

CIND820-Nehal's project-Diabetes dataset Preprocessing

July 2, 2024

CIND 820- Big Data Analytics Project

Using Machine Learning for Prediction of Early Readmission of Diabetic Patients

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```
[ ]: !pip install pandas
import sys
!{sys.executable} -m pip install -U pandas-profiling
!jupyter nbextension enable --py widgetsnbextension
!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 2.6 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 11.8 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 14.1 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 26.1 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: cycycler>=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=545e6d18eaa6b9a18faf890428aab505d70135df2158336ed321617327a4b698
 Stored in directory: /root/.cache/pip/wheels/dd/91/29/a79cecb328d01739e64017b6
 fb9a1ab9d8cb1853098ec5966d
 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)

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

```
[ ]: #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))
```

<IPython.core.display.HTML object>

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
1	No	Ch	>30
2	No	No	NO
3	No	Ch	NO
4	No	Ch	NO
5	No	No	>30
6	No	Ch	NO
7	No	No	>30
8	No	Ch	NO
9	No	Ch	NO

[10 rows x 50 columns]

```
[ ]: #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	acetoheamide	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: int64(13), object(37)

memory usage: 38.8+ MB

None

```
[ ]: #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'
]

```

```

[ ]: # Define mappings according to the IDS_mapping file
admission_type_mapping = {
    1: 'Emergency',
    2: 'Urgent',
    3: 'Elective',
    4: 'Newborn',
    5: 'Not Available',
    6: 'NULL',
    7: 'Trauma Center',
    8: 'Not Mapped'
}

discharge_disposition_mapping = {
    1: 'Discharged to home',
    2: 'Discharged/transferred to another short term hospital',
    3: 'Discharged/transferred to SNF',
    4: 'Discharged/transferred to ICF',
    5: 'Discharged/transferred to another type of inpatient care institution',
    6: 'Discharged/transferred to home with home health service',
    7: 'Left AMA',
    8: 'Discharged/transferred to home under care of Home IV provider',
    9: 'Admitted as an inpatient to this hospital',
    10: 'Neonate discharged to another hospital for neonatal aftercare',
    11: 'Expired',
    12: 'Still patient or expected to return for outpatient services',
    13: 'Hospice / home',
    14: 'Hospice / medical facility',
    15: 'Discharged/transferred within this institution to Medicare approved_
↪swing bed',
    16: 'Discharged/transferred/referred another institution for outpatient_
↪services',
    17: 'Discharged/transferred/referred to this institution for outpatient_
↪services',
    18: 'NULL',
    19: 'Expired at home. Medicaid only, hospice.',
    20: 'Expired in a medical facility. Medicaid only, hospice.',
    21: 'Expired, place unknown. Medicaid only, hospice.',
    22: 'Discharged/transferred to another rehab fac including rehab units of a_
↪hospital.',
    23: 'Discharged/transferred to a long term care hospital.',
    24: 'Discharged/transferred to a nursing facility certified under Medicaid_
↪but not certified under Medicare.',
    25: 'Not Mapped',
    26: 'Unknown/Invalid',
    27: 'Discharged/transferred to a federal health care facility.',
    28: 'Discharged/transferred/referred to a psychiatric hospital of_
↪psychiatric distinct part unit of a hospital',

```

```

    29: 'Discharged/transferred to a Critical Access Hospital (CAH)',
    30: 'Discharged/transferred to another Type of Health Care Institution not_
↳Defined Elsewhere'
}

admission_source_mapping = {
    1: 'Physician Referral',
    2: 'Clinic Referral',
    3: 'HMO Referral',
    4: 'Transfer from a hospital',
    5: 'Transfer from a Skilled Nursing Facility (SNF)',
    6: 'Transfer from another health care facility',
    7: 'Emergency Room',
    8: 'Court/Law Enforcement',
    9: 'Not Available',
    10: 'Transfer from critical access hospital',
    11: 'Normal Delivery',
    12: 'Premature Delivery',
    13: 'Sick Baby',
    14: 'Extramural Birth',
    15: 'Not Available',
    17: 'NULL',
    18: 'Transfer From Another Home Health Agency',
    19: 'Readmission to Same Home Health Agency',
    20: 'Not Mapped',
    21: 'Unknown/Invalid',
    22: 'Transfer from hospital inpt/same fac reslt in a sep claim',
    23: 'Born inside this hospital',
    24: 'Born outside this hospital',
    25: 'Transfer from Ambulatory Surgery Center',
    26: 'Transfer from Hospice'
}

# Create temporary columns for display purposes
df_copy = df.copy()
df_copy['admission_type'] = df_copy['admission_type_id'].
↳map(admission_type_mapping)
df_copy['discharge_disposition'] = df_copy['discharge_disposition_id'].
↳map(discharge_disposition_mapping)
df_copy['admission_source'] = df_copy['admission_source_id'].
↳map(admission_source_mapping)

# Display the first 10 records after mapping
print(df_copy[['admission_type', 'discharge_disposition', 'admission_source']].
↳head())

```

```
admission_type discharge_disposition admission_source
```

0	NULL	Not Mapped	Physician Referral
1	Emergency	Discharged to home	Emergency Room
2	Emergency	Discharged to home	Emergency Room
3	Emergency	Discharged to home	Emergency Room
4	Emergency	Discharged to home	Emergency Room

```
[ ]: #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]

```
[ ]: #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	

```
[ ]: #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

```

```

[ ]: #Plotting categorical variable, including missing values category
pie_chart_columns = [
    'gender', 'readmitted', 'change', 'diabetesMed',
    'max_glu_serum', 'A1Cresult', 'examide',
    'citoglipton', 'insulin', 'metformin'
]

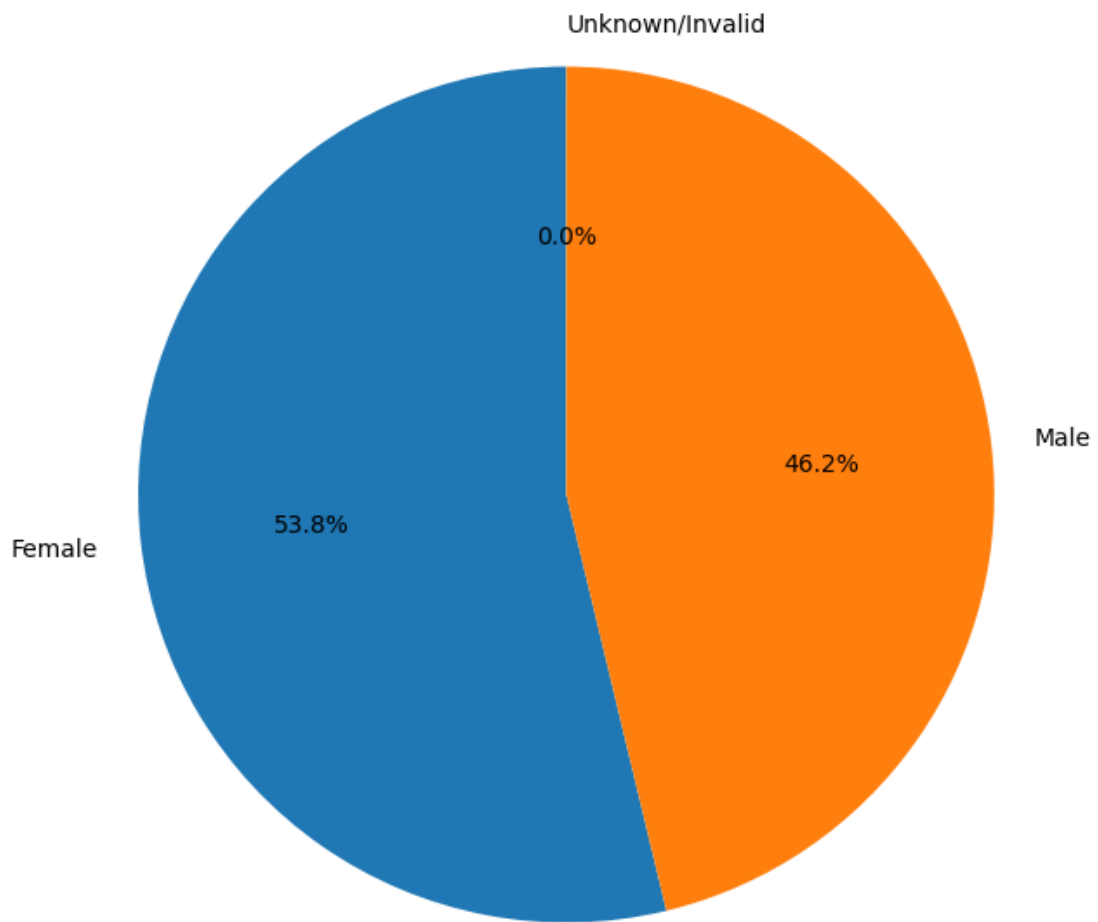
# Plotting pie charts
for col in pie_chart_columns:
    plt.figure(figsize=(8, 8))
    df[col].value_counts().plot.pie(autopct='%1.1f%%', startangle=90)
    plt.title(f'Distribution of {col}')
    plt.ylabel('')
    plt.show()

bar_chart_columns = [
    'race', 'age', 'weight', 'payer_code', 'medical_specialty',
    'diag_1', 'diag_2', 'diag_3', 'repaglinide', 'nateglinide',
    'chlorpropamide', 'glimepiride', 'acetoexamide', 'glipizide',
    'glyburide', 'tolbutamide', 'pioglitazone', 'rosiglitazone',
    'acarbose', 'miglitol', 'troglitazone', 'tolazamide',
    'glyburide-metformin', 'glipizide-metformin', 'glimepiride-pioglitazone',
    'metformin-rosiglitazone', 'metformin-pioglitazone'
]

