Préparation des données

Le but de cette étude est de proposer un modèle de prédiction de la réadmission non planifiée à 30 jours chez les patients diabétiques dans les hôpitaux américains en utilisant les données générées par le Data Warehouse. L'analyse sera basée sur des facteurs de risque tels que les données démographiques du patient, les détails d'admission, le diagnostic et les données médicales. Dans un sens plus large, le but de l'étude est de permettre aux centres de santé de mieux anticiper et traiter les réadmissions non planifiées tout en améliorant la qualité de leurs soins et leur rentabilité.

Importer des bibliothèques

In [1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import scipy.stats as stats
import os
import warnings
warnings.filterwarnings("ignore")

import statsmodels.api as sm
from statsmodels.stats.anova import anova_lm
import scipy.stats as stats
import matplotlib.pyplot as plt
from sklearn.preprocessing import StandardScaler, PowerTransformer, LabelEncoder, OneHotEncoder, MinMaxScale
pd.set_option('display.max_columns', None)
pd.set_option('display.max_rows', None)
```

Importer le fichier CSV extrait de DWH

In [2]:
```
df2 = pd.read_csv('CSV_Files/out.csv')
df2.head()
```

Out[2]:

	RACE	GENDER	AGE_INT	ADMISSION_TYPE	DISCHARGE_DISPOSITION	ADMISSION_SOURCE	TIME_IN_HOSPITAL	PAYER_CODE	MEDI
0	Caucasian	Female	65	Urgent	Discharged to home	Physician Referral	3	MC	
1	Caucasian	Female	75	Emergency	Discharged/transferred to another rehab fac in...	Emergency Room	7	MC	
2	Caucasian	Female	95	Emergency	Discharged to home	Emergency Room	4	MC	Em
3	Caucasian	Male	75	Emergency	Discharged/transferred to another short term h...	Emergency Room	10	MC	I
4	Caucasian	Male	55	Emergency	Left AMA	Transfer from another health care facility	6	MC	

In [3]:
```
df2.columns
```

Out[3]:
```
Index(['RACE', 'GENDER', 'AGE_INT', 'ADMISSION_TYPE', 'DISCHARGE_DISPOSITION',
       'ADMISSION_SOURCE', 'TIME_IN_HOSPITAL', 'PAYER_CODE',
       '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', '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'],
      dtype='object')
```

Exploration et nettoyage des données pour appliquer les modèles de machine learning

On va effectuer des tâches supplémentaire de nettoyage des données telles que la suppression de mauvaises données, le traitement des valeurs manquantes...

In [4]:
```
df2.shape
```

Out[4]: (26755, 47)

In [5]:
```
df2.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 26755 entries, 0 to 26754
Data columns (total 47 columns):
RACE                        26755 non-null object
GENDER                      26755 non-null object
AGE_INT                     26755 non-null int64
ADMISSION_TYPE              26752 non-null object
DISCHARGE_DISPOSITION       26749 non-null object
ADMISSION_SOURCE            25935 non-null object
TIME_IN_HOSPITAL            26755 non-null int64
PAYER_CODE                  26755 non-null object
MEDICAL_SPECIALTY           26755 non-null object
NUM_LAB_PROCEDURES          26755 non-null int64
NUM_PROCEDURES              26755 non-null int64
NUM_MEDICATIONS             26755 non-null int64
NUMBER_OUTPATIENT           26755 non-null int64
NUMBER_EMERGENCY            26755 non-null int64
NUMBER_INPATIENT            26755 non-null int64
DIAG_1                      26755 non-null object
DIAG_2                      26755 non-null object
DIAG_3                      26755 non-null object
NUMBER_DIAGNOSES            26755 non-null int64
MAX_GLU_SERUM               26755 non-null object
A1CRESULT                   26755 non-null object
METFORMIN                   26755 non-null object
REPAGLINIDE                 26755 non-null object
NATEGLINIDE                 26755 non-null object
CHLORPROPAMIDE              26755 non-null object
GLIMEPIRIDE                 26755 non-null object
ACETOHEXAMIDE               26755 non-null object
GLIPIZIDE                   26755 non-null object
GLYBURIDE                   26755 non-null object
TOLBUTAMIDE                 26755 non-null object
PIOGLITAZONE                26755 non-null object
ROSIGLITAZONE               26755 non-null object
ACARBOSE                    26755 non-null object
MIGLITOL                    26755 non-null object
TROGLITAZONE                26755 non-null object
TOLAZAMIDE                  26755 non-null object
EXAMIDE                     26755 non-null object
CITOGLIPTON                 26755 non-null object
INSULIN                     26755 non-null object
GLYBURIDE_METFORMIN         26755 non-null object
GLIPIZIDE_METFORMIN         26755 non-null object
GLIMEPIRIDE_PIOGLITAZONE    26755 non-null object
METFORMIN_ROSIGLITAZONE     26755 non-null object
METFORMIN_PIOGLITAZONE      26755 non-null object
CHANGE                      26755 non-null object
DIABETESMED                 26755 non-null object
READMITTED                  26755 non-null object
dtypes: int64(9), object(38)
memory usage: 9.6+ MB
```

Il y a 47 caractéristiques dans ces données. Il contient des valeurs numériques (int) et des valeurs catégorielles (objet).

