClassifier(class_weight='balanced_subsample', random_state=42)
random_forest.fit(X_train, y_train)
y_pred_rf = random_forest.predict(X_test)

# Evaluate the model
accuracy_rf = accuracy_score(y_test, y_pred_rf)
conf_matrix_rf = confusion_matrix(y_test, y_pred_rf)
class_report_rf = classification_report(y_test, y_pred_rf)

print(f'Random Forest Accuracy: {accuracy_rf}')
print('Random Forest Confusion Matrix:')
print(conf_matrix_rf)
print('Random Forest Classification Report:')
print(class_report_rf)

```

Random Forest Accuracy: 0.8880809668861157

Random Forest Confusion Matrix:

```

[[18066   3]
 [ 2275  10]]

```

Random Forest Classification Report:

	precision	recall	f1-score	support
0	0.89	1.00	0.94	18069
1	0.77	0.00	0.01	2285
accuracy			0.89	20354
macro avg	0.83	0.50	0.47	20354
weighted avg	0.87	0.89	0.84	20354

In []: **from** sklearn.ensemble **import** GradientBoostingClassifier

```

# The forth ML algorithm Boosting Classifier
gradient_boosting = GradientBoostingClassifier(random_state=42)
gradient_boosting.fit(X_train, y_train)
y_pred_gb = gradient_boosting.predict(X_test)

# Evaluate the model
accuracy_gb = accuracy_score(y_test, y_pred_gb)
conf_matrix_gb = confusion_matrix(y_test, y_pred_gb)
class_report_gb = classification_report(y_test, y_pred_gb)

print(f'Gradient Boosting Accuracy: {accuracy_gb}')
print('Gradient Boosting Confusion Matrix:')
print(conf_matrix_gb)

```

```
print('Gradient Boosting Classification Report:')
print(class_report_gb)
```

Gradient Boosting Accuracy: 0.8881300972781763

Gradient Boosting Confusion Matrix:

```
[[18051   18]
 [ 2259   26]]
```

Gradient Boosting Classification Report:

	precision	recall	f1-score	support
0	0.89	1.00	0.94	18069
1	0.59	0.01	0.02	2285
accuracy			0.89	20354
macro avg	0.74	0.51	0.48	20354
weighted avg	0.86	0.89	0.84	20354

```
In [ ]: from imblearn.over_sampling import SMOTE
        from collections import Counter
```

```
# As we can see from initial results of the previous 4 ML algorithms that the class imbalance is affecting on the perfor
# specially on the RECALL which represents the the people who were readmitted within a month time
# and were wrongly predicted as readmitted after a month time
# So, we need to handle the class imbalance by more representing the minority class using SMOTE
smote = SMOTE(random_state=42)
X_train_smote, y_train_smote = smote.fit_resample(X_train, y_train)

# Check the class distribution after resampling
print("Resampled training set class distribution:", Counter(y_train_smote))
```

```
In [ ]: # Random undersampling
# Here I tried to handle the class imbalance by more representing the minority class and less representation of the major
# using Random undersampling
from sklearn.model_selection import train_test_split
from imblearn.under_sampling import RandomUnderSampler
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import classification_report, confusion_matrix, accuracy_score
X = df_onehot_coded.drop(columns=['readmitted_>30', 'readmitted_NO', 'readmitted_<30'])
y = df_onehot_coded['readmitted_<30']

# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

# Apply Random Under-Sampling to the training data
```

```

rus = RandomUnderSampler(random_state=42)
X_train_rus, y_train_rus = rus.fit_resample(X_train, y_train)

# Logistic Regression with RUS
log_reg_rus = LogisticRegression(max_iter=1000, random_state=42)
log_reg_rus.fit(X_train_rus, y_train_rus)