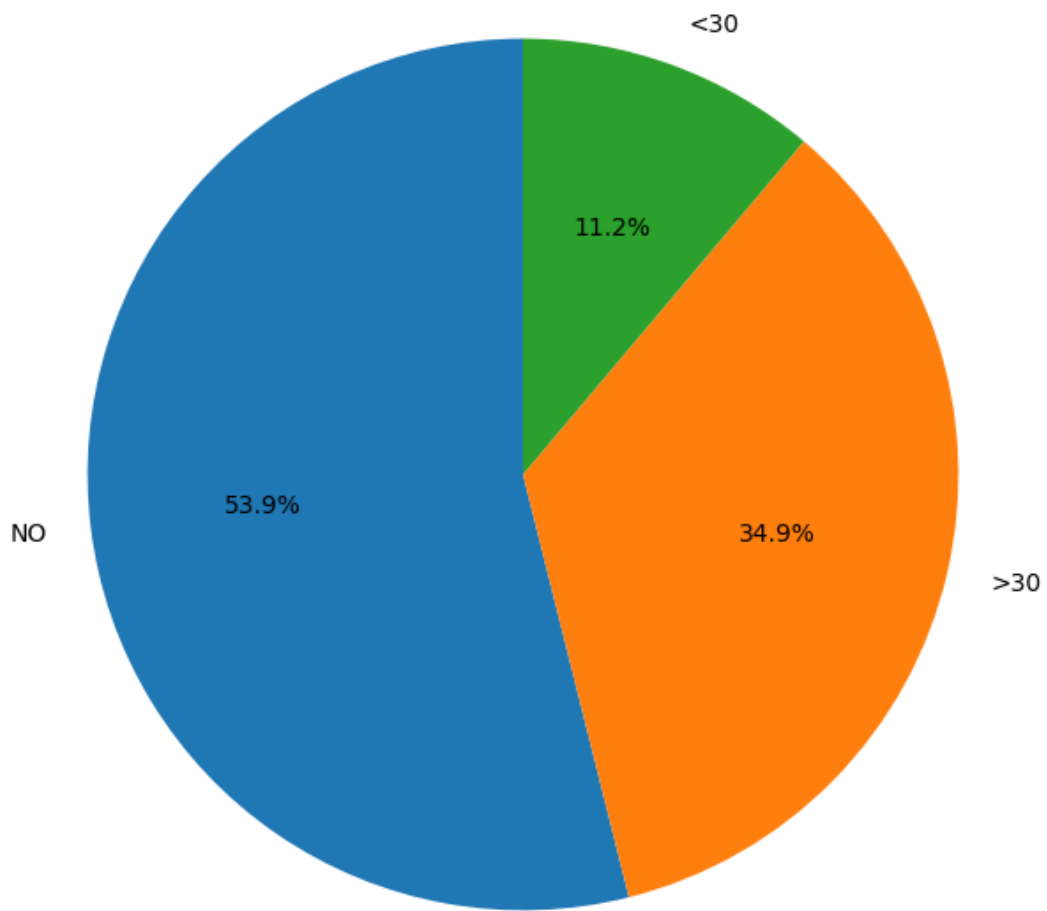
# Plotting bar charts
for col in bar_chart_columns:
    plt.figure(figsize=(12, 6))
    sns.countplot(data=df, x=col)
    plt.title(f'Count of {col}')
    plt.xticks(rotation=90)
    plt.show()

```

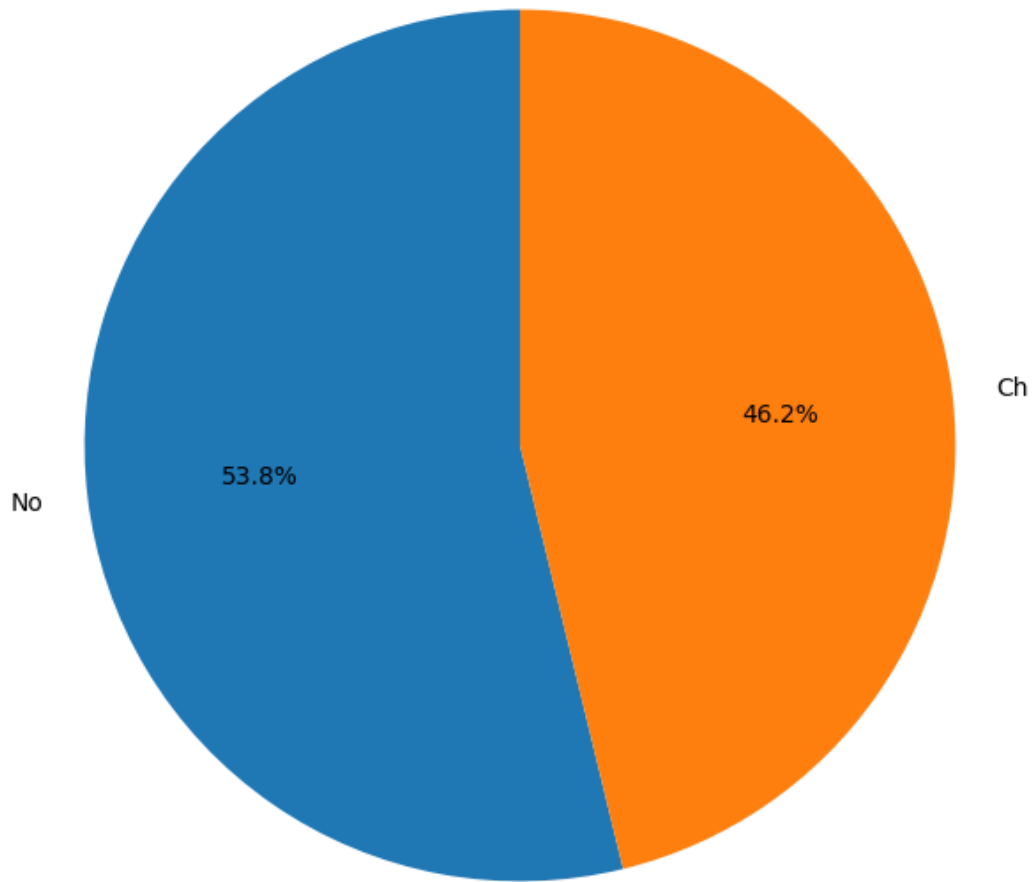

Distribution of gender



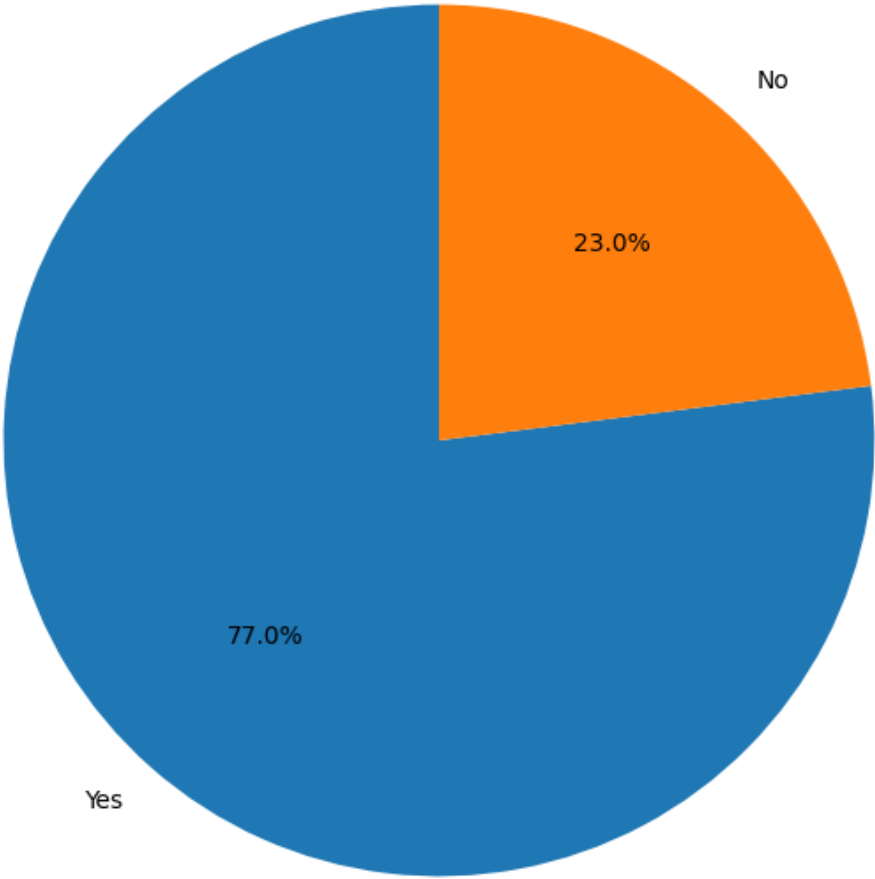
Distribution of readmitted



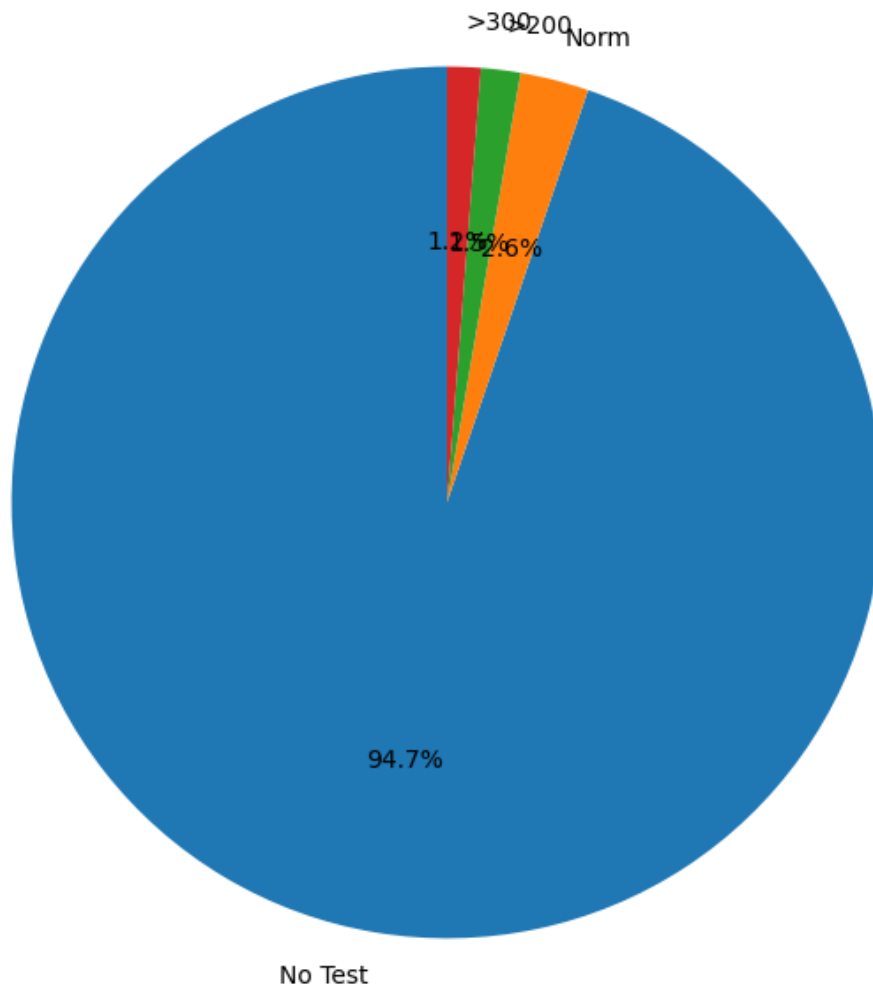
Distribution of change



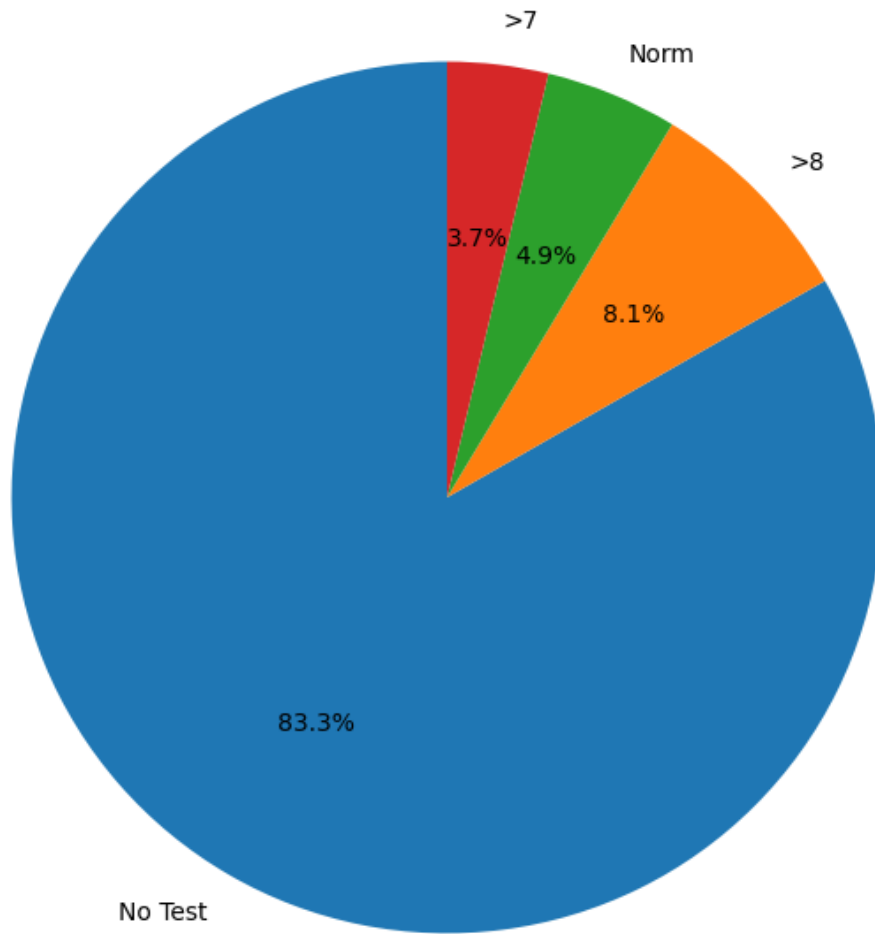
Distribution of diabetesMed



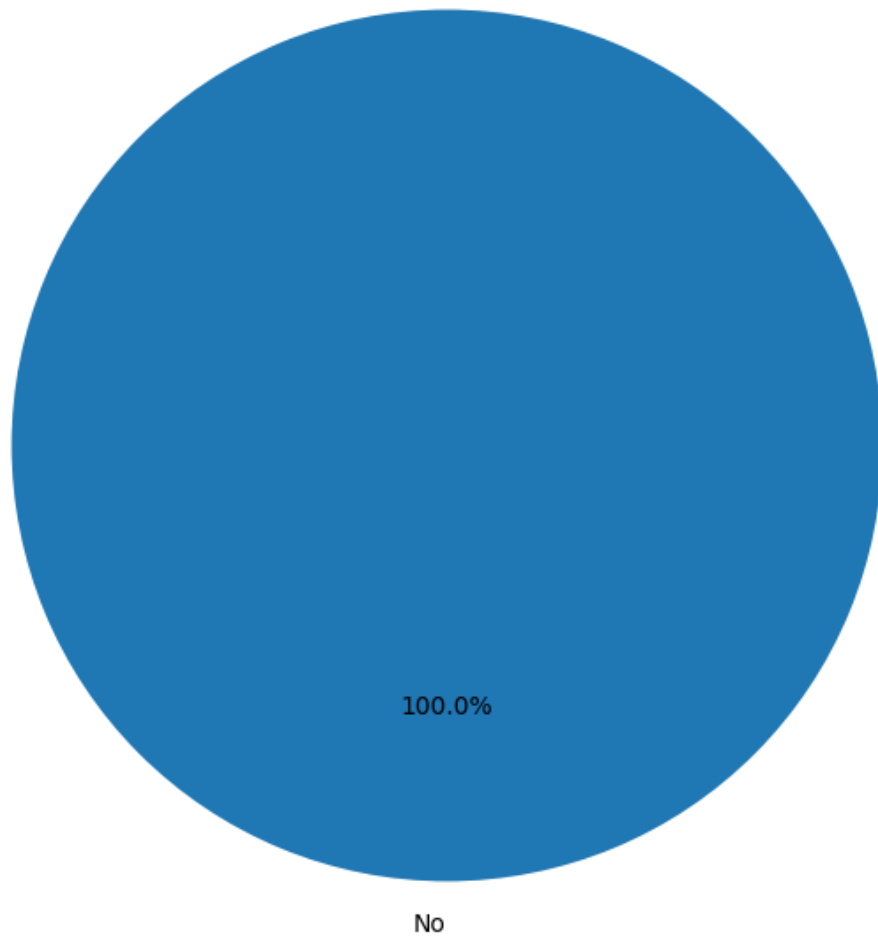
Distribution of max_glu_serum



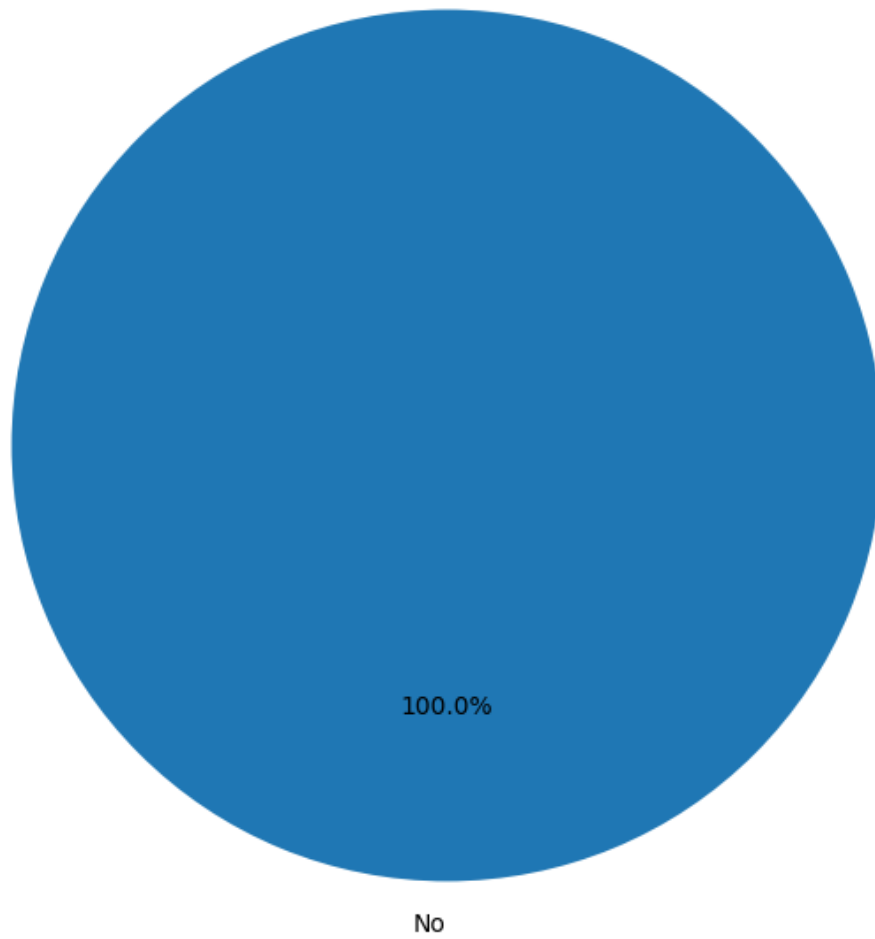
Distribution of A1Cresult