Il y a 26755 échantillons présents dans cet ensemble de données. Il ne semble pas y avoir de valeurs nulles, nous allons creuser profondément et en savoir plus.

In [6]:
```
df2.describe()
```

Out[6]:

	AGE_INT	TIME_IN_HOSPITAL	NUM_LAB_PROCEDURES	NUM_PROCEDURES	NUM_MEDICATIONS	NUMBER_OUTPATIENT	NUMBER_
count	26755.000000	26755.000000	26755.000000	26755.000000	26755.000000	26755.000000	
mean	66.608671	4.317922	40.756681	1.475575	16.246720	0.290712	
std	15.582391	2.949791	19.965546	1.749729	8.609362	0.998707	
min	5.000000	1.000000	1.000000	0.000000	1.000000	0.000000	
25%	55.000000	2.000000	29.000000	0.000000	10.000000	0.000000	
50%	65.000000	4.000000	42.000000	1.000000	15.000000	0.000000	
75%	75.000000	6.000000	54.000000	2.000000	20.000000	0.000000	
max	95.000000	14.000000	132.000000	6.000000	81.000000	38.000000	

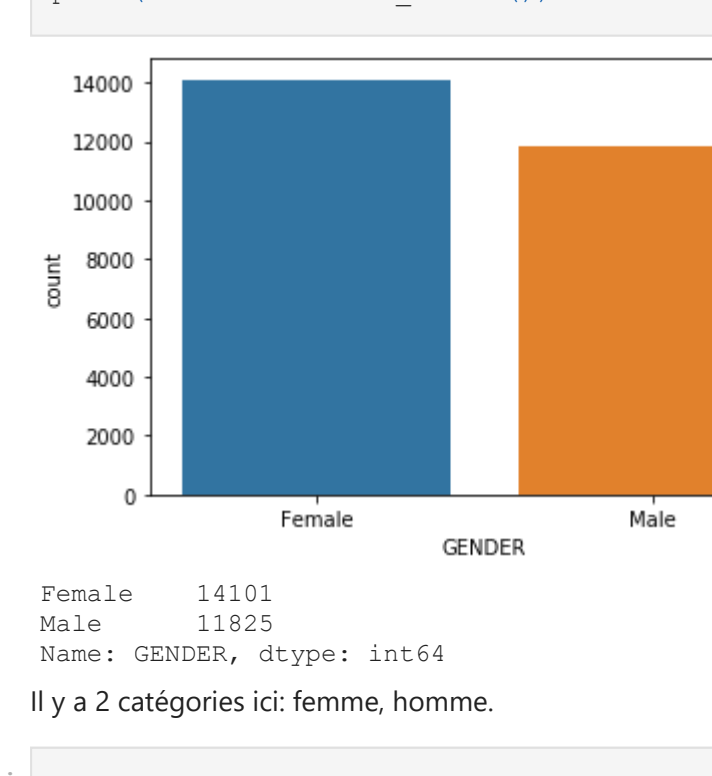
'RACE', 'GENDER', 'AGE_INT', 'ADMISSION_TYPE', 'DISCHARGE_DISPOSITION',
'ADMISSION_SOURCE', 'TIME_IN_HOSPITAL', 'PAYER_CODE',
'MEDICAL_SPECIALTY', 'NUM_LAB_PROCEDURES', 'NUM_PROCEDURES',
'NUM_MEDICATIONS', 'NUMBER_OUTPATIENT', 'NUMBER_EMERGENCY',
'NUMBER_INPATIENT', 'DIAG_1', 'DIAG_2', 'DIAG_3', 'NUMBER_DIAGNOSES',
'MAX_GLU_SERUM', 'A1CRESULT', 'METFORMIN', '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'

Nous avons 47 variables, alors jetons un coup d'œil à chacun.