# Evaluate the model
y_pred_lr = log_reg_rus.predict(X_test)
accuracy_lr = accuracy_score(y_test, y_pred_lr)
conf_matrix_lr = confusion_matrix(y_test, y_pred_lr)
class_report_lr = classification_report(y_test, y_pred_lr)

print('Logistic Regression with RUS')
print(f'Accuracy: {accuracy_lr}')
print('Confusion Matrix:')
print(conf_matrix_lr)
print('Classification Report:')
print(class_report_lr)

```

Logistic Regression with RUS

Accuracy: 0.6109364252726737

Confusion Matrix:

[[11141 6928]

[991 1294]]

Classification Report:

	precision	recall	f1-score	support
0	0.92	0.62	0.74	18069
1	0.16	0.57	0.25	2285
accuracy			0.61	20354
macro avg	0.54	0.59	0.49	20354
weighted avg	0.83	0.61	0.68	20354

```

In [ ]: from sklearn.tree import DecisionTreeClassifier
# Decision Tree with RUS
decision_tree_rus = DecisionTreeClassifier(random_state=42)
decision_tree_rus.fit(X_train_rus, y_train_rus)

# Evaluate the model
y_pred_dt = decision_tree_rus.predict(X_test)
accuracy_dt = accuracy_score(y_test, y_pred_dt)
conf_matrix_dt = confusion_matrix(y_test, y_pred_dt)

```

```
class_report_dt = classification_report(y_test, y_pred_dt)
```

```
print('Decision Tree with RUS')
print(f'Accuracy: {accuracy_dt}')
print('Confusion Matrix:')
print(conf_matrix_dt)
print('Classification Report:')
print(class_report_dt)
```

Decision Tree with RUS

Accuracy: 0.5648029871278373

Confusion Matrix:

```
[[10218  7851]
 [ 1007  1278]]
```

Classification Report:

	precision	recall	f1-score	support
0	0.91	0.57	0.70	18069
1	0.14	0.56	0.22	2285
accuracy			0.56	20354
macro avg	0.53	0.56	0.46	20354
weighted avg	0.82	0.56	0.64	20354

```
In [ ]: from sklearn.ensemble import RandomForestClassifier
# Random Forest with RUS
random_forest_rus = RandomForestClassifier(class_weight='balanced_subsample', random_state=42)
random_forest_rus.fit(X_train_rus, y_train_rus)

# Evaluate the model
y_pred_rf = random_forest_rus.predict(X_test)
accuracy_rf = accuracy_score(y_test, y_pred_rf)
conf_matrix_rf = confusion_matrix(y_test, y_pred_rf)
class_report_rf = classification_report(y_test, y_pred_rf)

print('Random Forest with RUS')
print(f'Accuracy: {accuracy_rf}')
print('Confusion Matrix:')
print(conf_matrix_rf)
print('Classification Report:')
print(class_report_rf)
```

Random Forest with RUS

Accuracy: 0.6215485899577479

Confusion Matrix:

```
[[11270  6799]
```

```
 [  904 1381]]
```

Classification Report:

	precision	recall	f1-score	support
0	0.93	0.62	0.75	18069
1	0.17	0.60	0.26	2285
accuracy			0.62	20354
macro avg	0.55	0.61	0.50	20354
weighted avg	0.84	0.62	0.69	20354

```
In [ ]: from sklearn.ensemble import GradientBoostingClassifier
# Gradient Boosting with RUS
gradient_boosting_rus = GradientBoostingClassifier(random_state=42)
gradient_boosting_rus.fit(X_train_rus, y_train_rus)

# Evaluate the model
y_pred_gb = gradient_boosting_rus.predict(X_test)
accuracy_gb = accuracy_score(y_test, y_pred_gb)
conf_matrix_gb = confusion_matrix(y_test, y_pred_gb)
class_report_gb = classification_report(y_test, y_pred_gb)

print('Gradient Boosting with RUS')
print(f'Accuracy: {accuracy_gb}')
print('Confusion Matrix:')
print(conf_matrix_gb)
print('Classification Report:')
print(class_report_gb)
```

Gradient Boosting with RUS
Accuracy: 0.6251351085781665
Confusion Matrix:
[[11281 6788]
 [842 1443]]

Classification Report:

	precision	recall	f1-score	support
0	0.93	0.62	0.75	18069
1	0.18	0.63	0.27	2285
accuracy			0.63	20354
macro avg	0.55	0.63	0.51	20354
weighted avg	0.85	0.63	0.69	20354