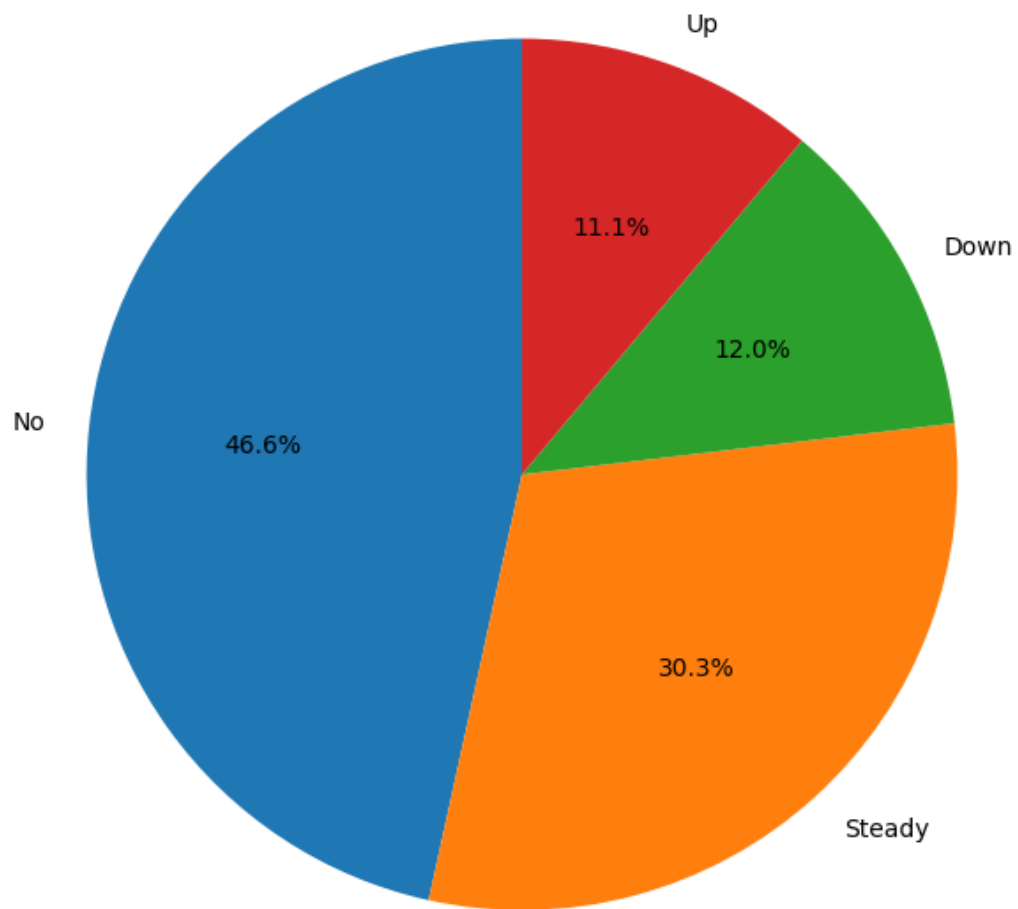
Distribution of examide



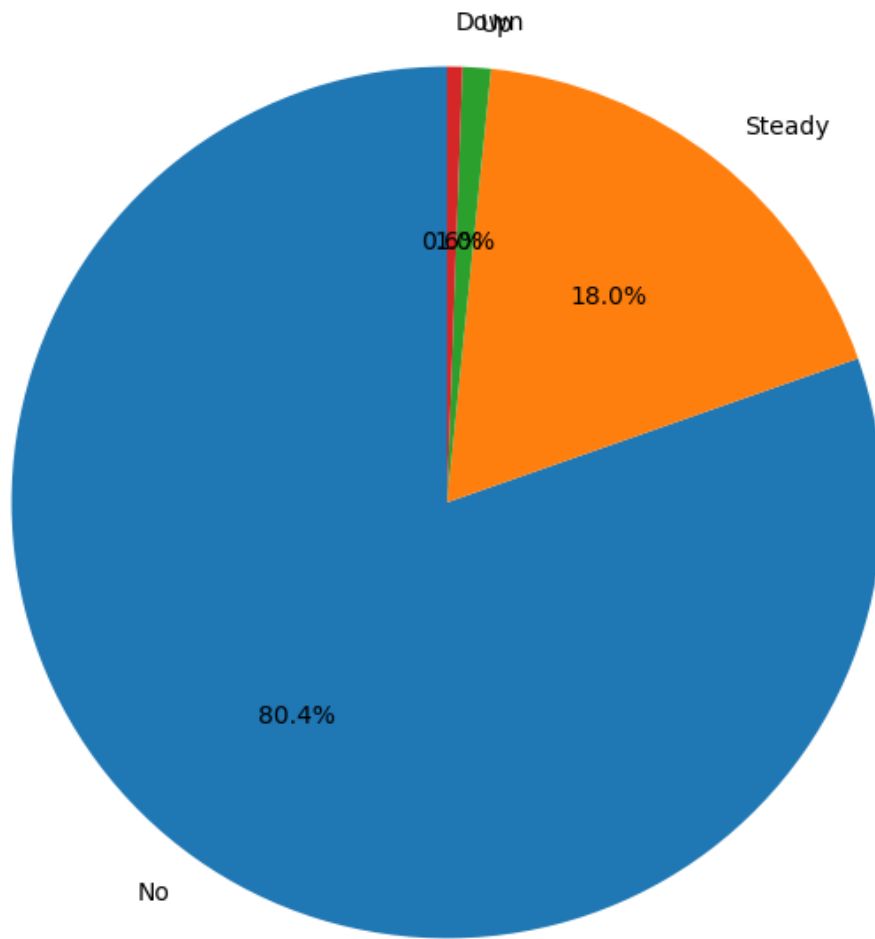
Distribution of citoglipton

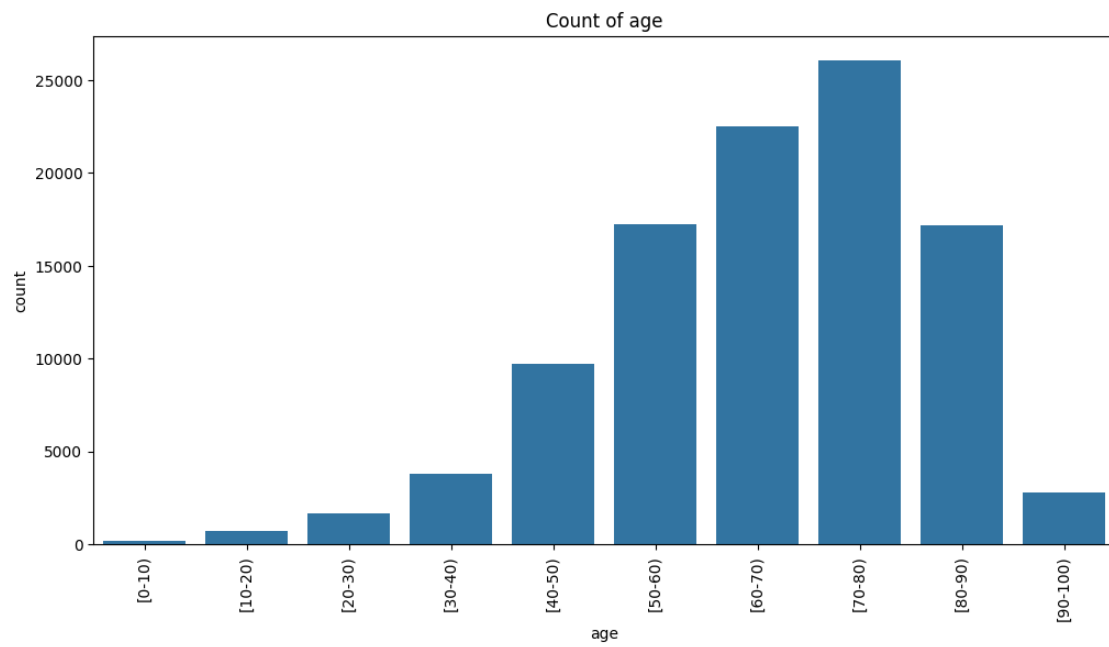
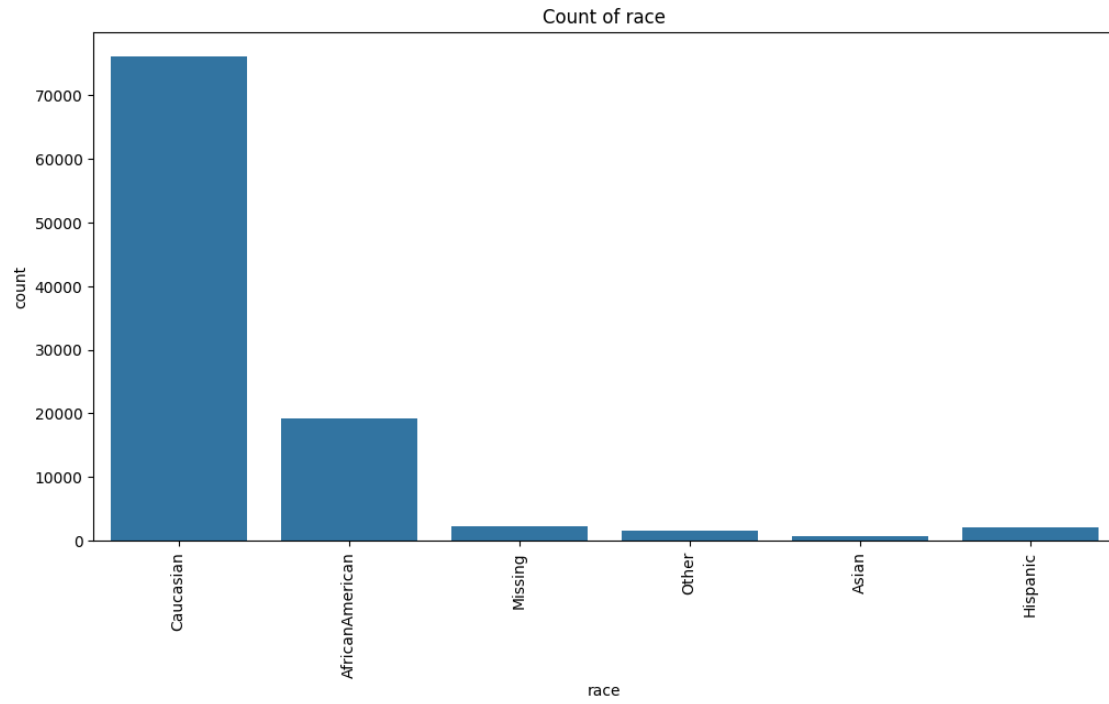


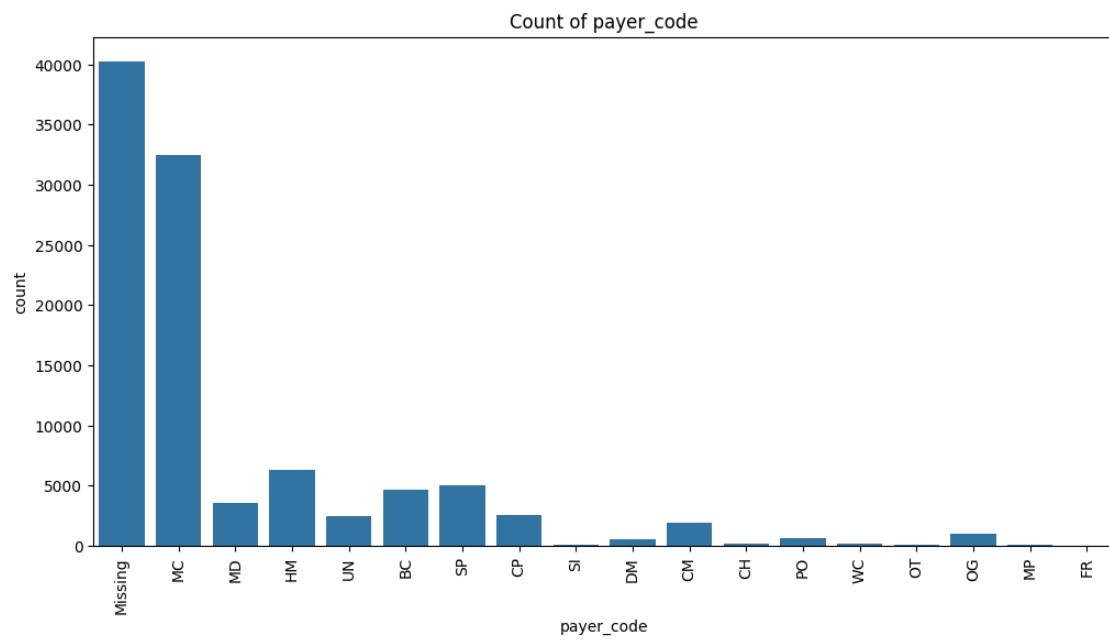
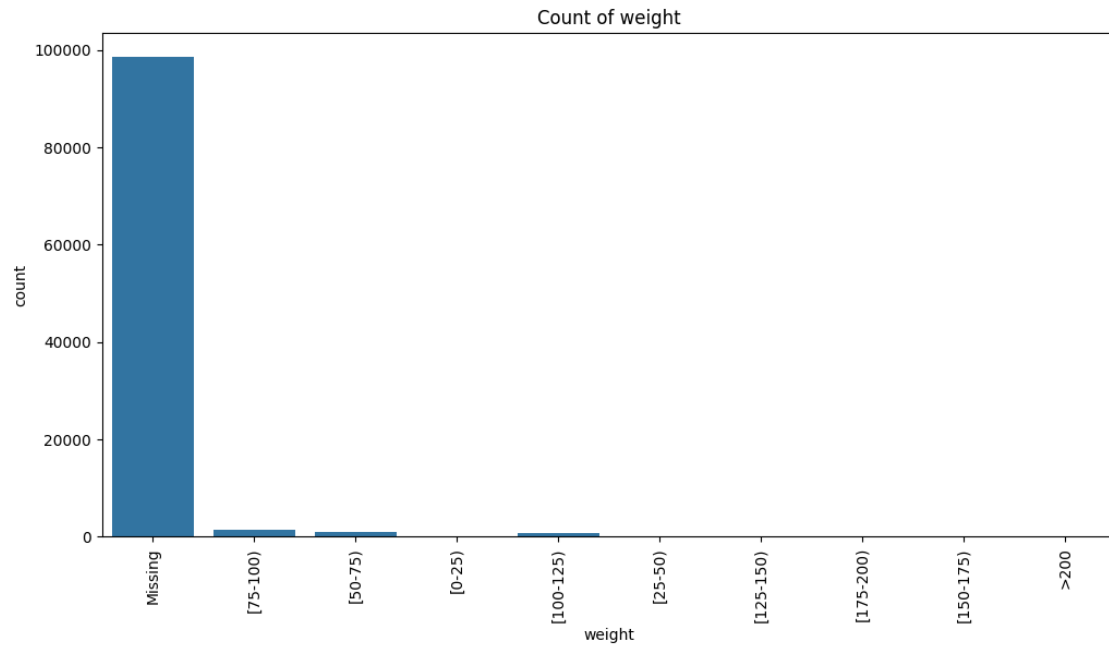
Distribution of insulin

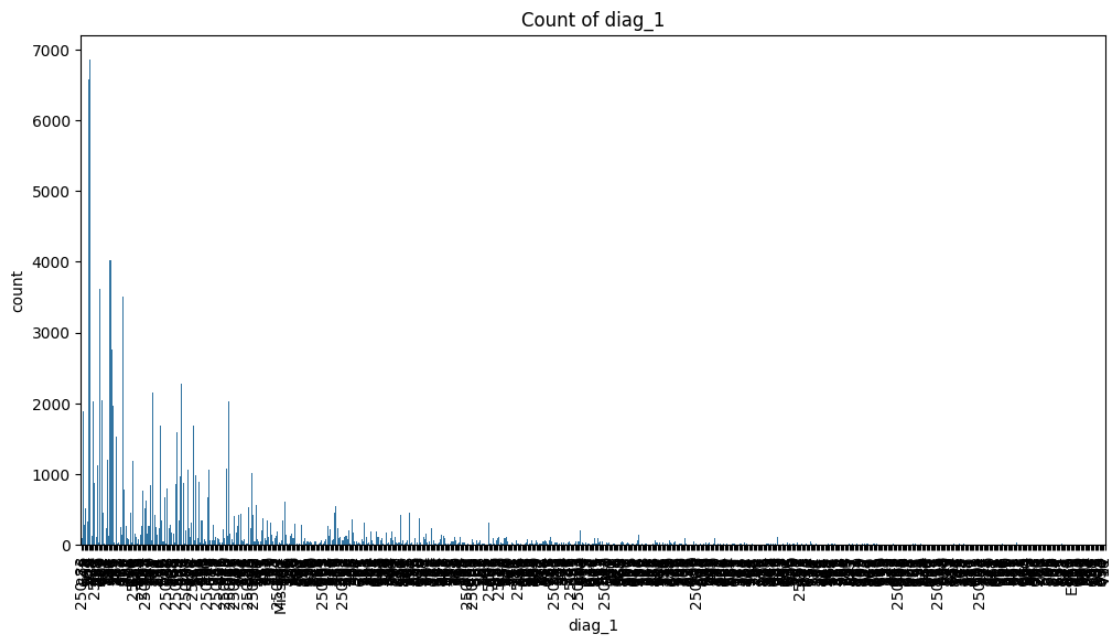
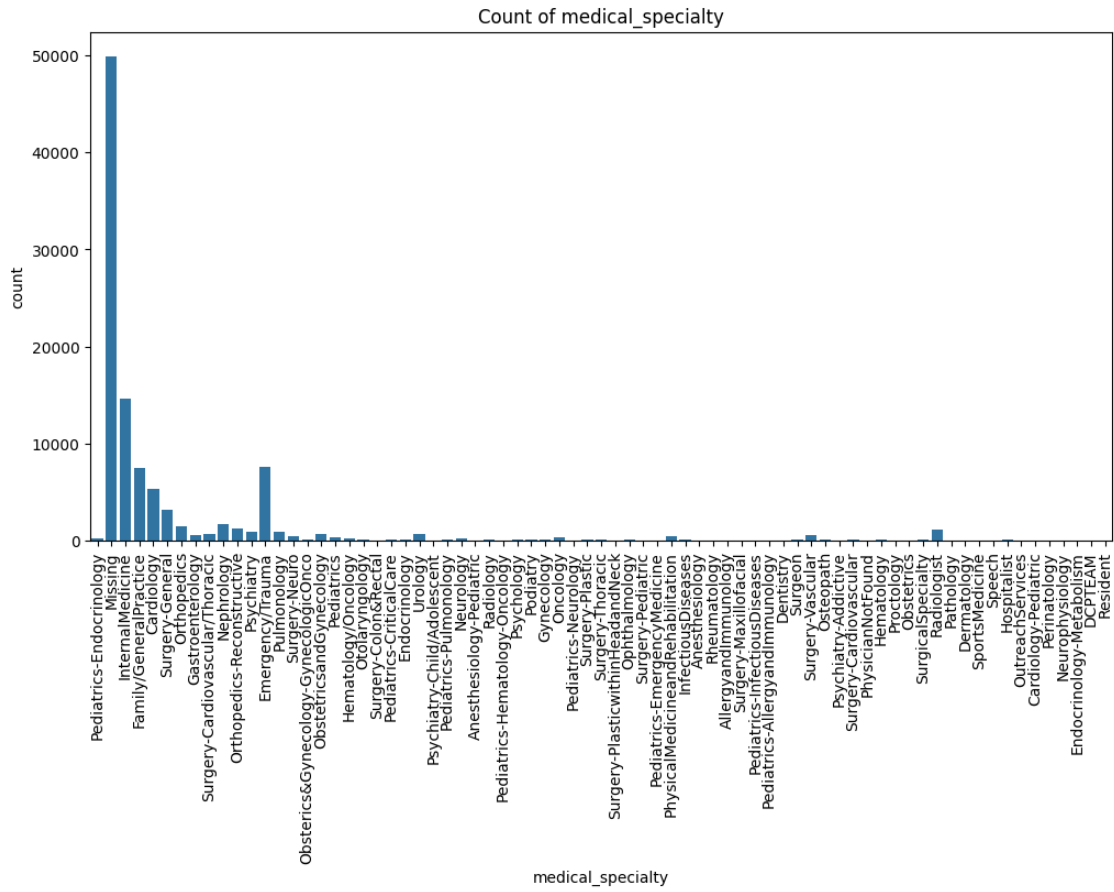


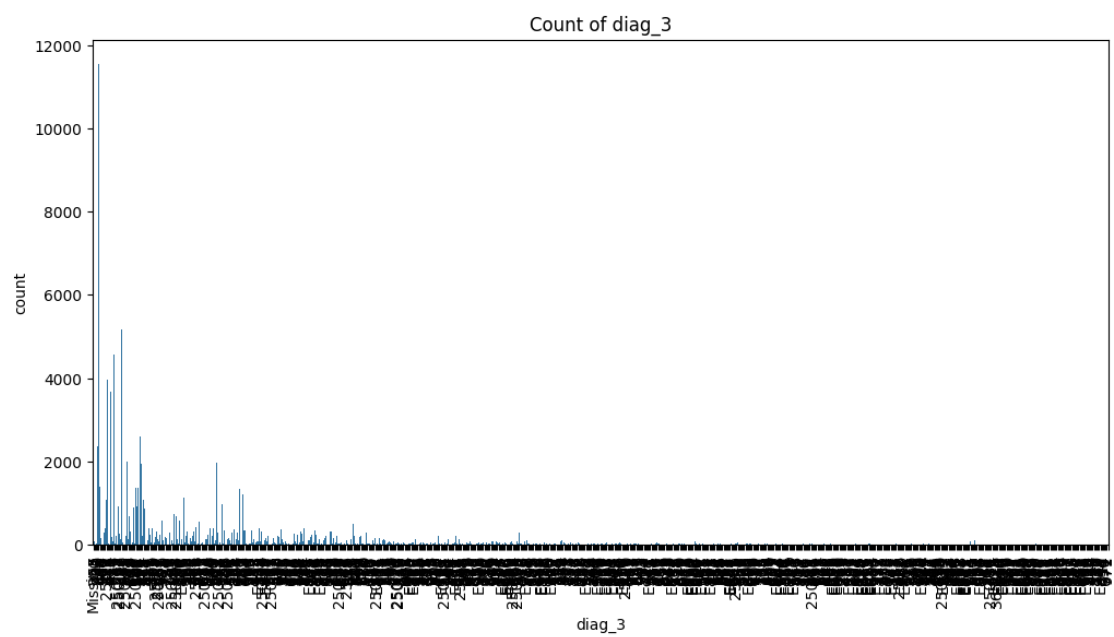
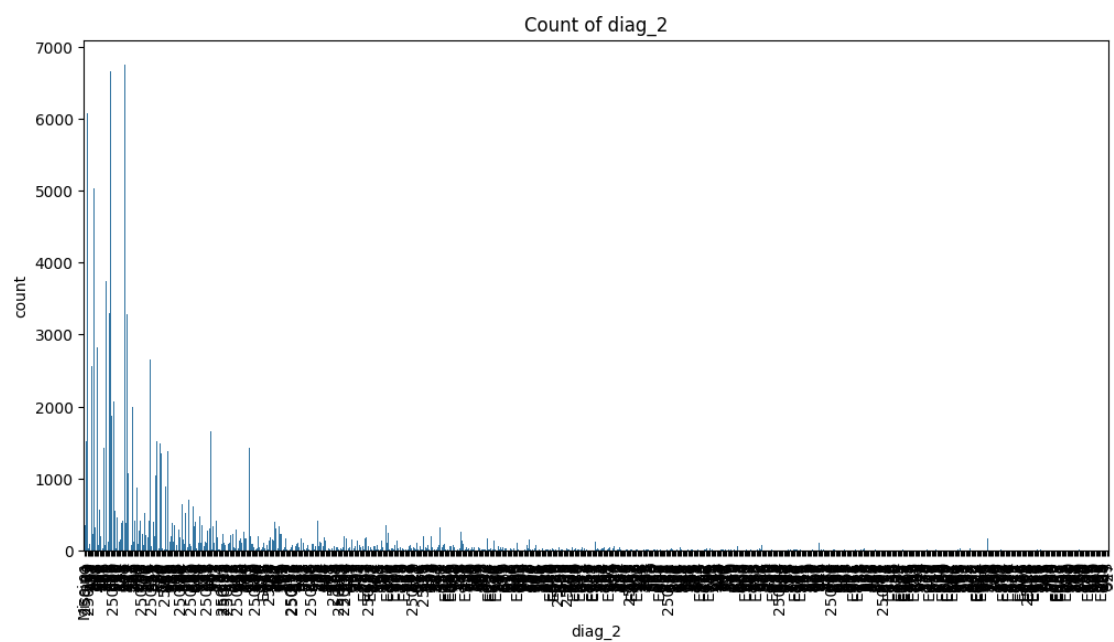
Distribution of metformin

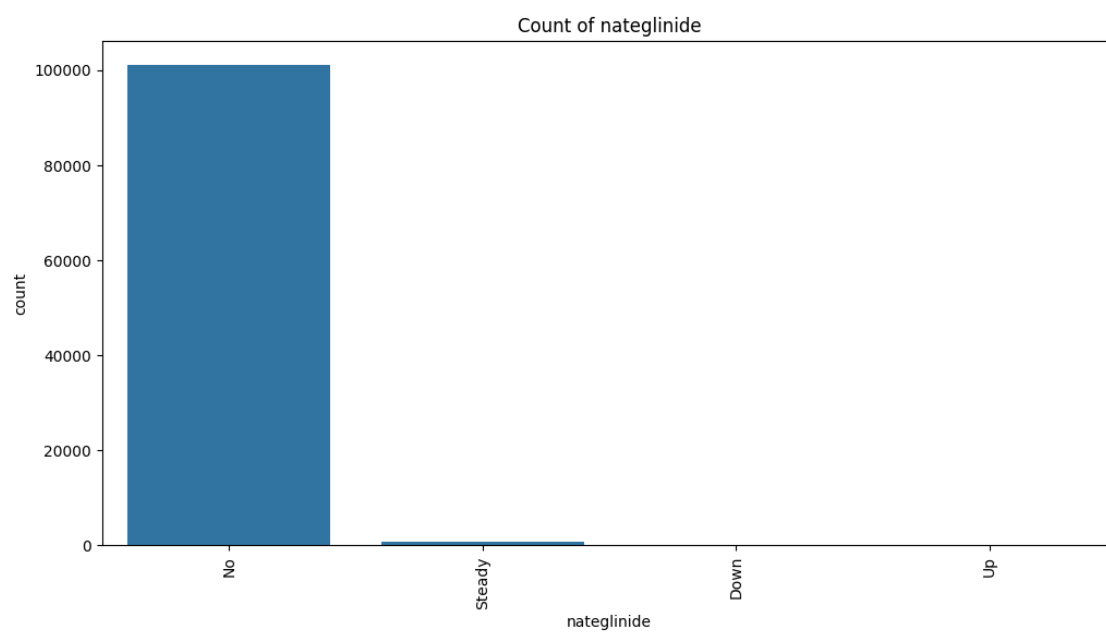
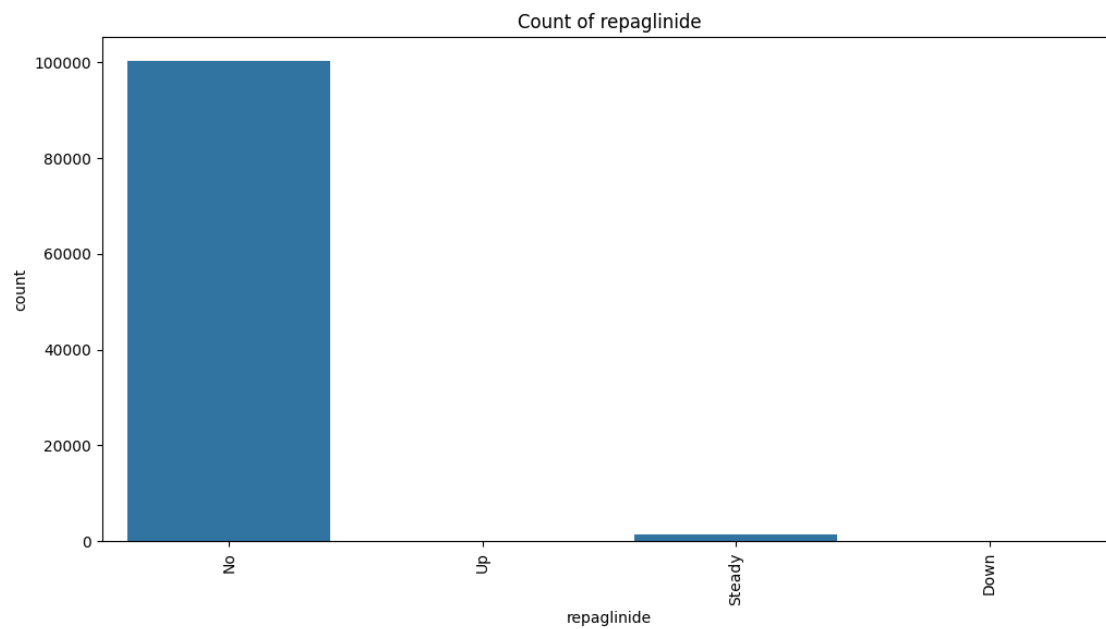


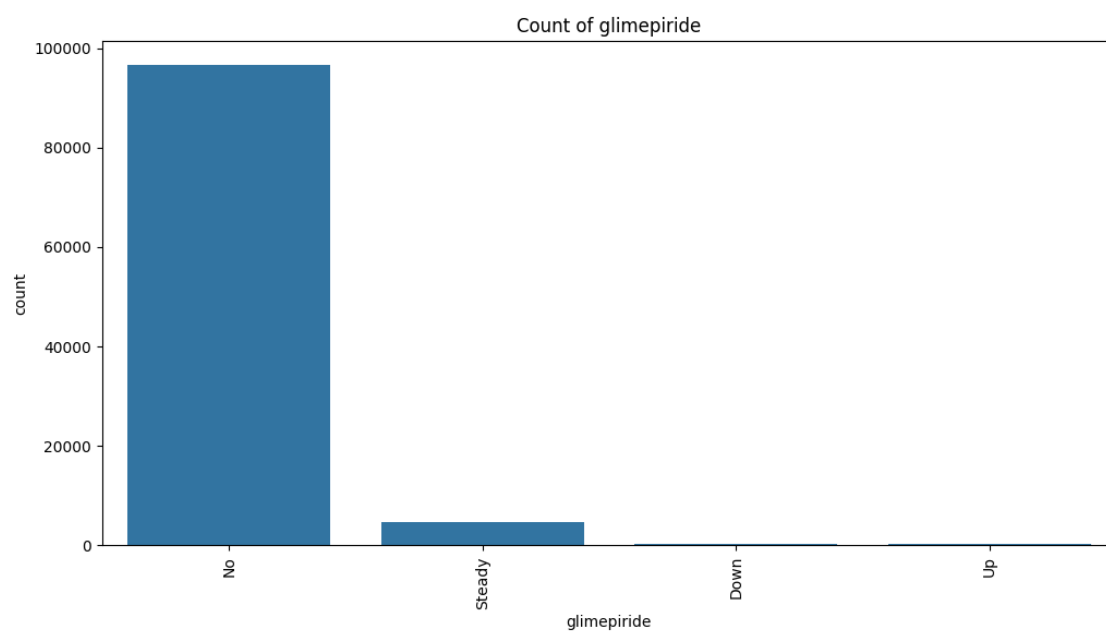