1. RACE : C'est une variable catégorielle.

In [7]:
```
print(df2['RACE'].value_counts())
df2['RACE'].value_counts().plot(kind='pie',autopct='%.2f%%',figsize=(15,5))
plt.show()
```

```
Caucasian          20183
AfricanAmerican     5359
Hispanic             487
Other                476
Asian                250
Name: RACE, dtype: int64
```



Il y a 5 catégories distinctes pour la variable RACE.

Pour le remplissage des valeurs nulles, nous avons essayé de remplacer par mode, en effectuant une substitution selon la distribution prob, en supprimant les valeurs nulles mais en supprimant les valeurs nulles semblant obtenir les meilleurs résultats.

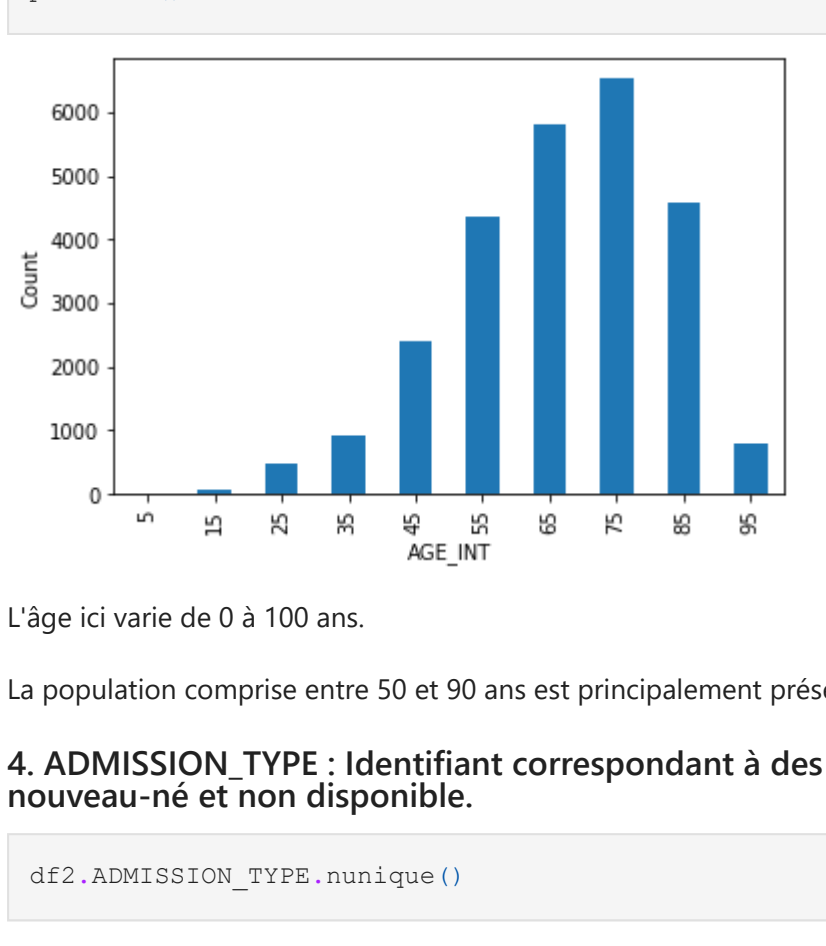
In [8]:
```
df2 = df2.dropna()
```

In [9]:
```
df2.shape
```

Out[9]: (25926, 47)

2. GENDER: C'est une caractéristique catégorique représentant le sexe du patient.

In [10]:
```
sns.countplot(df2.GENDER)
plt.show()
print(df2.GENDER.value_counts())
```



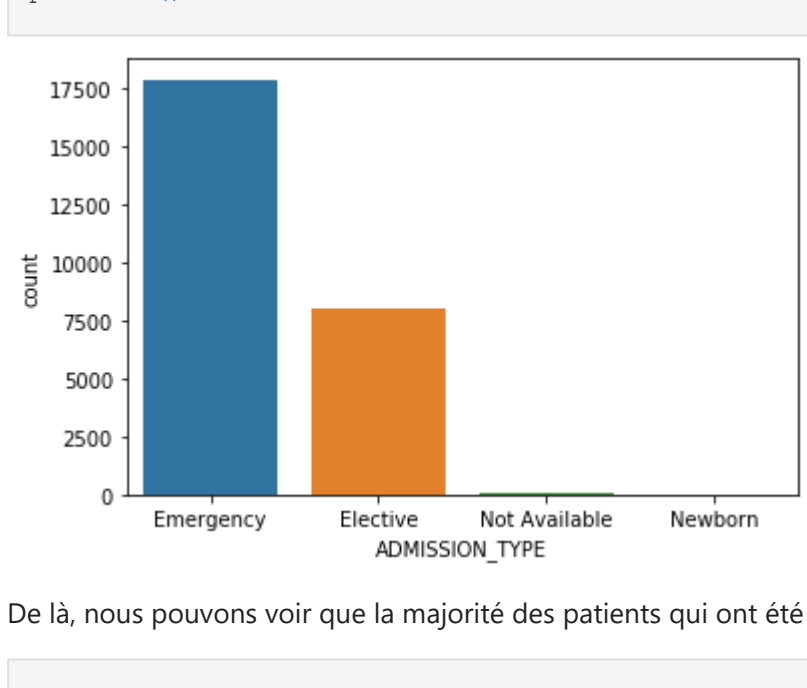

```
Female    14101
Male      11825
Name: GENDER, dtype: int64
```

Il y a 2 catégories ici: femme, homme.

In [11]:
```
#encoding gender
df2['GENDER'] = df2['GENDER'].replace({'Female' : 0, 'Male' : 1})
```

3. AGE_INT: C'est l'age du personne; on a déja traiter ces valeurs avec SQL

In [12]:
```
# check 'age' feature
df2.groupby('AGE_INT').size().plot(kind='bar')
plt.ylabel('Count')
plt.show()
```



L'âge ici varie de 0 à 100 ans.

La population comprise entre 50 et 90 ans est principalement présente dans cet ensemble de données.

4. ADMISSION_TYPE : Identifiant correspondant à des valeurs distinctes, par exemple, urgence, urgent, électif, nouveau-né et non disponible.

In [13]:
```
df2.ADMISSION_TYPE.nunique()
```

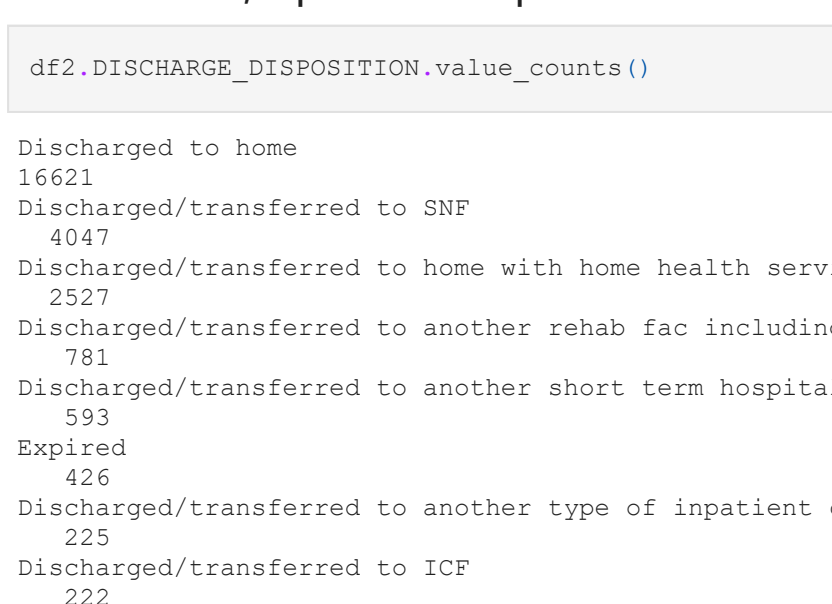
Out[13]: 5

Pour une analyse plus approfondie, nous pouvons fusionner ces catégories en moins de catégories.