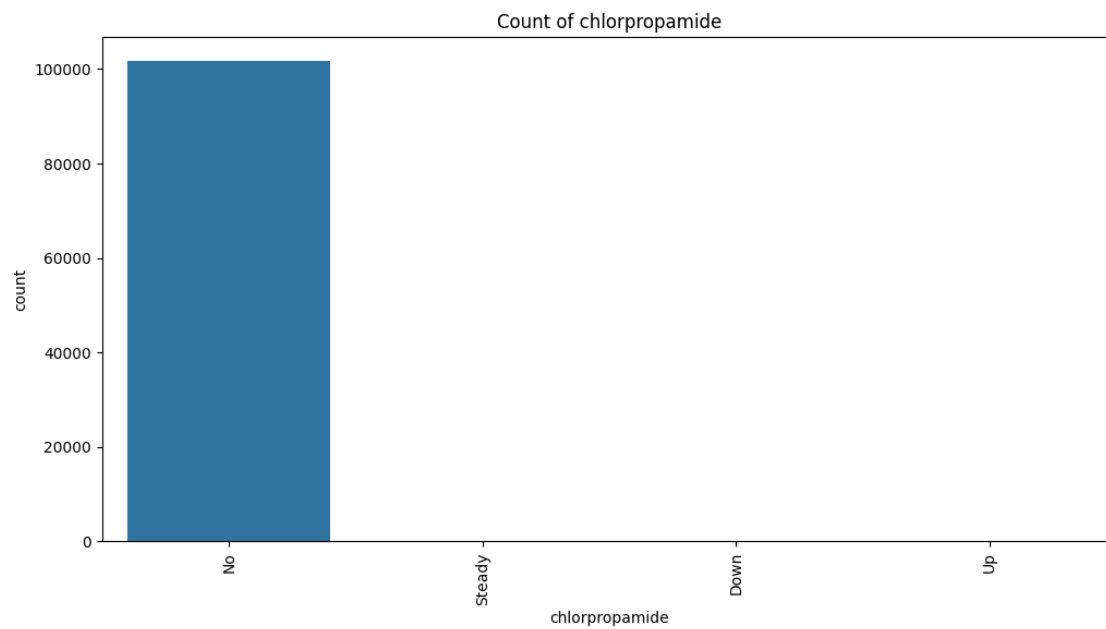


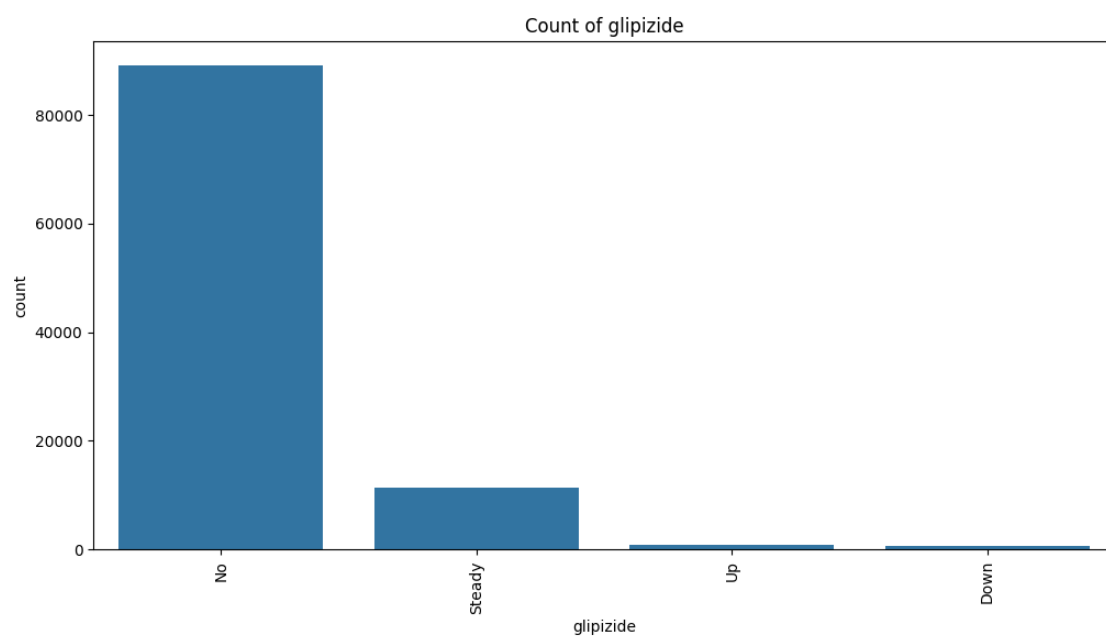
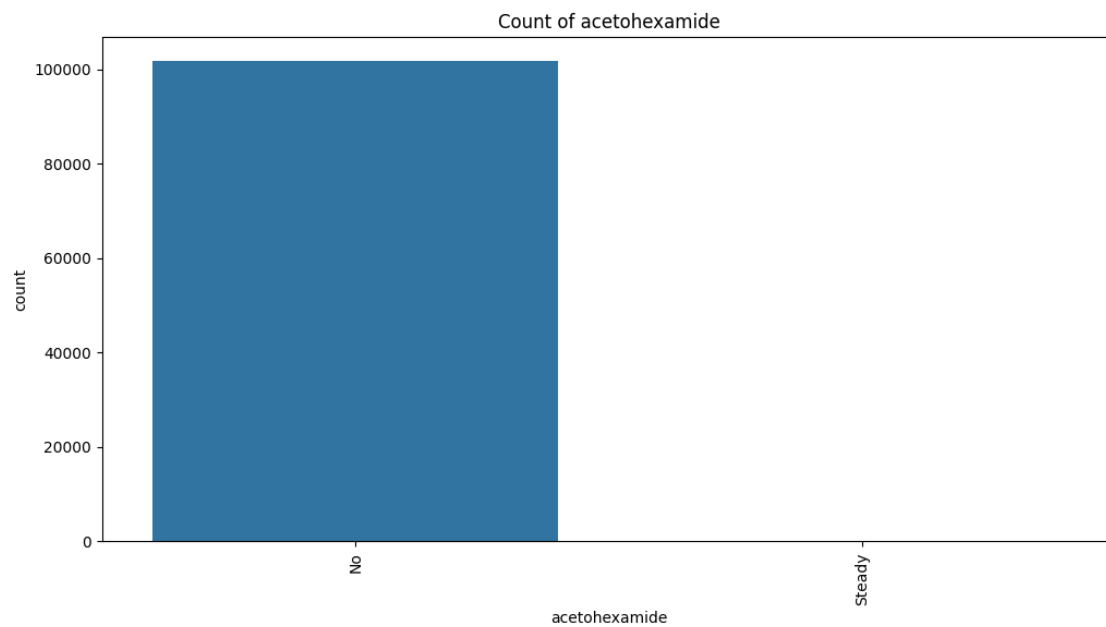


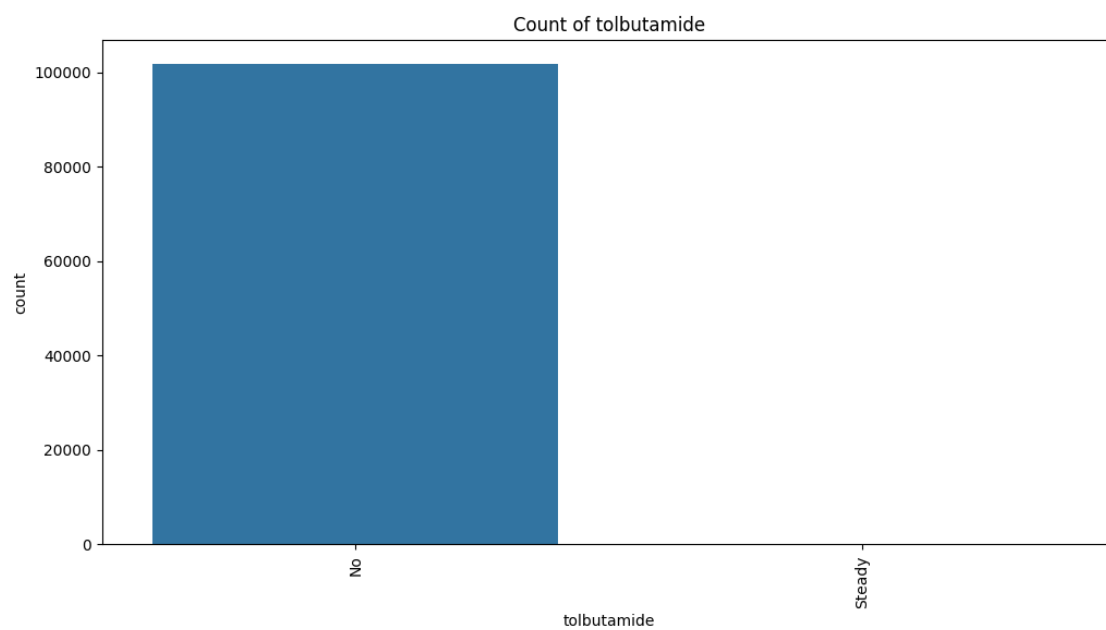
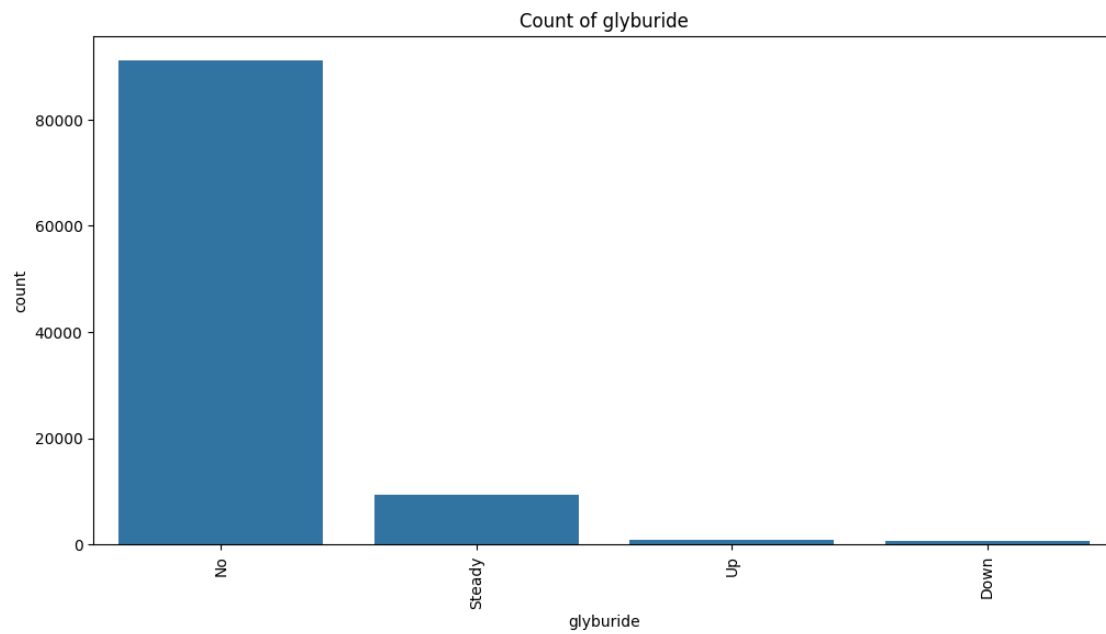


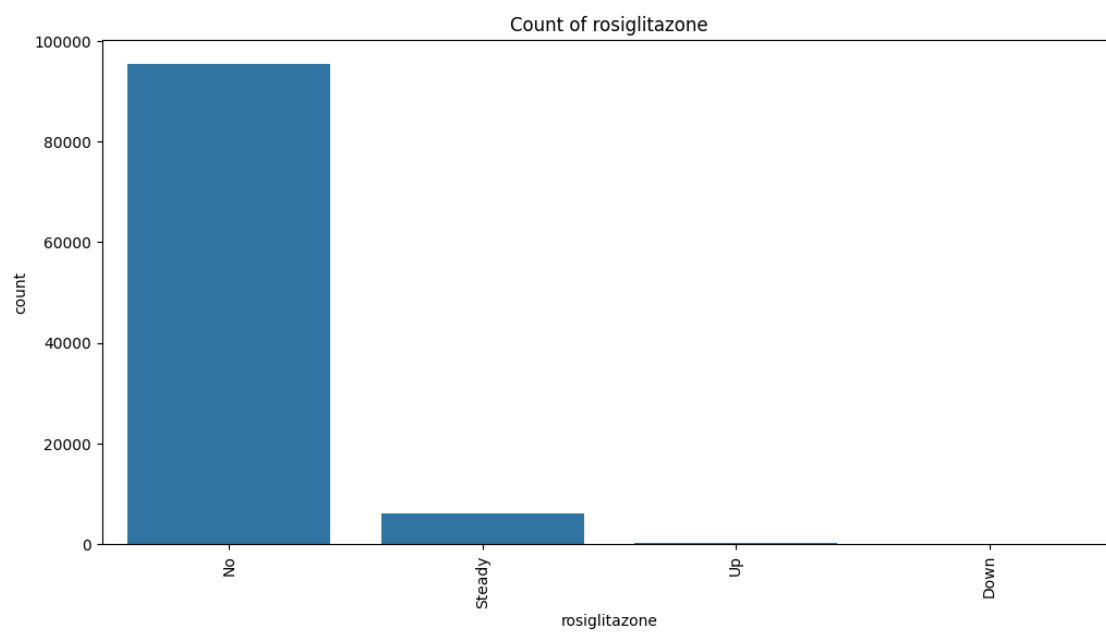
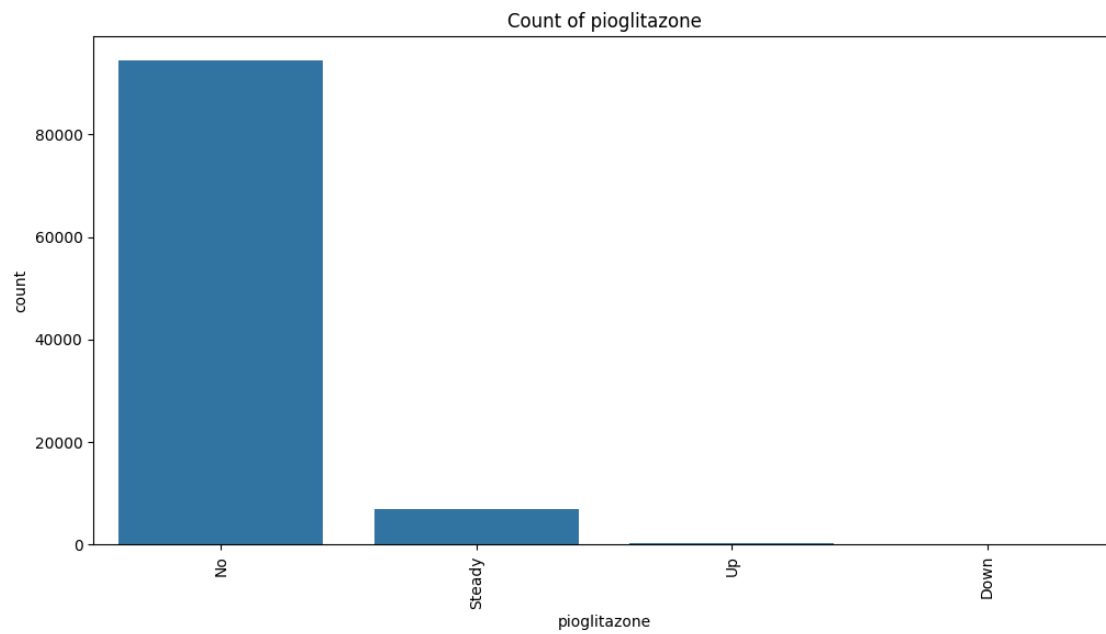


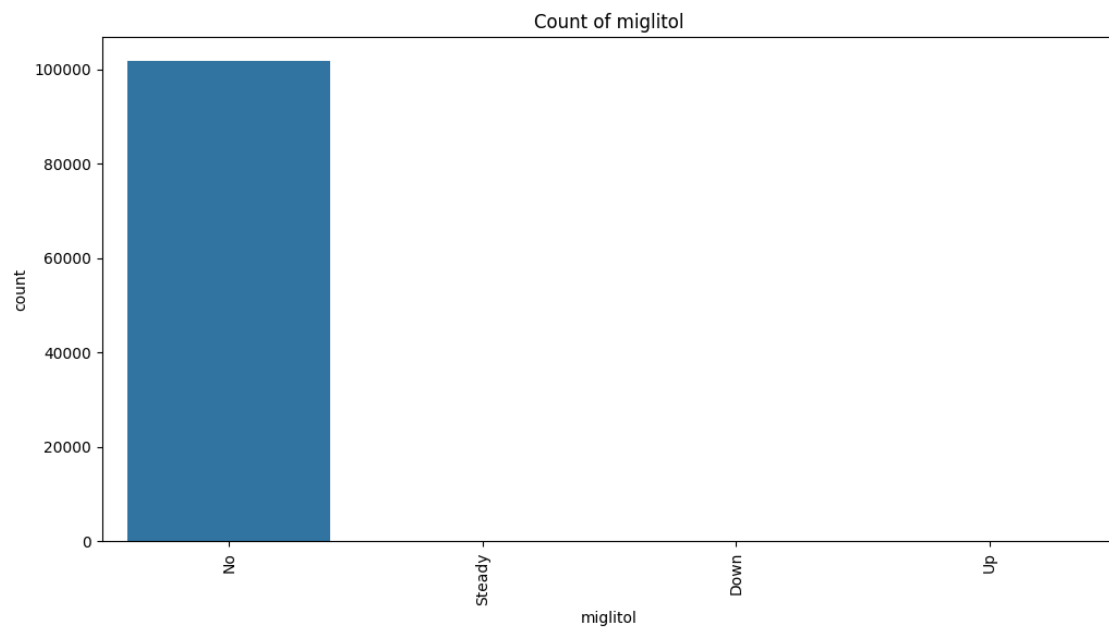
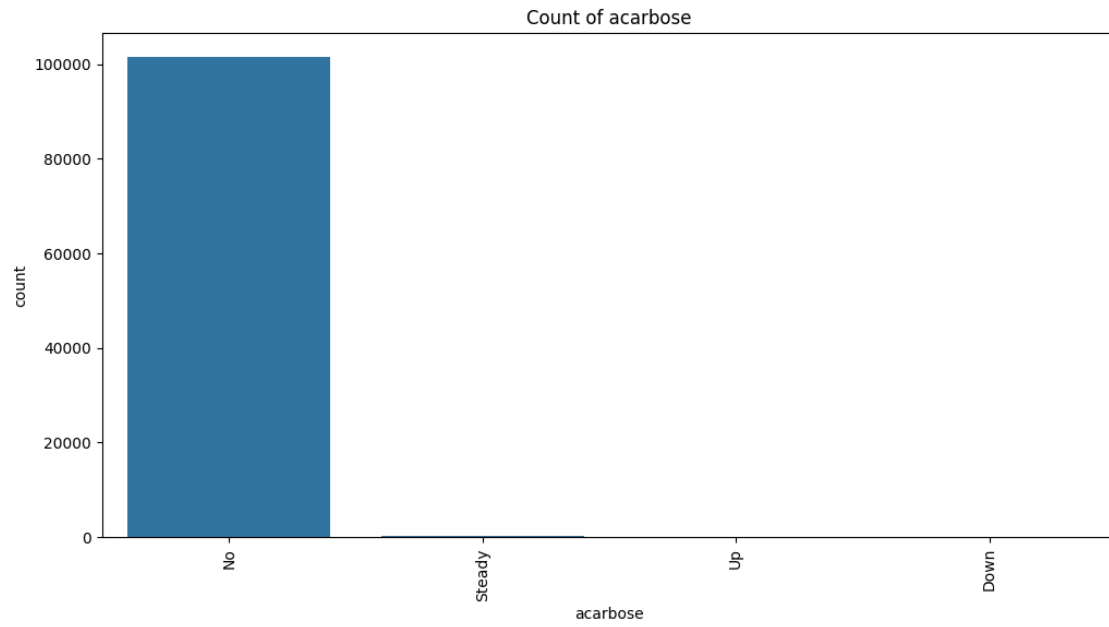


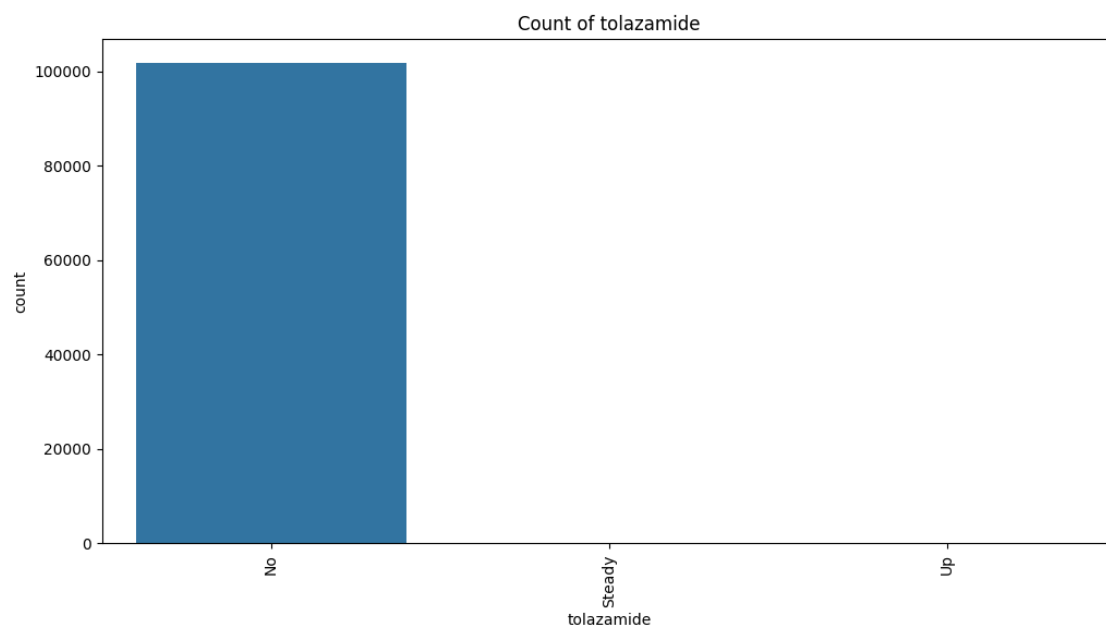
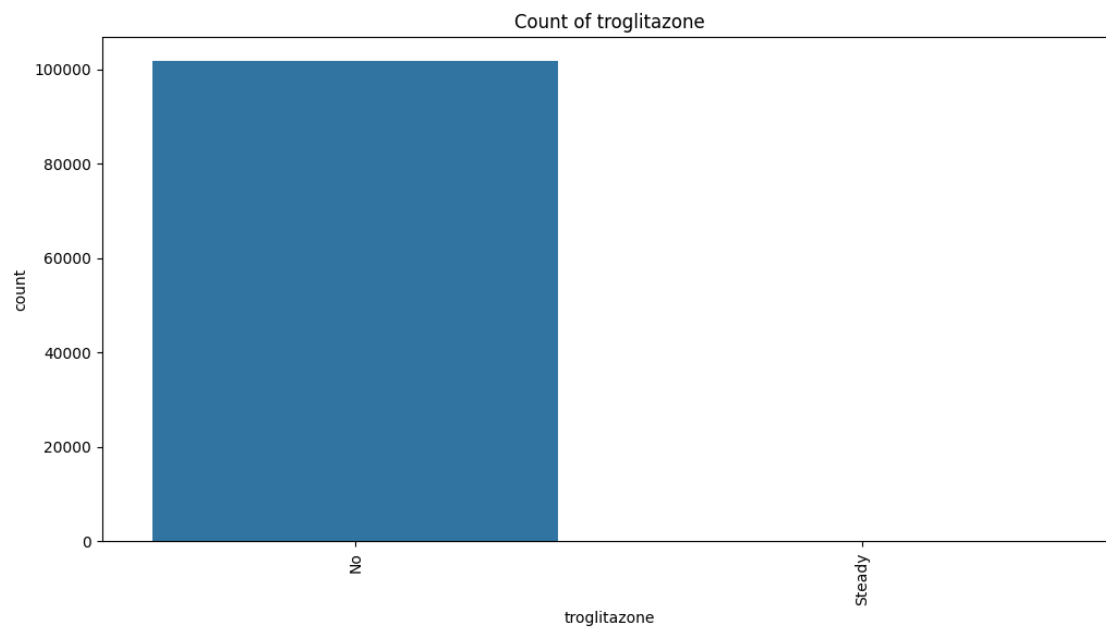


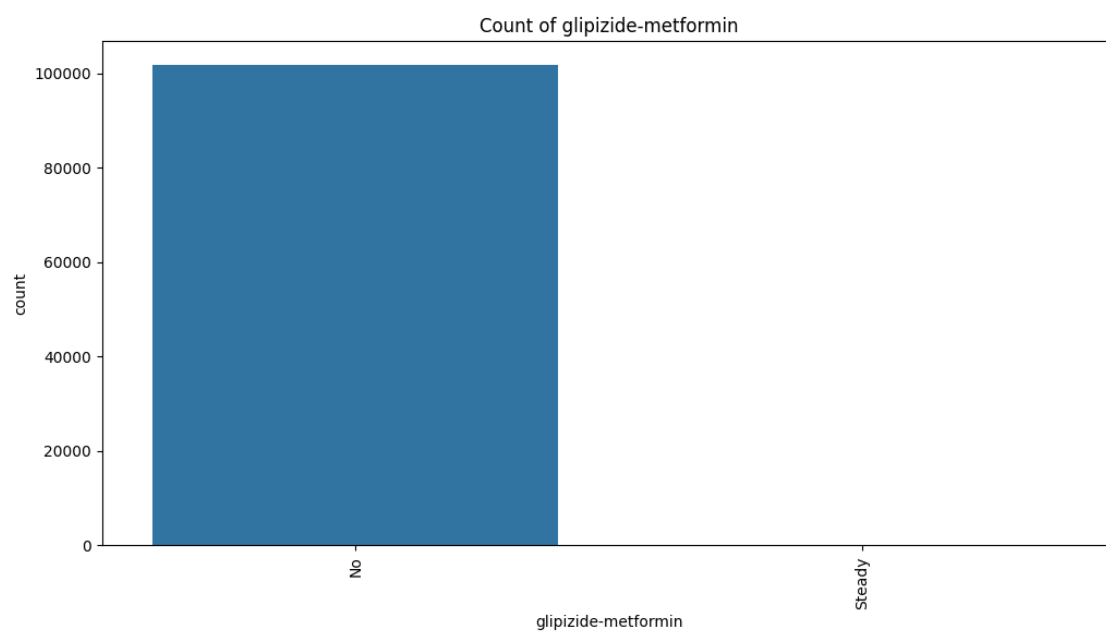
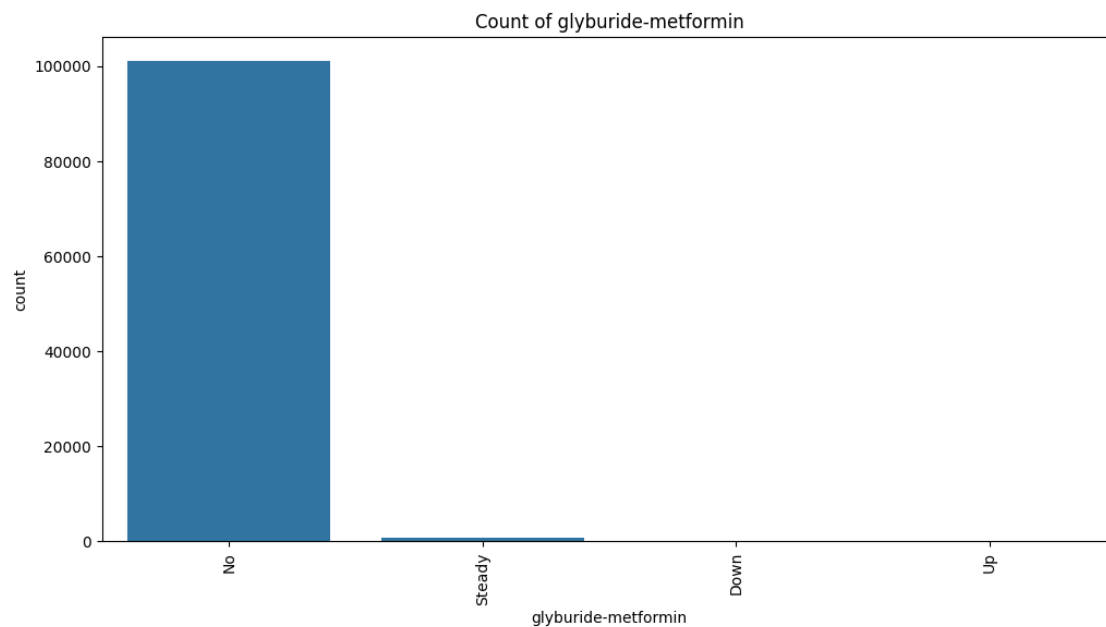


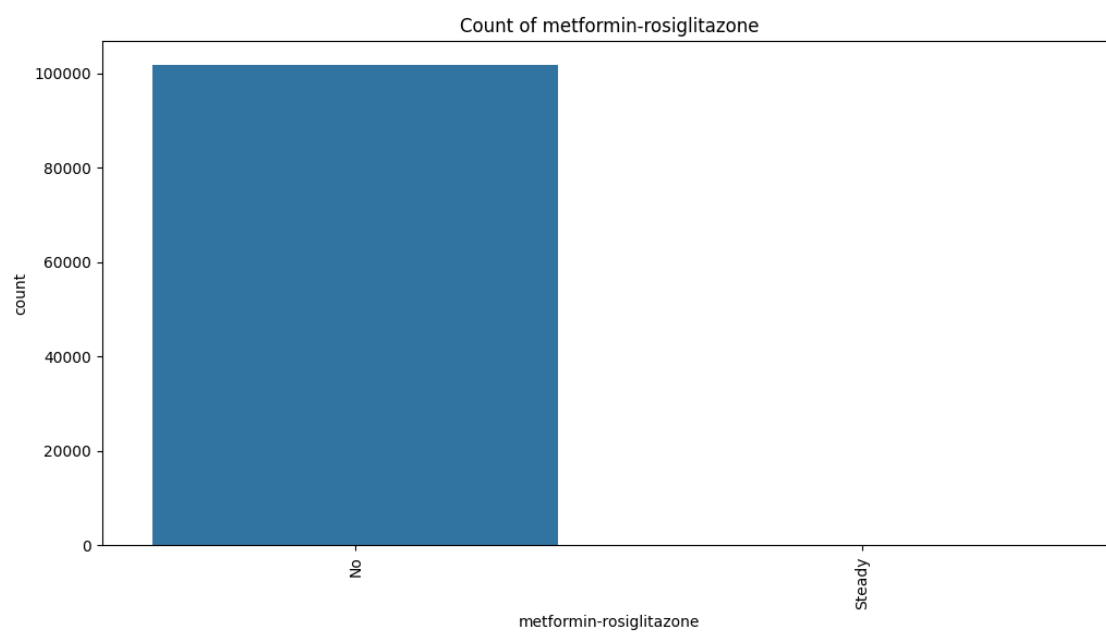
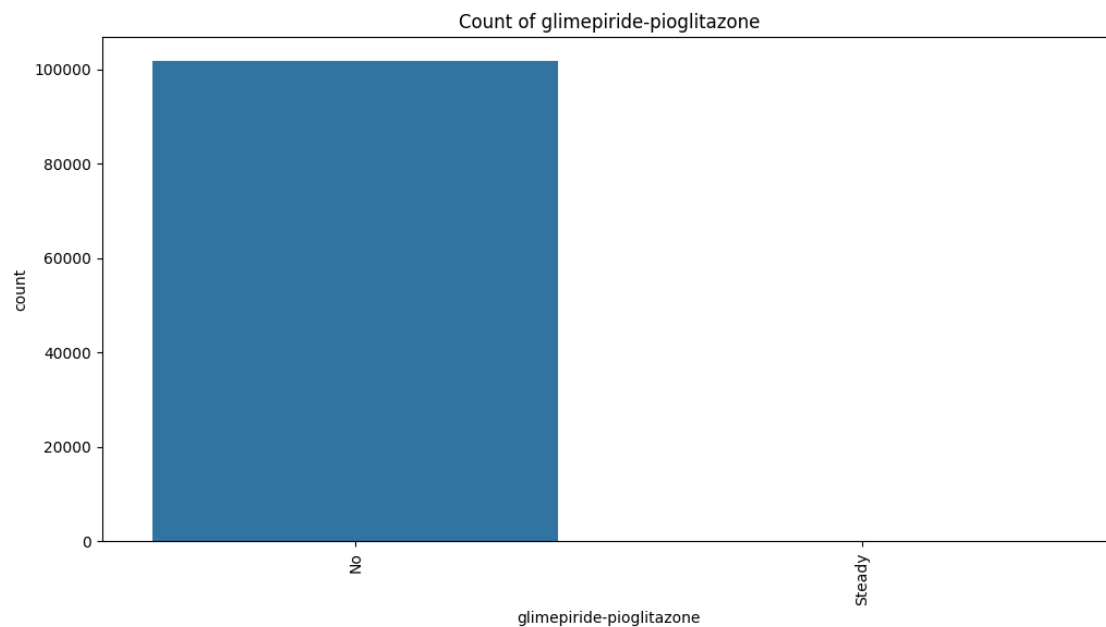


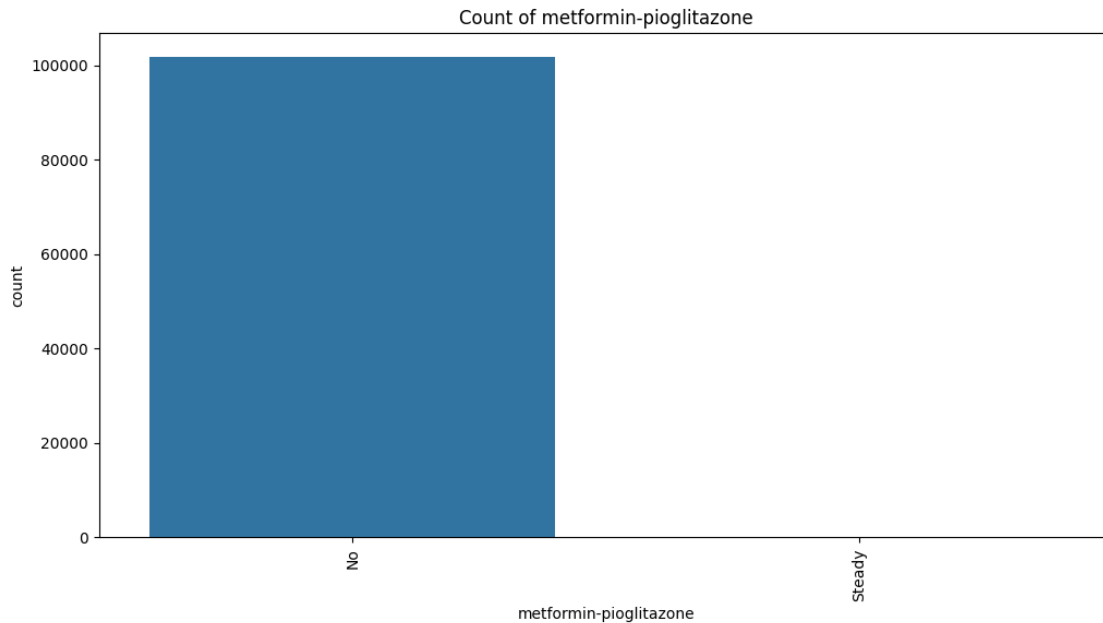