Emeregncy/Urgent/Trauma Center ---> Emergency

In [14]:
```
df2['ADMISSION_TYPE']=df2['ADMISSION_TYPE'].replace({'Urgent':'Emergency','Emergency':'Emergency'})
```

In [15]:
```
sns.countplot(df2['ADMISSION_TYPE'])
plt.show()
```



De là, nous pouvons voir que la majorité des patients qui ont été admis dans cet hôpital ont un type d'admission en urgence.

In [16]:
```
df2[df2['ADMISSION_TYPE']== 'Newborn'][['GENDER','AGE_INT','ADMISSION_TYPE']]
```

Out[16]:

	GENDER	AGE_INT	ADMISSION_TYPE
4665	1	65	Newborn

Supprimer la catégorie newborn parce que ADMISSION_TYPE == newborn et l'âge et le sexe qui y correspondent donnent des informations contradictoires.

In [17]:
```
df2=df2[df2['ADMISSION_TYPE']!='Newborn']
```

In [18]:
```
df2.ADMISSION_TYPE.value_counts()
```

Out[18]:
```
Emergency        17874
Elective          8014
Not Available       37
Name: ADMISSION_TYPE, dtype: int64
```

5. DISCHARGE_DISPOSITION: Identifiant entier correspondant à 26 valeurs distinctes, par exemple, déchargé vers le domicile, expiré et non disponible

In [19]:
```
df2.DISCHARGE_DISPOSITION.value_counts()
```

Out[19]:
```
Discharged to home
16621
Discharged/transferred to SNF
  4047
Discharged/transferred to home with home health service
  2527
Discharged/transferred to another rehab fac including rehab units of a hospital .
   781
Discharged/transferred to another short term hospital
   593
Expired
   426
Discharged/transferred to another type of inpatient care institution
   225
Discharged/transferred to ICF
   222
Left AMA
   155
Discharged/transferred to a long term care hospital.
   139
Hospice / home
   115
Hospice / medical facility
    38
Discharged/transferred/referred to a psychiatric hospital of psychiatric distinct part unit of a hospital
    11
Expired at home. Medicaid only, hospice.
     8
Discharged/transferred to home under care of Home IV provider
     6
Discharged/transferred to a nursing facility certified under Medicaid but not certified under Medicare.
     5
Discharged/transferred within this institution to Medicare approved swing bed
     3
Not Mapped
     1
Admitted as an inpatient to this hospital
     1
Discharged/transferred to a federal health care facility.
     1
Name: DISCHARGE_DISPOSITION, dtype: int64
```

discharge_disposition_id description

1 Discharged to home

2 Discharged/transferred to another short term hospital

3 Discharged/transferred to SNF(skilled nursing facility)

4 Discharged/transferred to ICF(intermediate care facility)

5 Discharged/transferred to another type of inpatient care institution

6 Discharged/transferred to home with home health service

7 Left AMA(Against Medical Advice)

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

30 Discharged/transferred to another Type of Health Care Institution not Defined Elsewhere

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).

Nous pouvons fusionner plusieurs groupes ici pour réduire le nombre de catégories:

1 ---> Discharged to home

2/3/4/5/6/16/22/23/24/30/27/28/29 ---> Transferred to another medical facility

7 ---> Left AMA(Against Medical Advice)

6/8 ---> Discharged to home with home health service

9/12/15/17 ---> Still patient/referred to this institution

11/19/20/21 ---> Expired

18/25/26 ---> Not Available

13/14 ---> Hospice

In [20]:
```
df2['DISCHARGE_DISPOSITION']=df2['DISCHARGE_DISPOSITION'].replace({'Discharged to home':'Discharged to home'
                                  'Discharged/transferred to another short term hospital':'Transferred
                                  'Discharged/transferred to SNF':'Transferred to another medical faci
                                  'Discharged/transferred to ICF':'Transferred to another medical faci
                                  'Discharged/transferred to another type of inpatient care institutio
                                  'Discharged/transferred to another rehab fac including rehab units o
                                  'Discharged/transferred to a long term care hospital.':'Transferred
                                  'Discharged/transferred to a nursing facility certified under Medica
                                  'Discharged/transferred to a federal health care facility.':'Transfe
                                  'Discharged/transferred/referred to a psychiatric hospital of psychi
                                  'Discharged/transferred within this institution to Medicare approved
                                  'Discharged/transferred to home under care of Home IV provider':'Dis
                                  'Expired':'Expired',
                                  'Expired at home. Medicaid only, hospice.':'Expired',
                                  'Left AMA':'Left AMA',
                                  'Admitted as an inpatient to this hospital':'Still patient/referred
                                  'Hospice / home':'Hospice',
                                  'Hospice / medical facility':'Hospice',
                                  'Not Mapped':'Not Available'})
```

In [21]:
```
df2.DISCHARGE_DISPOSITION.value_counts()
```

```
Discharged to home                              14621
Transferred to another medical facility          6024
Discharged to home with home health service      2527
Expired                                           434
Left AMA                                          155
Hospice                                           153
Still patient/referred to this institution          4
Not Available                                       1
```

Les patients qui ont expiré doivent être retirés du système car ils créeront un biais car ils ne seront pas admis.