```
[ ]: # converting numeric columns to numeric data types and categorical columns to
      category data type
for col in numeric_columns:
    df[col] = pd.to_numeric(df[col], errors='coerce')

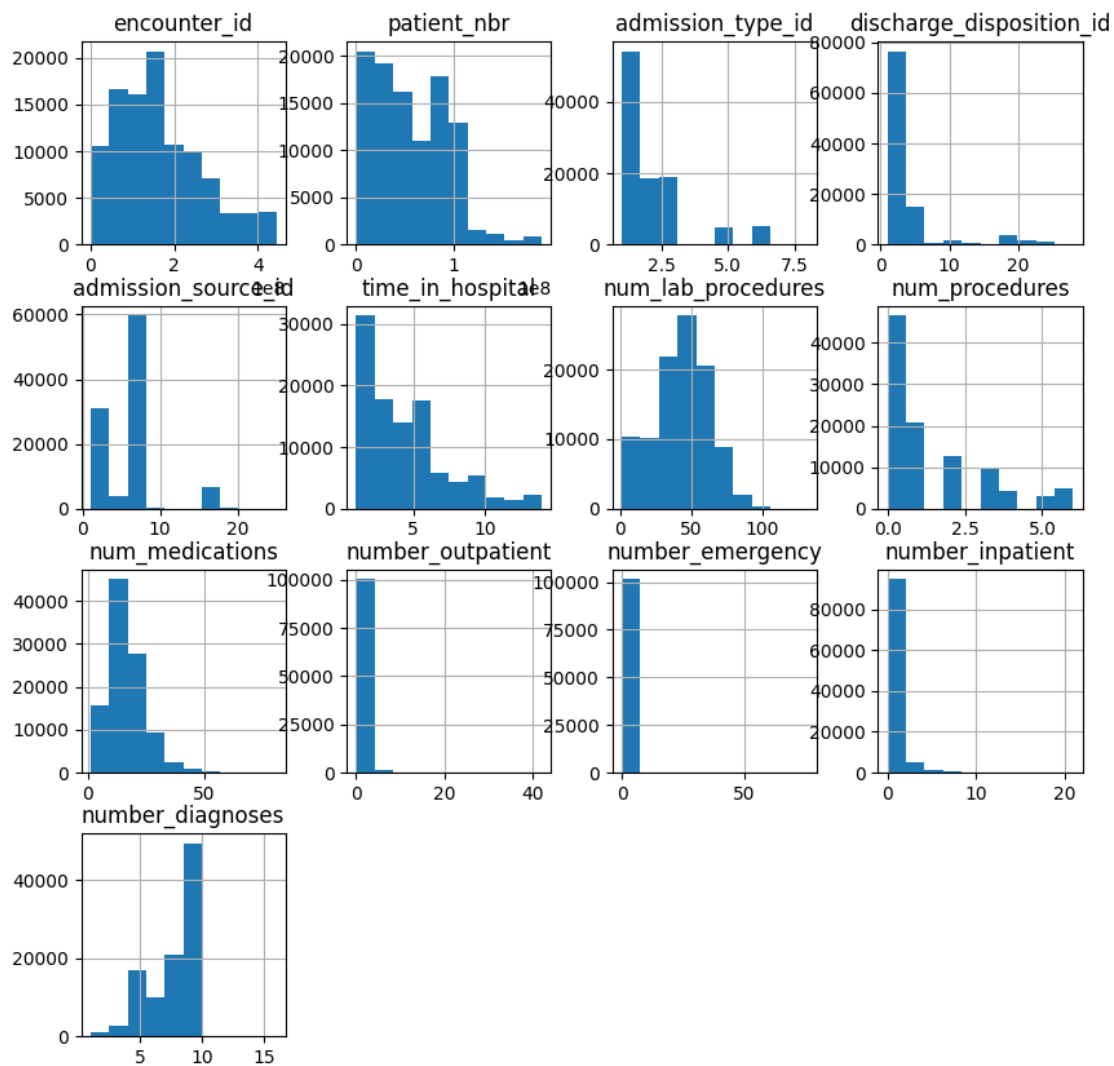
for col in categorical_columns:
    if col in df.columns:
        df[col] = df[col].astype('category')
print(df.dtypes)
print(df[numeric_columns].dtypes)
```

```
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

```
[ ]: #Visualizing the distribution of the numeric variables
df[numeric_columns].hist(figsize=(10, 10))
plt.show()
```



```
[ ]: # 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	

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

Number of duplicate records: 0

```
[ ]: # Panda profiling report
import ydata_profiling
from ydata_profiling import ProfileReport
profile = ProfileReport(df, title="YData Profiling Report", explorative=True)
profile.to_notebook_iframe()
profile.to_file("ydata_profiling_report.html")
files.download("ydata_profiling_report.html")
```

Summarize dataset: 0%| | 0/5 [00:00<?, ?it/s]

Generate report structure: 0%| | 0/1 [00:00<?, ?it/s]

Render HTML: 0%| | 0/1 [00:00<?, ?it/s]

<IPython.core.display.HTML object>

/usr/local/lib/python3.10/dist-packages/ydata_profiling/profile_report.py:363:

UserWarning: Try running command: 'pip install --upgrade Pillow' to avoid

ValueError

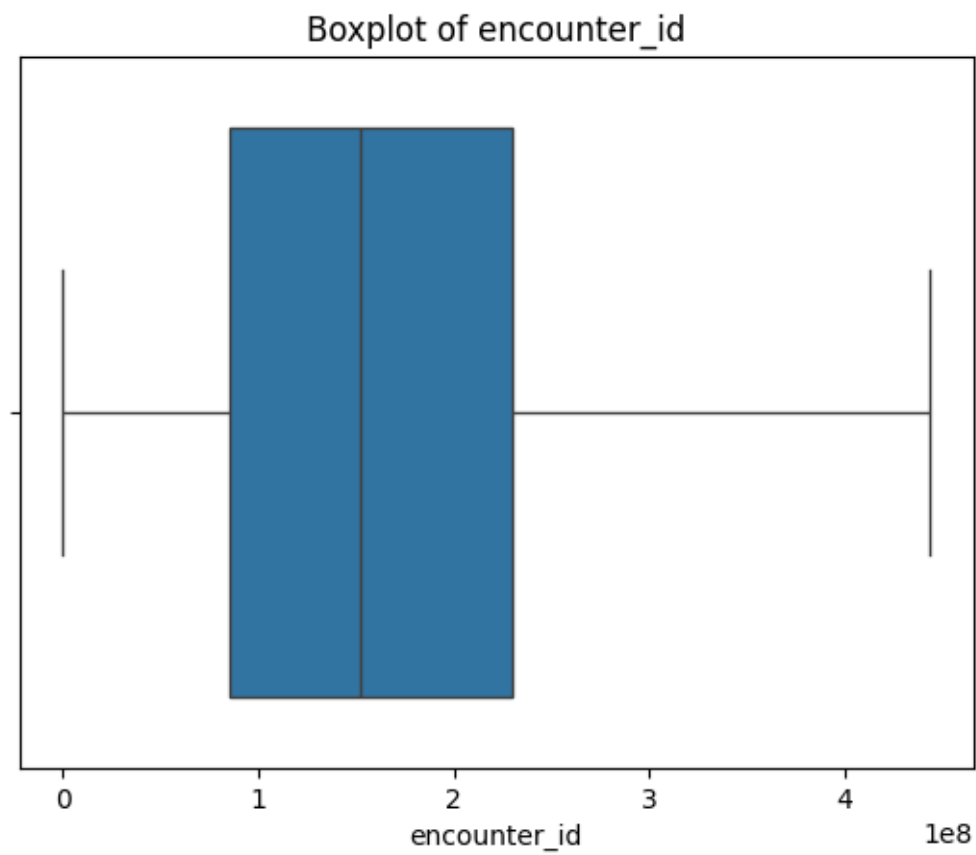
warnings.warn(

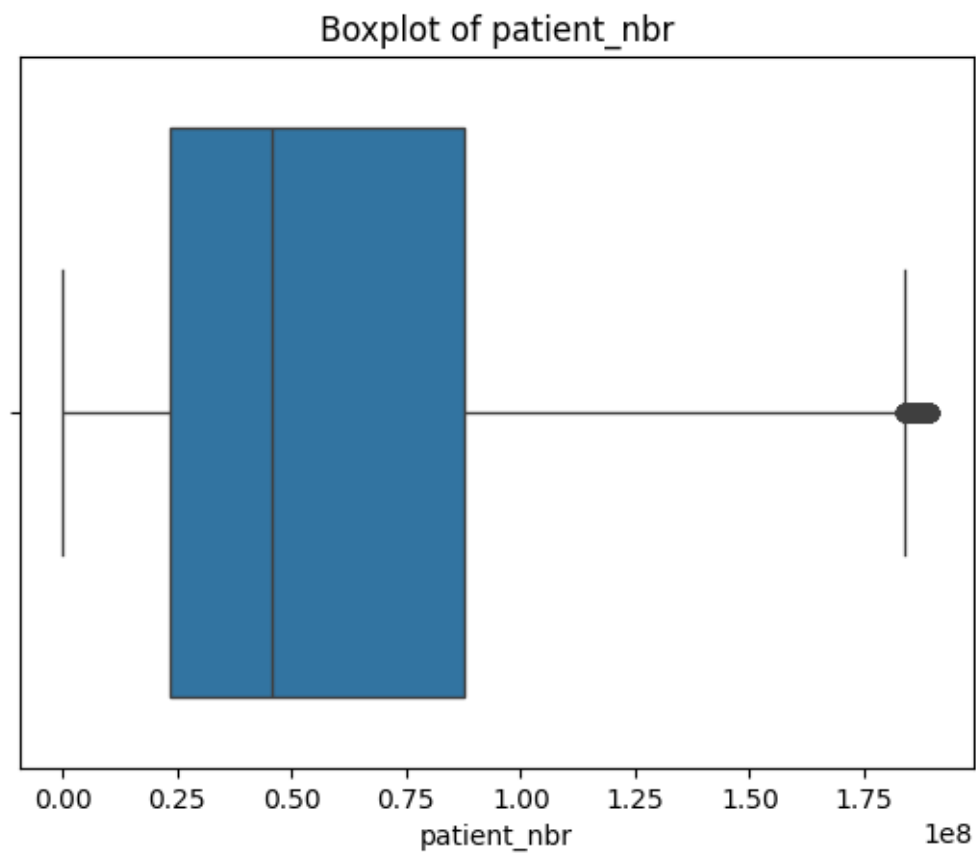
Export report to file: 0%| | 0/1 [00:00<?, ?it/s]

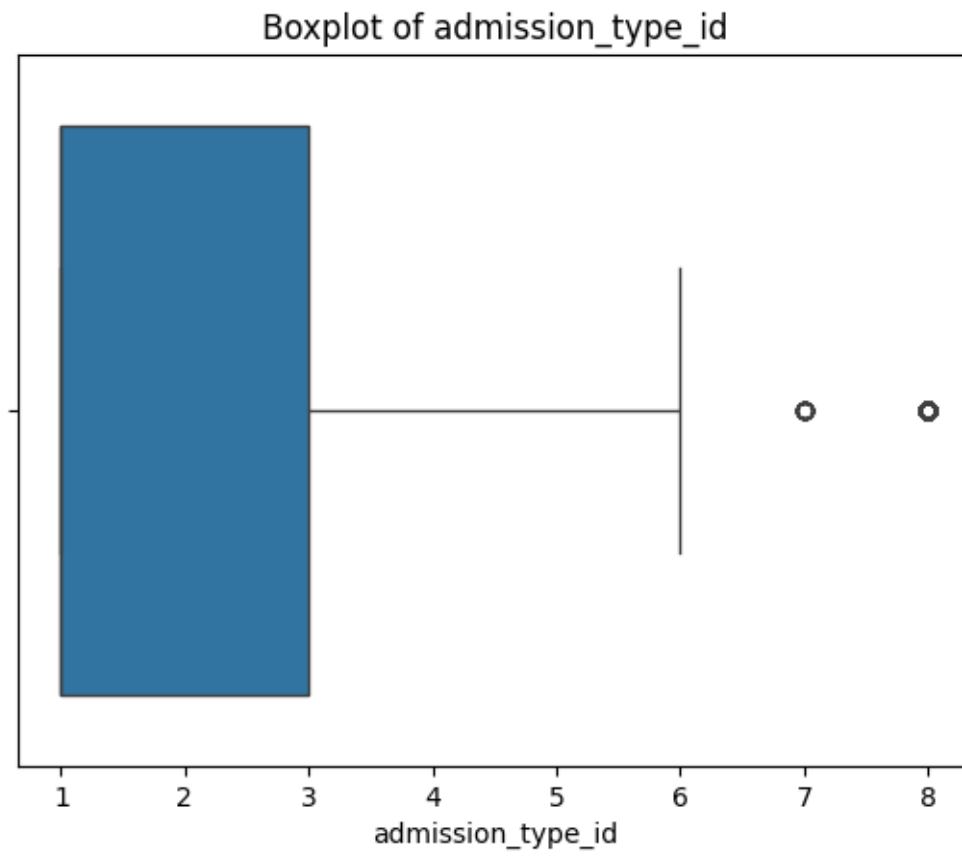
<IPython.core.display.Javascript object>

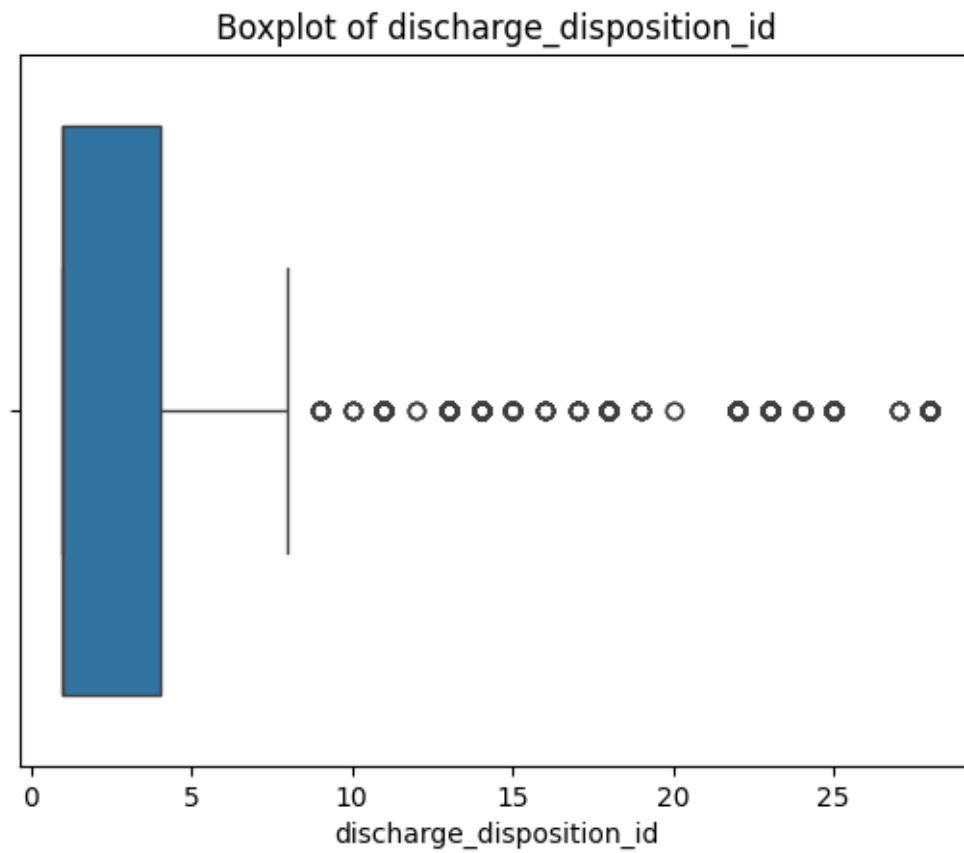
<IPython.core.display.Javascript object>

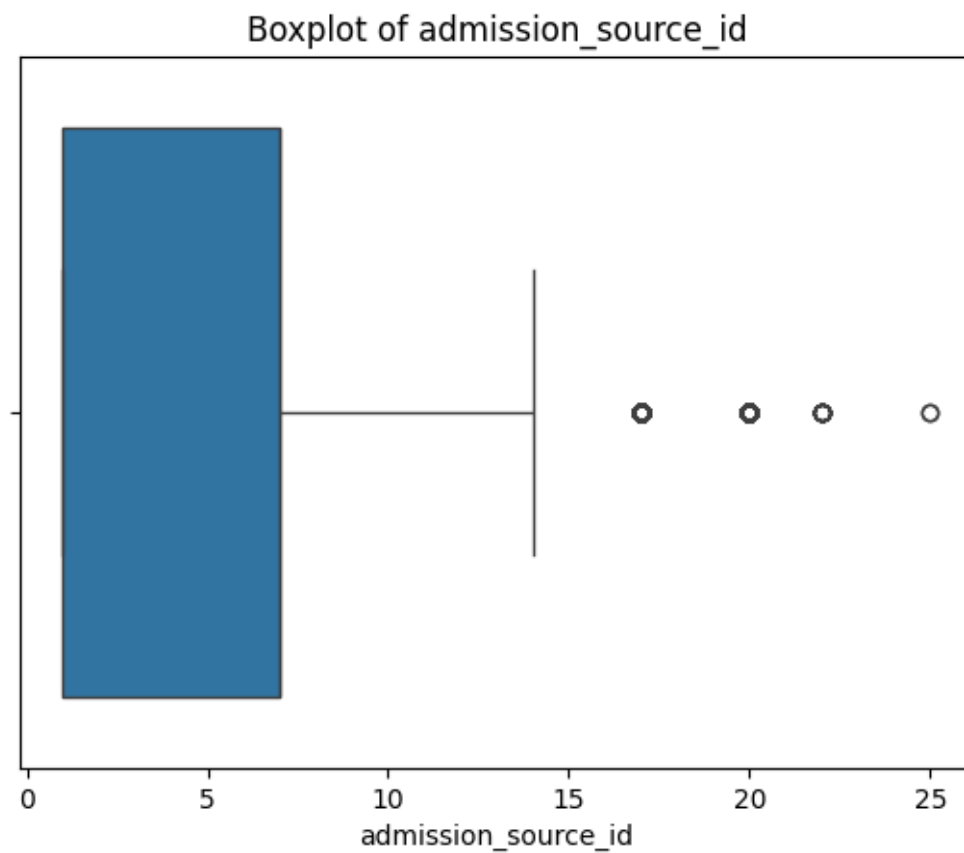
```
[ ]: #Identifying outliers visually in numeric columns using boxplots
for col in numeric_columns:
    sns.boxplot(x=df[col])
    plt.title(f'Boxplot of {col}')
    plt.show()
```

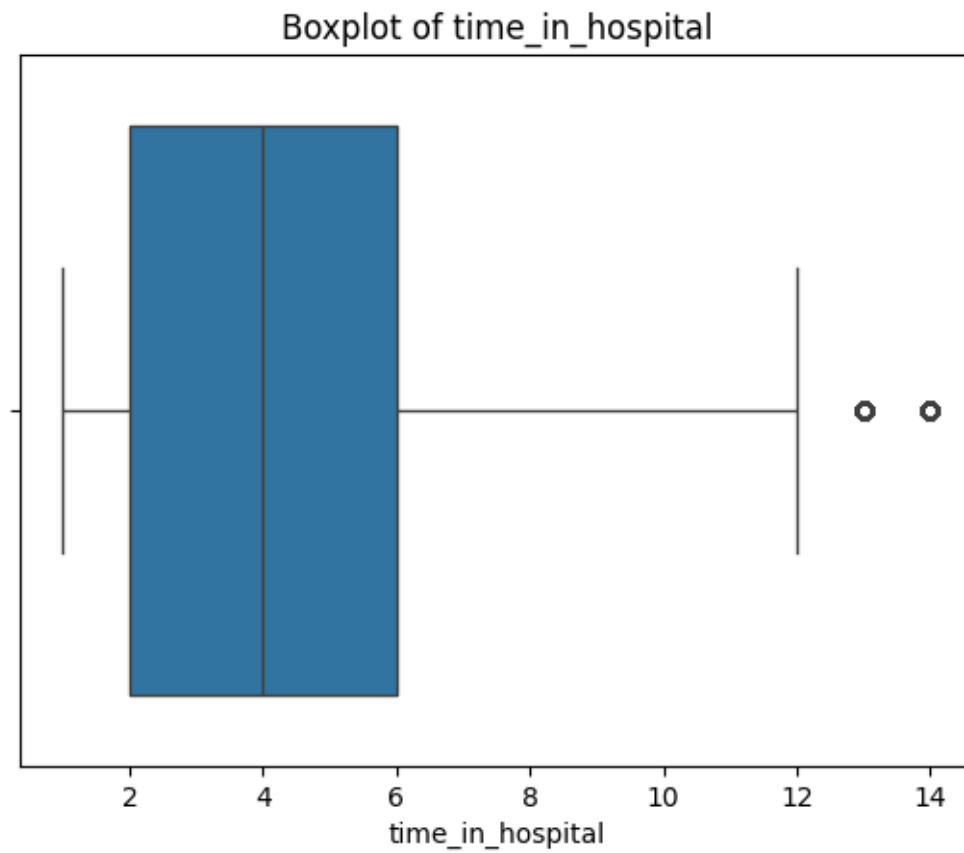




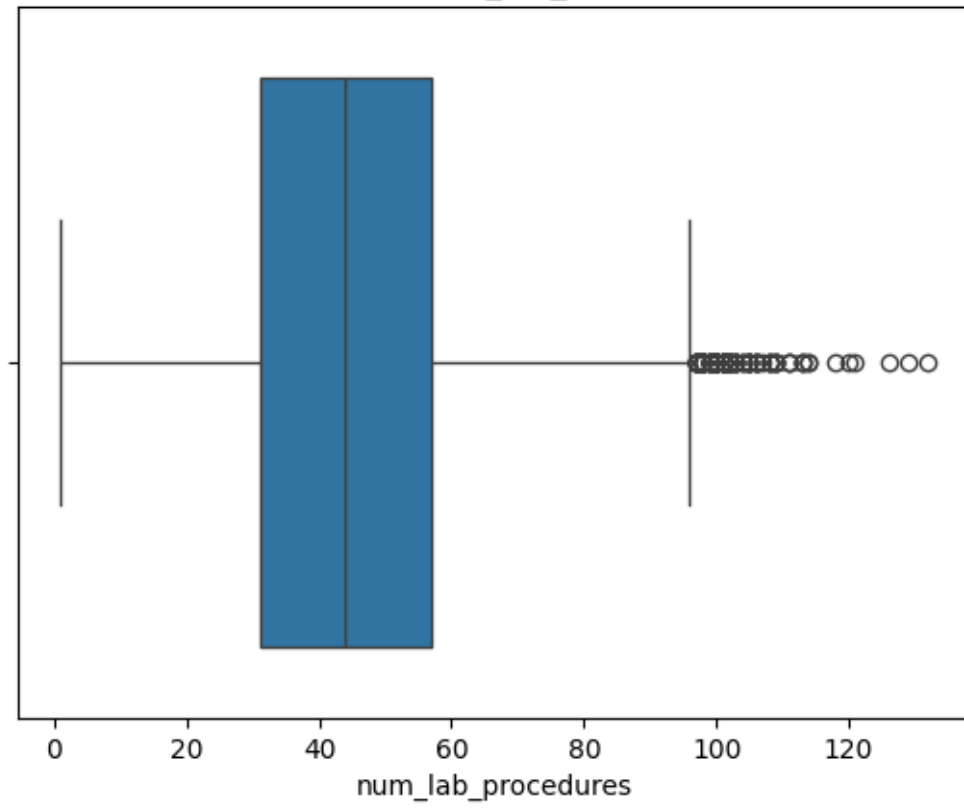




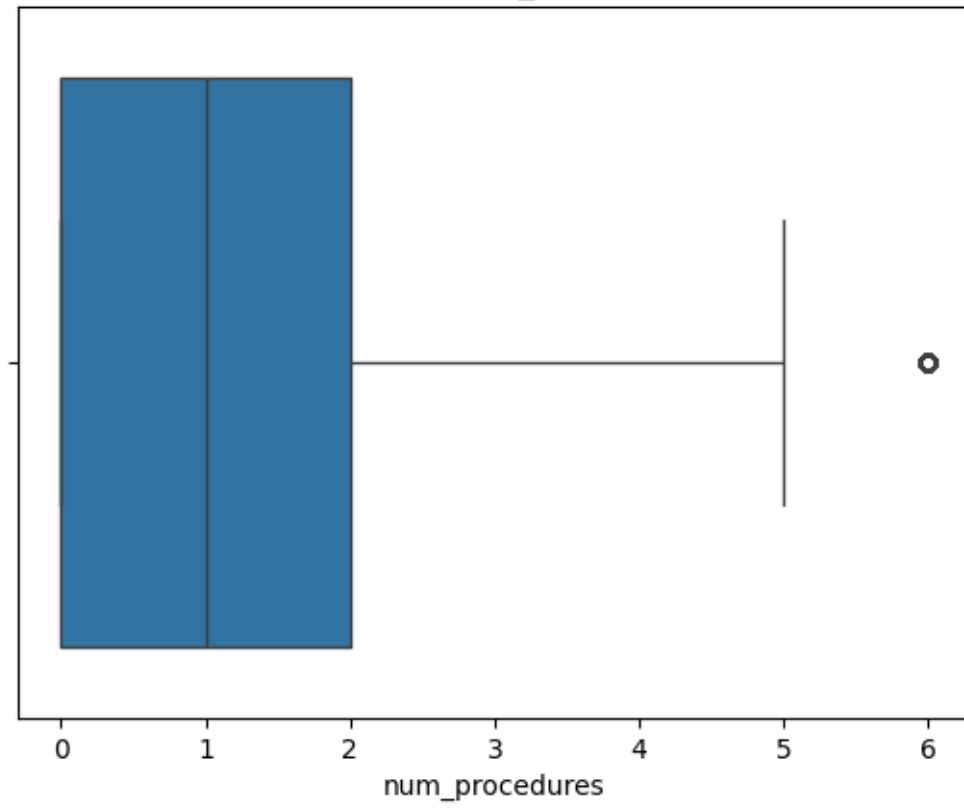




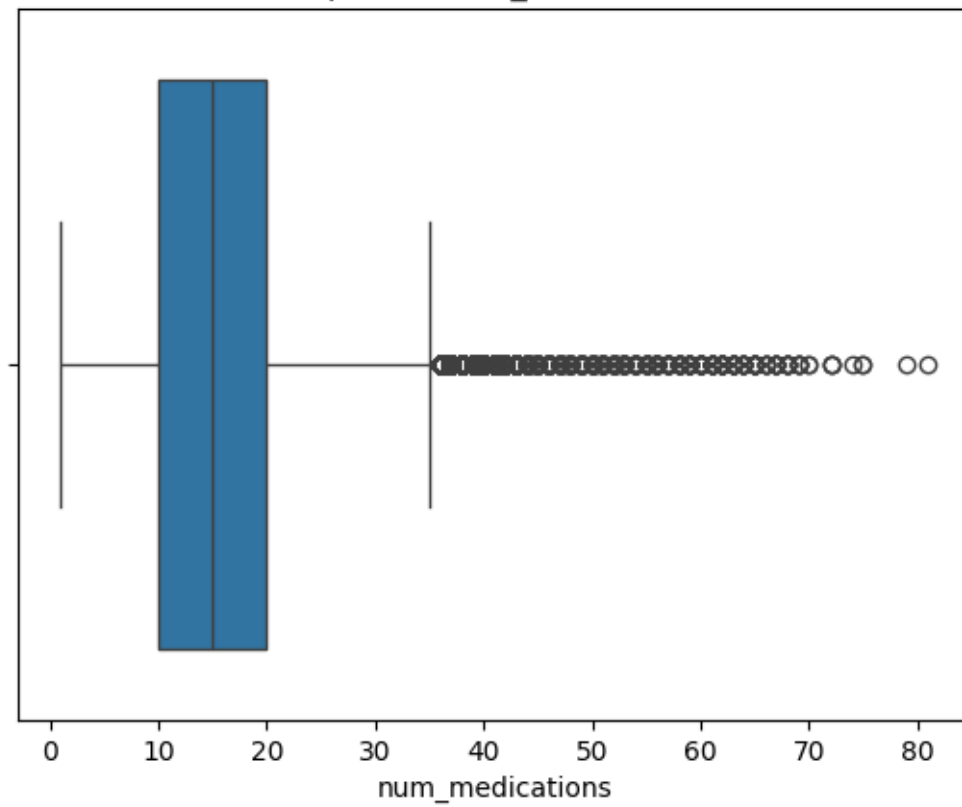
Boxplot of num_lab_procedures



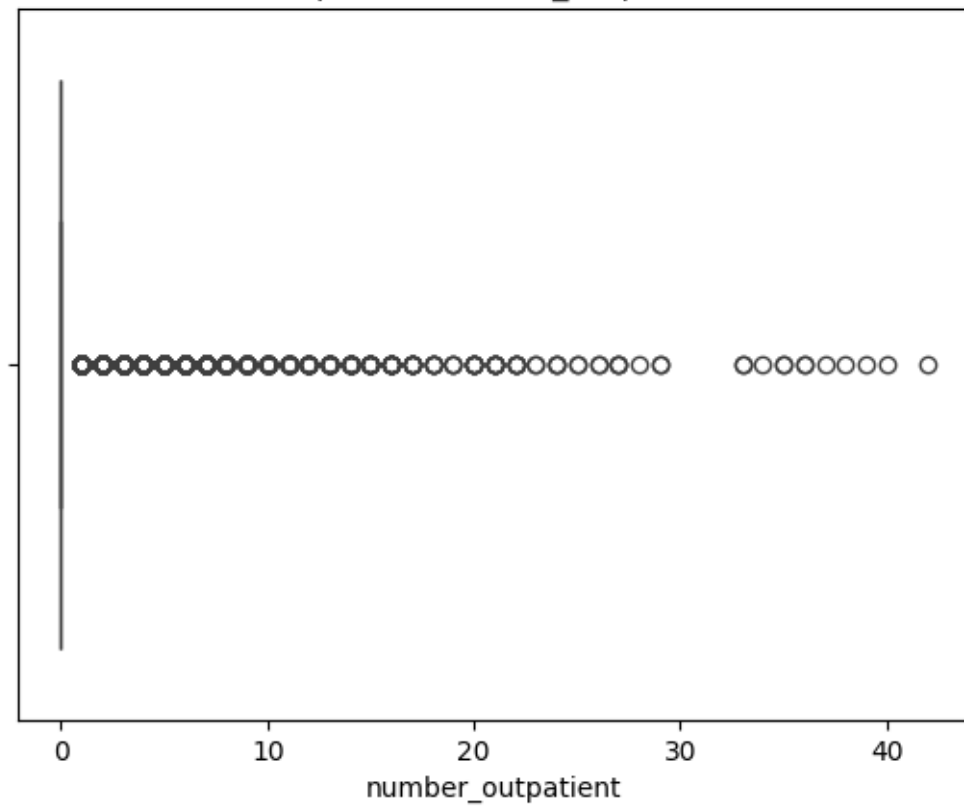
Boxplot of num_procedures



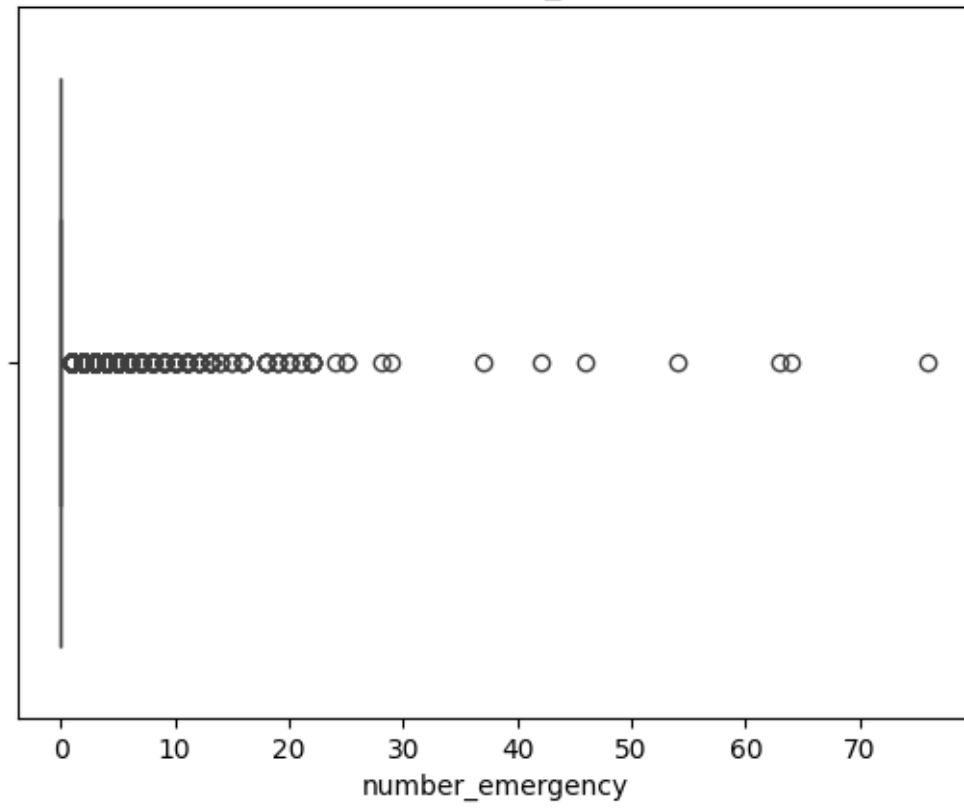
Boxplot of num_medications

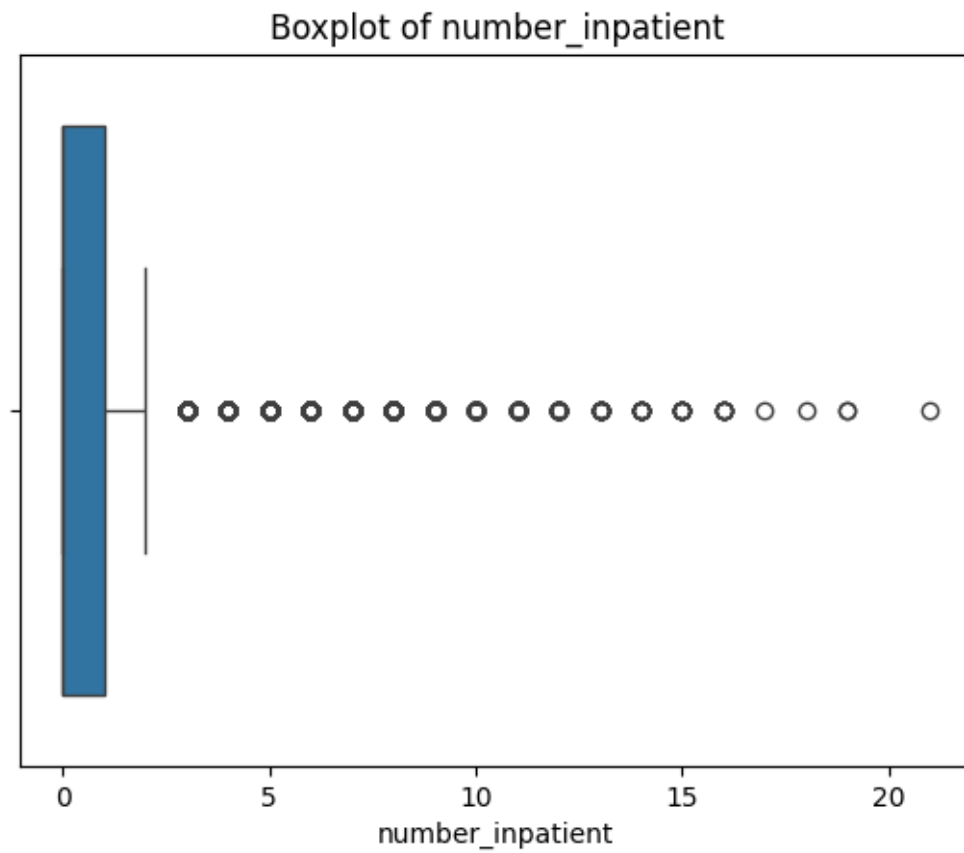


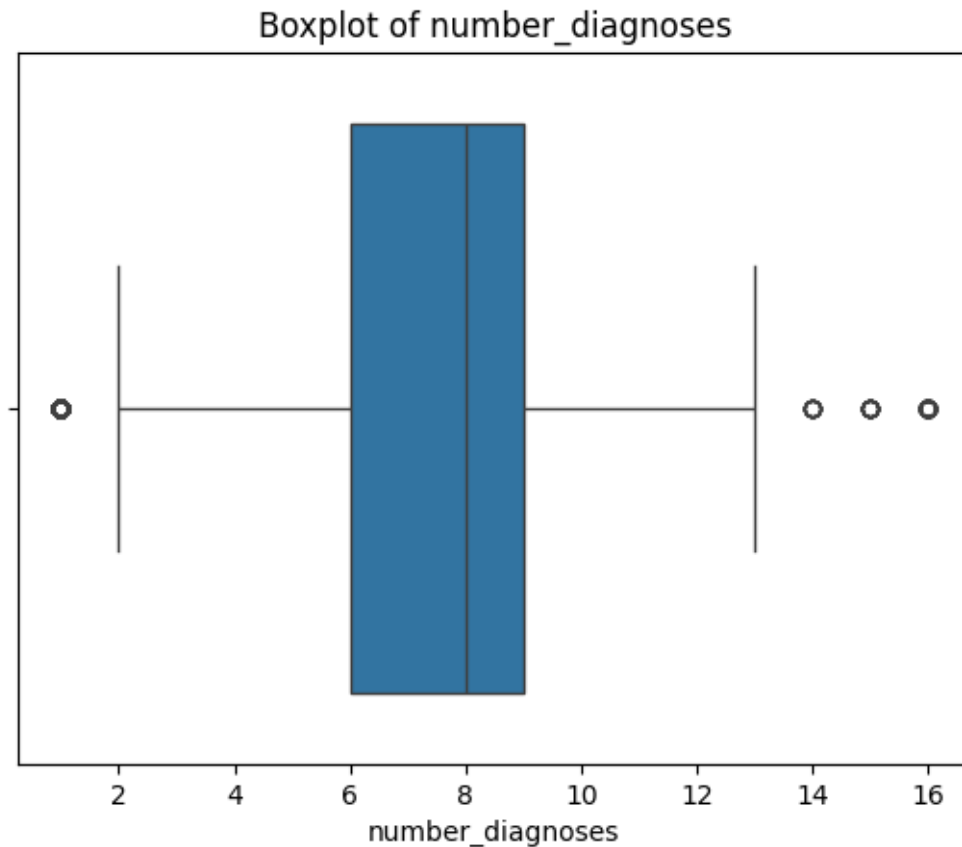
Boxplot of number_outpatient



Boxplot of number_emergency







```
[ ]: #Identifying outliers in numeric columns
      #Function to calculate and print outliers
      def outliers(df, numeric_columns):
          outliers_count = {}

          for col in numeric_columns:
              Q1 = df[col].quantile(0.25)
              Q3 = df[col].quantile(0.75)
              IQR = Q3 - Q1
              lower_bound = Q1 - 1.5 * IQR
              upper_bound = Q3 + 1.5 * IQR

              outliers = df[(df[col] < lower_bound) | (df[col] > upper_bound)]
              outliers_count[col] = outliers[col]

          print(f"{col}:")
          print(f"  Q1: {Q1}")
          print(f"  Q3: {Q3}")
          print(f"  IQR: {IQR}")
          print(f"  Lower Bound: {lower_bound}")
```

```

        print(f" Upper Bound: {upper_bound}")
        print(f" Outliers: {len(outliers)}")
        print()

    return outliers_count

#print outliers
outliers_count = outliers(df, numeric_columns)

```

```

encounter_id:
  Q1: 84961194.0
  Q3: 230270887.5
  IQR: 145309693.5
  Lower Bound: -133003346.25
  Upper Bound: 448235427.75
  Outliers: 0

```

```

patient_nbr:
  Q1: 23413221.0
  Q3: 87545949.75
  IQR: 64132728.75
  Lower Bound: -72785872.125
  Upper Bound: 183745042.875
  Outliers: 247

```

```

admission_type_id:
  Q1: 1.0
  Q3: 3.0
  IQR: 2.0
  Lower Bound: -2.0
  Upper Bound: 6.0
  Outliers: 341

```

```

discharge_disposition_id:
  Q1: 1.0
  Q3: 4.0
  IQR: 3.0
  Lower Bound: -3.5
  Upper Bound: 8.5
  Outliers: 9818

```

```

admission_source_id:
  Q1: 1.0
  Q3: 7.0
  IQR: 6.0
  Lower Bound: -8.0
  Upper Bound: 16.0

```

```
Outliers: 6956

time_in_hospital:
  Q1: 2.0
  Q3: 6.0
  IQR: 4.0
  Lower Bound: -4.0
  Upper Bound: 12.0
  Outliers: 2252

num_lab_procedures:
  Q1: 31.0
  Q3: 57.0
  IQR: 26.0
  Lower Bound: -8.0
  Upper Bound: 96.0
  Outliers: 143

num_procedures:
  Q1: 0.0
  Q3: 2.0
  IQR: 2.0
  Lower Bound: -3.0
  Upper Bound: 5.0
  Outliers: 4954

num_medications:
  Q1: 10.0
  Q3: 20.0
  IQR: 10.0
  Lower Bound: -5.0
  Upper Bound: 35.0
  Outliers: 2557

number_outpatient:
  Q1: 0.0
  Q3: 0.0
  IQR: 0.0
  Lower Bound: 0.0
  Upper Bound: 0.0
  Outliers: 16739

number_emergency:
  Q1: 0.0
  Q3: 0.0
  IQR: 0.0
  Lower Bound: 0.0
  Upper Bound: 0.0
```

Outliers: 11383

number_inpatient:

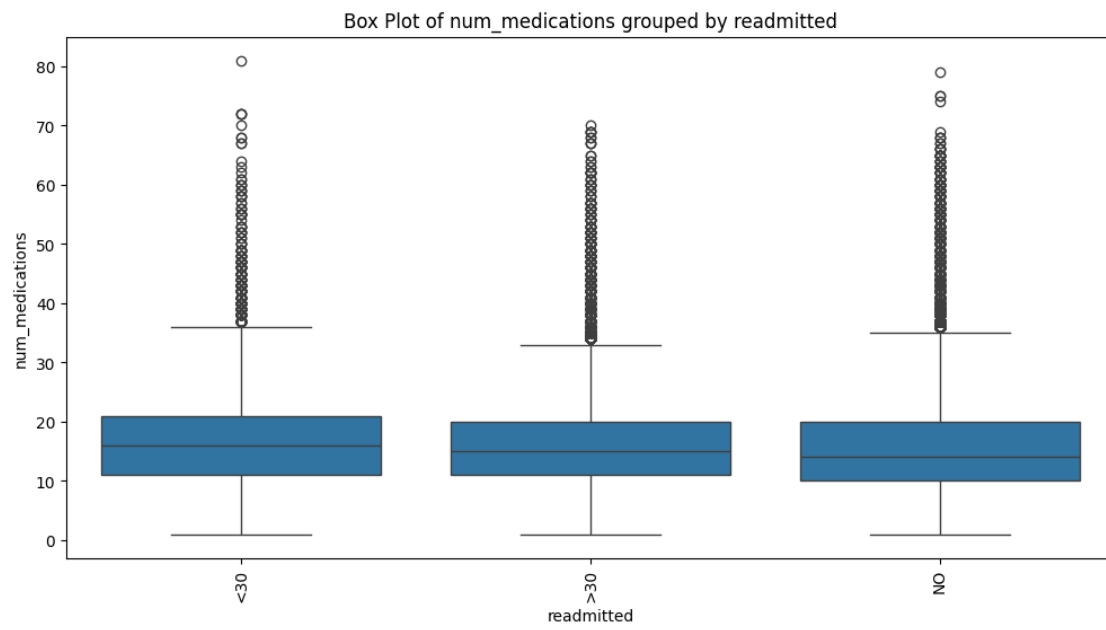
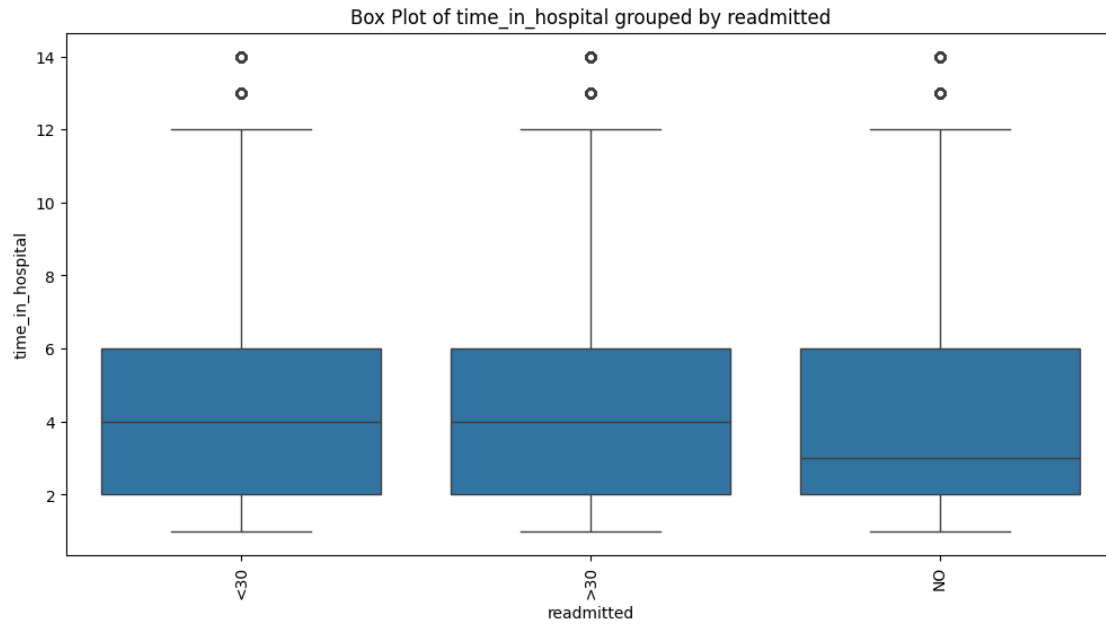
Q1: 0.0
Q3: 1.0
IQR: 1.0
Lower Bound: -1.5
Upper Bound: 2.5
Outliers: 7049

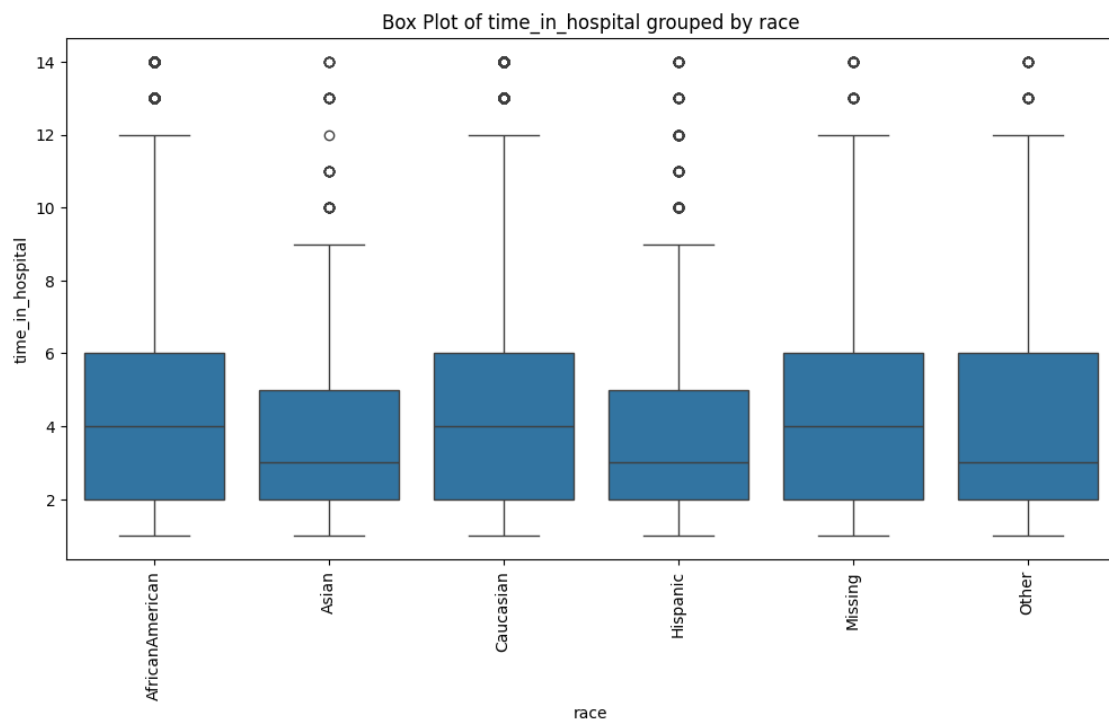
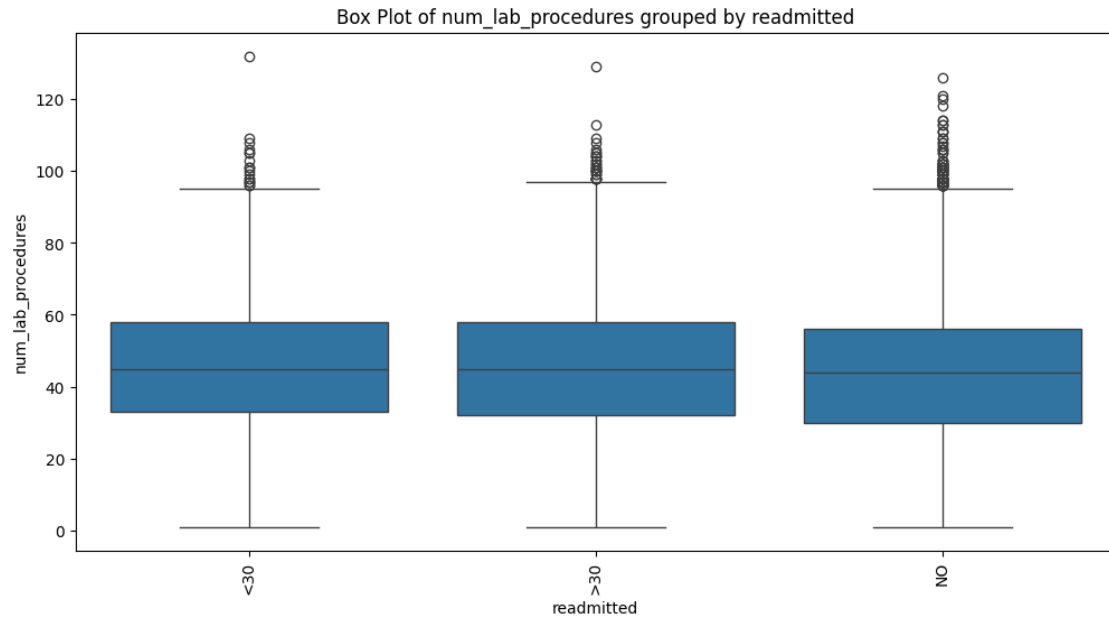
number_diagnoses:

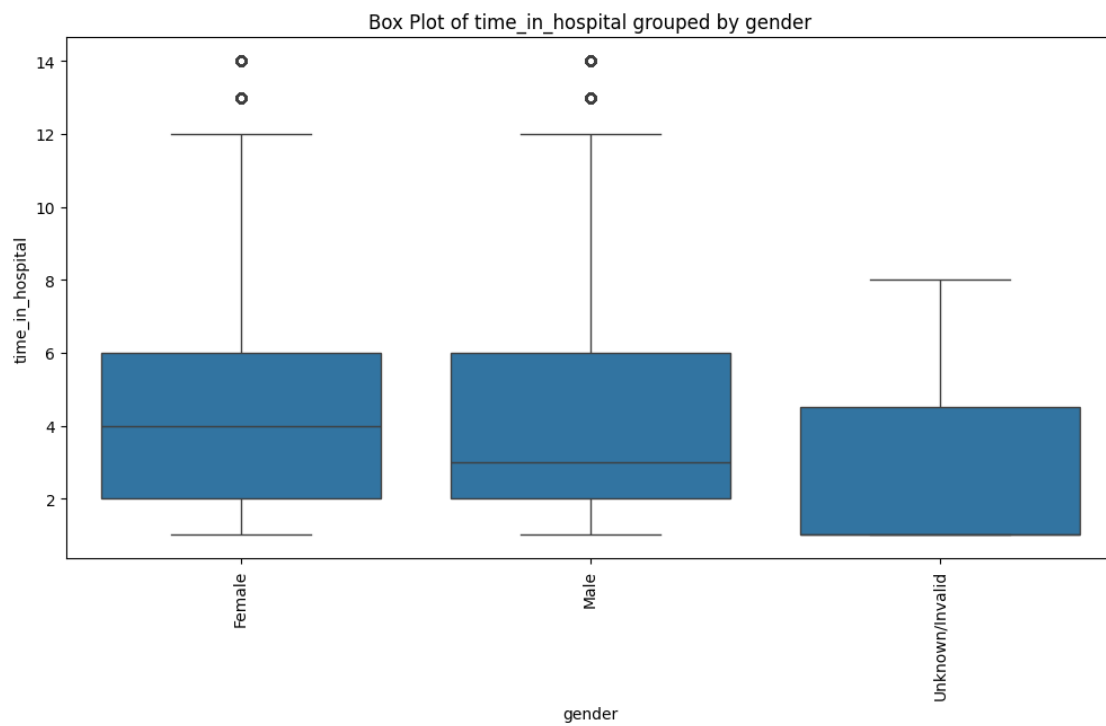
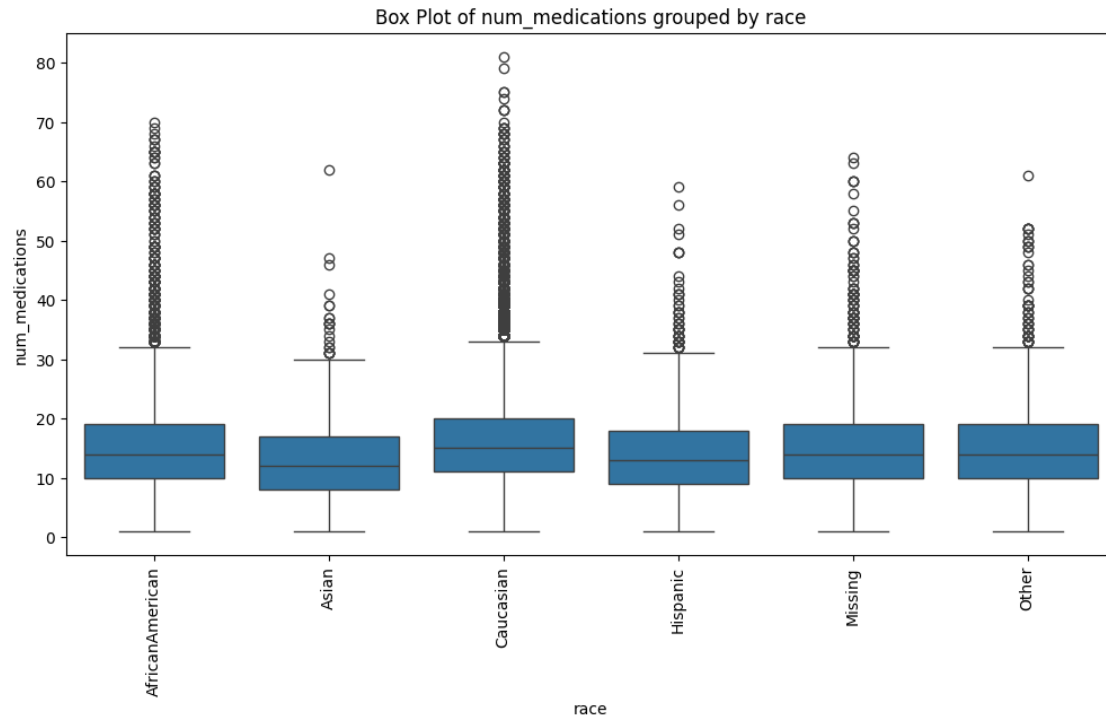
Q1: 6.0
Q3: 9.0
IQR: 3.0
Lower Bound: 1.5
Upper Bound: 13.5
Outliers: 281

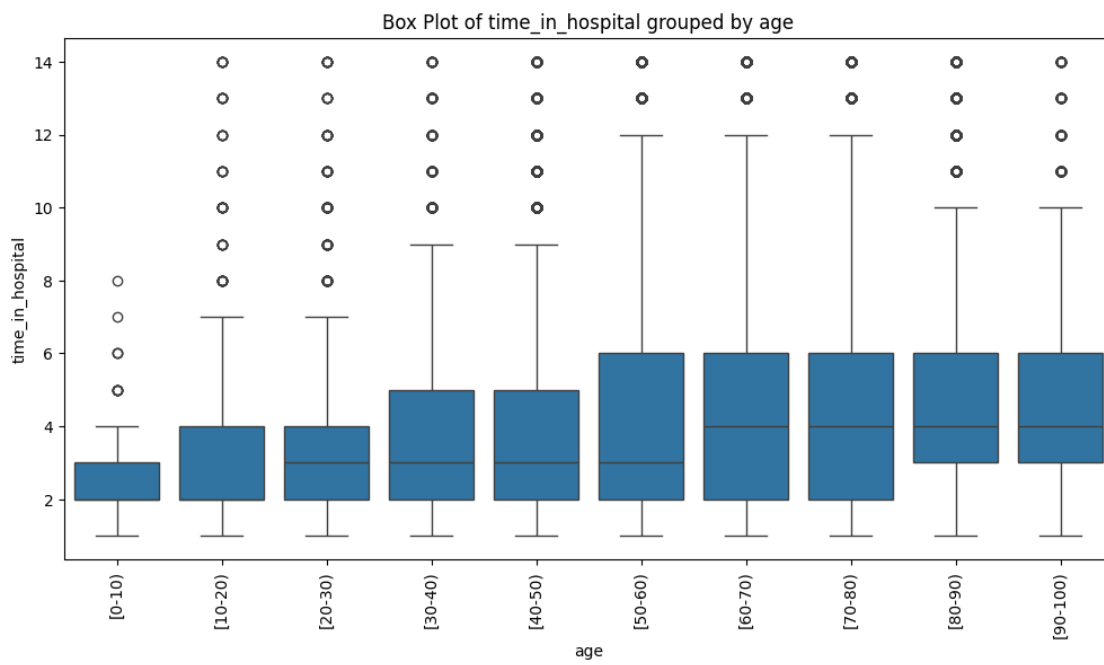
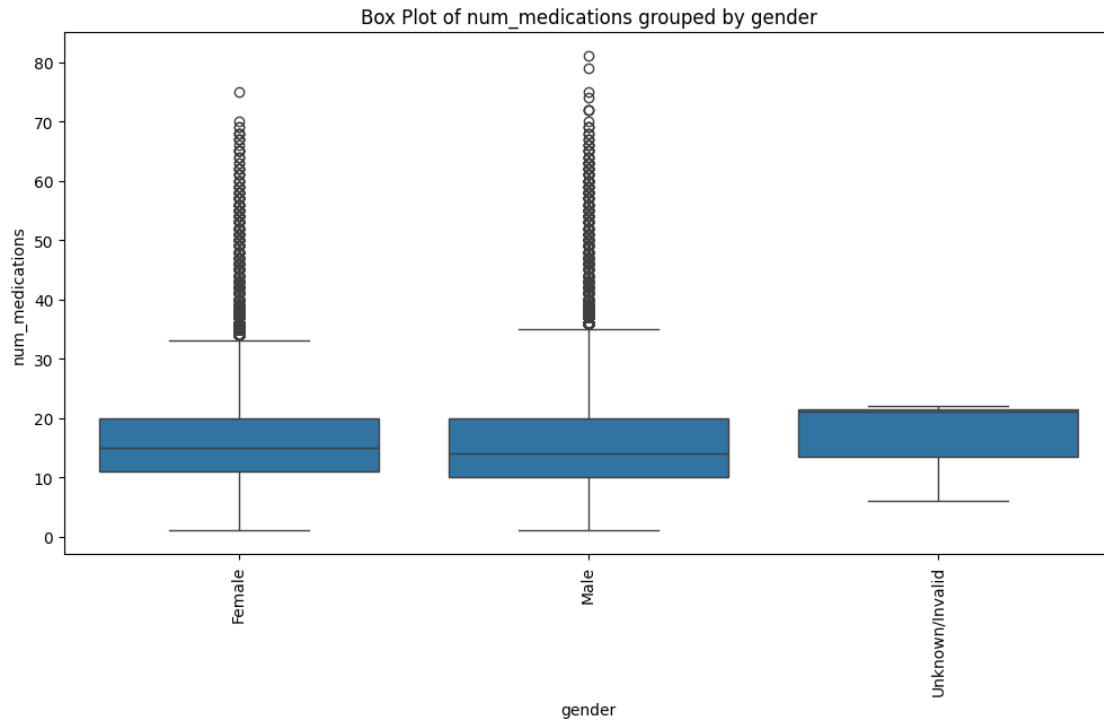
```
[ ]: # Visualizing outliers for selected important combinations
important_combinations = [
    ('readmitted', 'time_in_hospital'),
    ('readmitted', 'num_medications'),
    ('readmitted', 'num_lab_procedures'),
    ('race', 'time_in_hospital'),
    ('race', 'num_medications'),
    ('gender', 'time_in_hospital'),
    ('gender', 'num_medications'),
    ('age', 'time_in_hospital'),
    ('age', 'num_medications'),
    ('medical_specialty', 'time_in_hospital'),
    ('medical_specialty', 'num_lab_procedures'),
    ('medical_specialty', 'num_medications'),
    ('admission_type_id', 'time_in_hospital'),
    ('discharge_disposition_id', 'time_in_hospital'),
    ('admission_source_id', 'time_in_hospital')
]

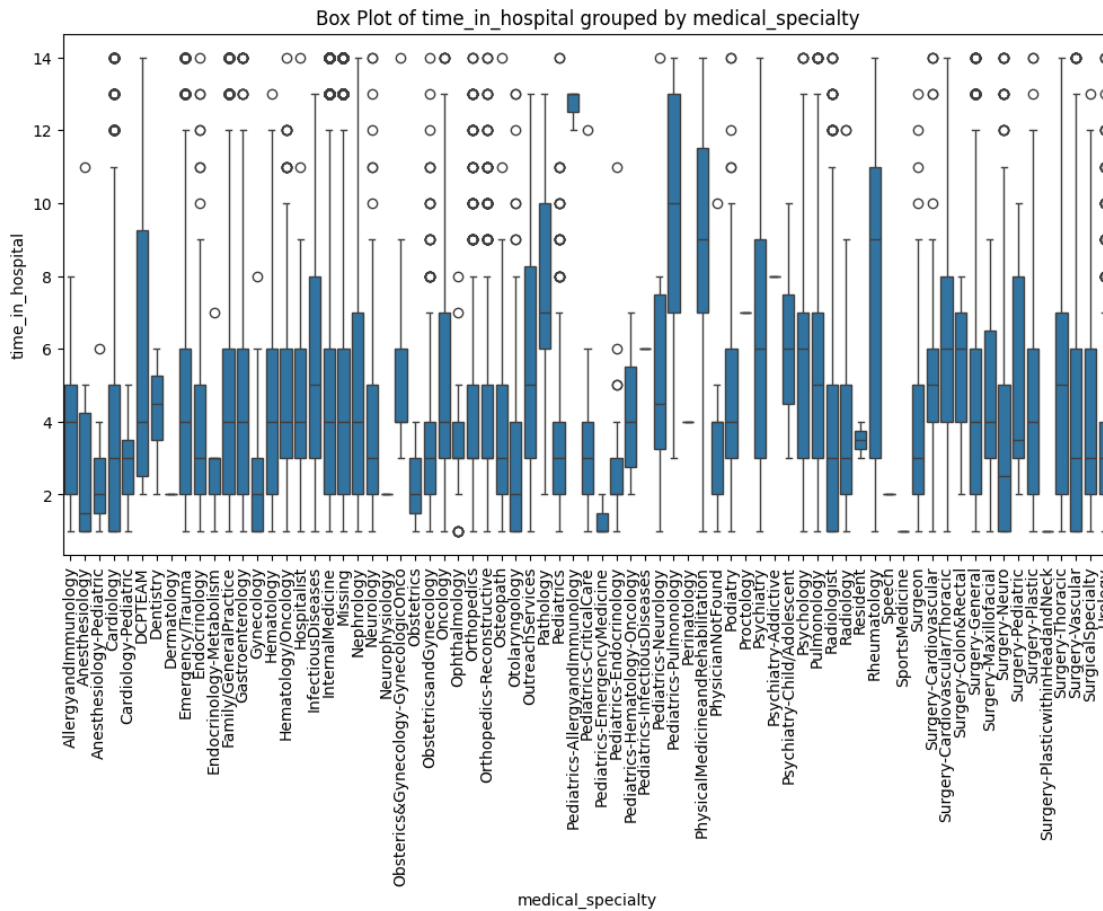
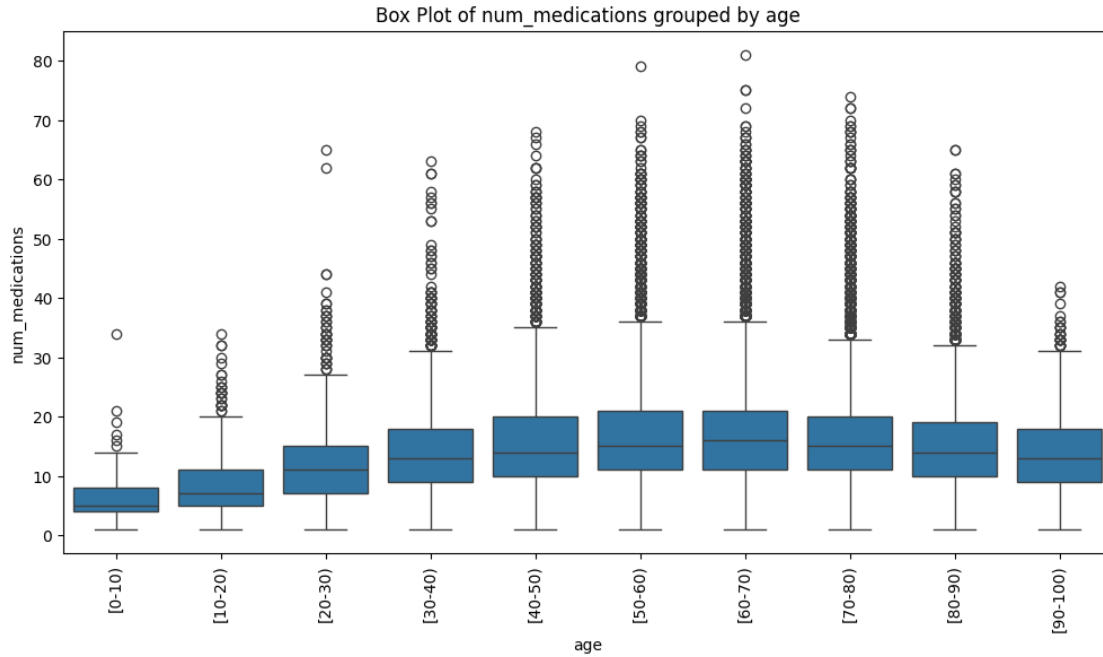
for categorical_col, numeric_col in important_combinations:
    plt.figure(figsize=(12, 6))
    sns.boxplot(x=categorical_col, y=numeric_col, data=df)
    plt.title(f'Box Plot of {numeric_col} grouped by {categorical_col}')
    plt.xticks(rotation=90)
    plt.show()
```

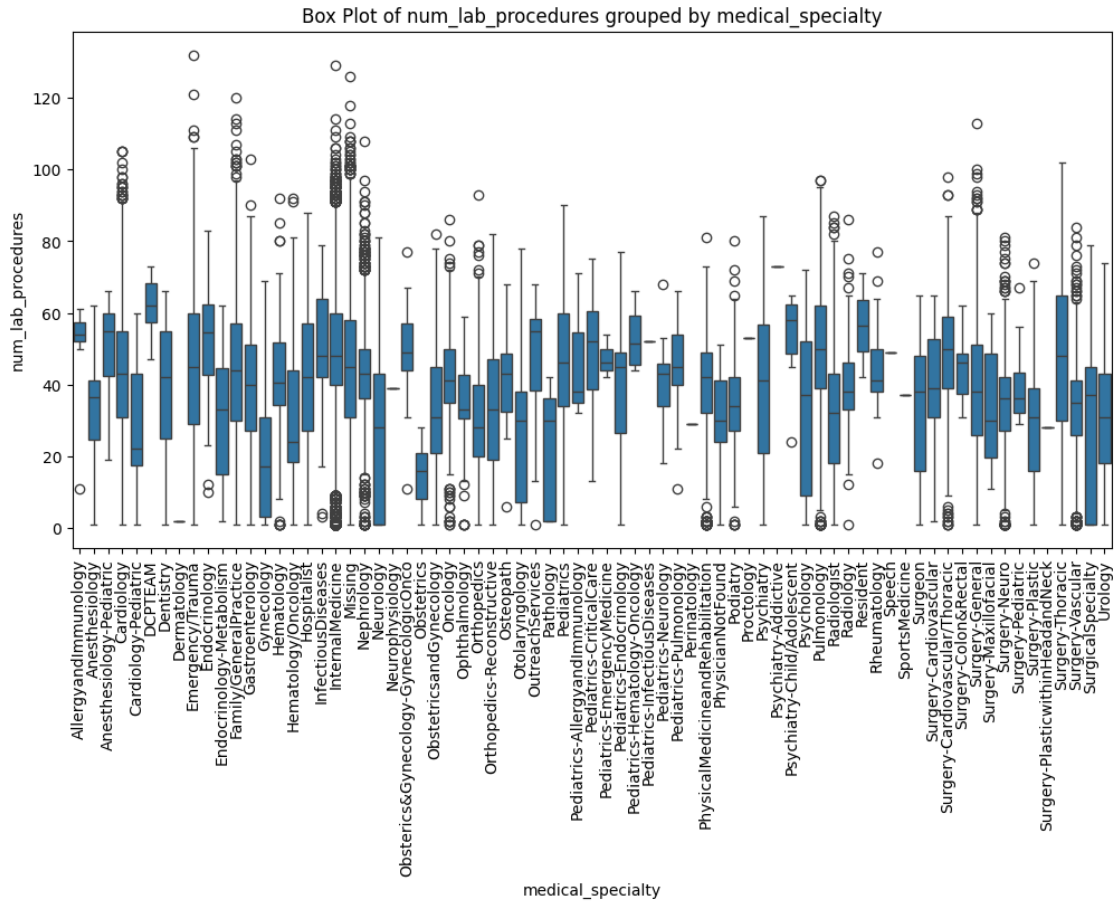


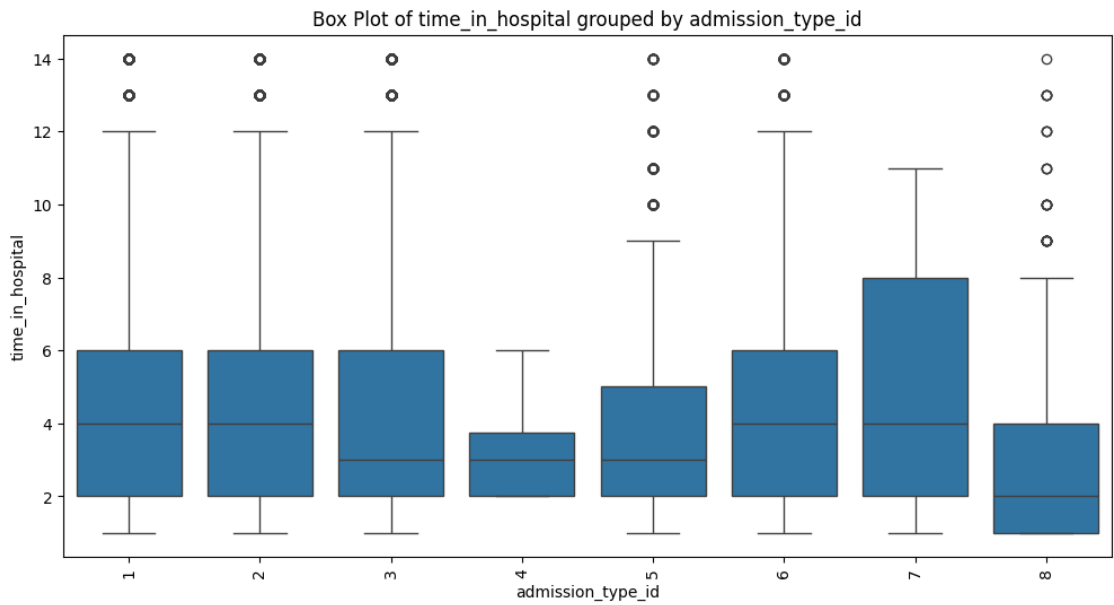
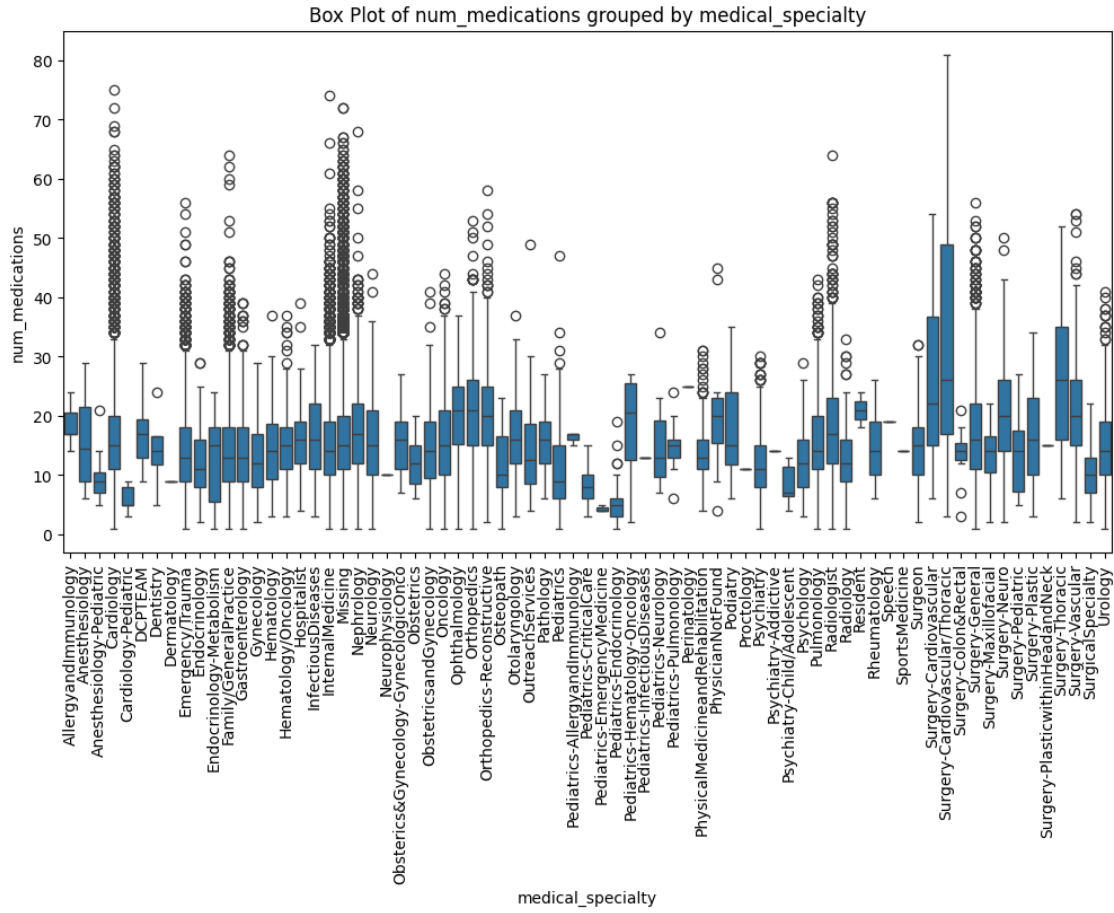


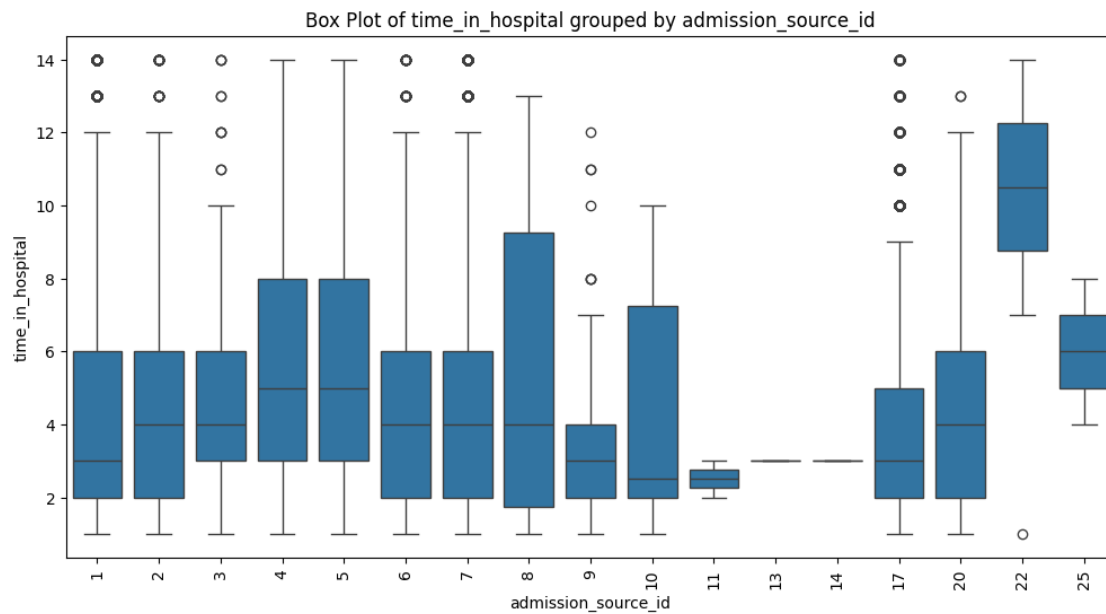
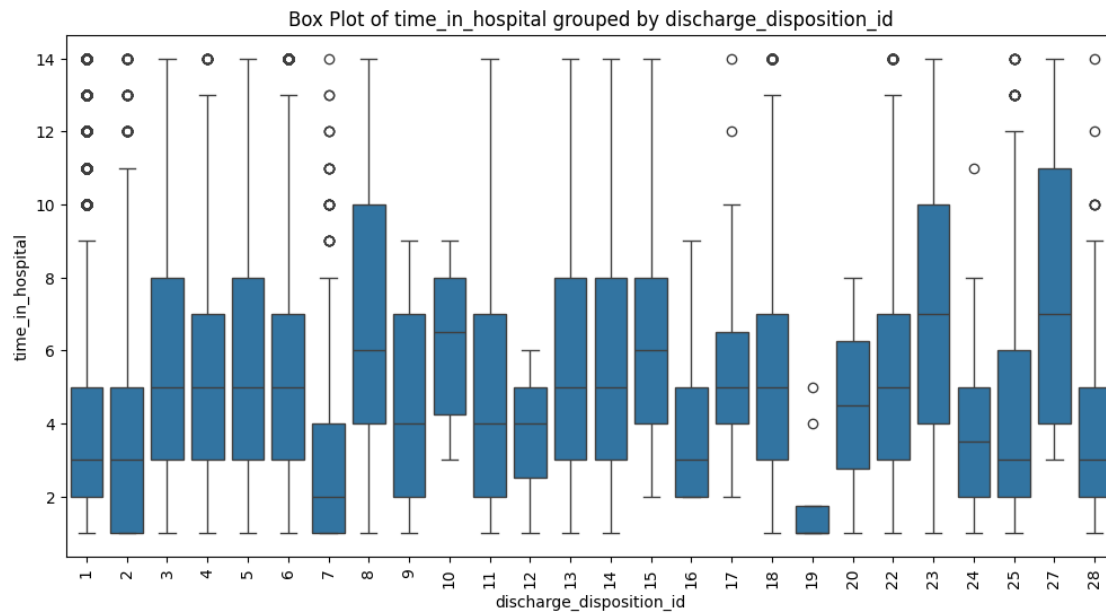












```
[ ]: # Here I wanted to clean the dataframe by removing irrelevant columns, columns_
      ↳ with high missing values
df_cleaned = df.copy()
columns_to_drop = ['encounter_id', 'patient_nbr', 'weight', 'payer_code']
df_cleaned.drop(columns=columns_to_drop, inplace=True)
```

```

# Here I put a threshold of 95% for List of columns dominated by "No" category
↳ since they have very low variance and no added value
columns_dominated_by_no = [
    'metformin', 'repaglinide', 'nateglinide', 'chlorpropamide',
    'glimepiride', 'acetoexamide', '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

```

[ ]: # Identify and verifying remaining categorical columns for onehot coding
categorical_columns = df_cleaned.select_dtypes(include=['category']).columns.
    ↪to list()
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', 'miglitol', 'insulin', 'change', 'diabetesMed', 'readmitted']

```

[ ]: # 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)
```

```
[ ]: # 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 x 2 columns]

```

[ ]: #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	0.0	1.0
1	1.0	0.0	1.0	0.0
2	1.0	0.0	0.0	1.0
3	1.0	0.0	0.0	1.0
4	1.0	0.0	0.0	1.0

[5 rows x 2406 columns]

```
[ ]: # 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
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diag_3_V85: min = 0.0, max = 1.0
diag_3_V86: min = 0.0, max = 1.0
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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
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A1Cresult_No Test: min = 0.0, max = 1.0
A1Cresult_Norm: min = 0.0, max = 1.0
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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
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glimepiride_Steady: min = 0.0, max = 1.0
glimepiride_Up: min = 0.0, max = 1.0
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glipizide_No: min = 0.0, max = 1.0
glipizide_Steady: min = 0.0, max = 1.0
glipizide_Up: min = 0.0, max = 1.0
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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
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