In [22]:
```
df2=df2[df2['DISCHARGE_DISPOSITION']!='Expired']
df2=df2[df2['DISCHARGE_DISPOSITION']!='Hospice']
```

6. ADMISSION_SOURCE: Identifiant entier correspondant à 17 valeurs distinctes, par exemple, recommandation d'un médecin, salle d'urgence et transfert d'un hôpital

In [23]:
```
df2.ADMISSION_SOURCE.value_counts(sort=False)
```

Out[23]:
```
Transfer from critical access hospital                           2
Emergency Room                                               13243
Transfer from another health care facility                    1449
Physician Referral                                            9577
Transfer from a hospital                                       620
Not Available                                                   42
Transfer from a Skilled Nursing Facility (SNF)                 340
Transfer from hospital inpt/same fac reslt in a sep claim        2
Clinic Referral                                                 47
Sick Baby                                                        1
Court/Law Enforcement                                            3
HMO Referral                                                    13
Name: ADMISSION_SOURCE, dtype: int64
```

1 Physician Referral

2 Clinic Referral

3 HMO Referral(Health Maintenance Organization)

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 critial 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

Nous pouvons fusionner plusieurs groupes ici pour réduire le nombre de catégories:

1/2/3 ---> Referral

4/5/6/10/18/19/25/26/22 ---> Transferred from another health care facility

7 ---> Emergency

9/15/17/20/21 ---> Not Available

8 ---> Court/Law Enforcement

Delivery ---> 11/12/14/13/23/24

In [24]:
```
df2['ADMISSION_SOURCE']=df2['ADMISSION_SOURCE'].replace({'Physician Referral':'Referral',
                                  'Clinic Referral':'Referral',
                                  'HMO Referral':'Referral',
                                  'Transfer from a hospital':'Transferred from another health care facility
                                  'Transfer from a Skilled Nursing Facility (SNF)':'Transferred from anothe
                                  'Transfer from another health care facility':'Transferred from another he
                                  'Court/Law Enforcement':'Emergency',
                                  'Transfer from critical access hospital':'Transferred from another health
                                  'Emergency Room':'Emergency',
                                  'Not Available':'Not Available',
                                  'Sick Baby':'Delivery',
                                  'Transfer from hospital inpt/same fac reslt in a sep claim':'Transferred
                                  })
```

In [25]:
```
df2.ADMISSION_SOURCE.value_counts()
```

Out[25]:
```
Emergency                                         13248
Referral                                           9634
Transferred from another health care facility      2413
Not Available                                        42
Delivery                                              1
Name: ADMISSION_SOURCE, dtype: int64
```

In [26]:
```
df2[df2['ADMISSION_SOURCE']=='Delivery'][['GENDER','AGE_INT','ADMISSION_SOURCE']]
```

Out[26]:

	GENDER	AGE_INT	ADMISSION_SOURCE
25302	1	75	Delivery

Supprimer la catégorie 'Delivery' car admission_source == delivery et l'âge correspondant donnent des informations contradictoires.

In [27]:
```
df2=df2[df2['ADMISSION_SOURCE']!='Delivery']
```

- Puisque nous avons 2 colonnes concernant l'admission, type_id et source_id, nous avons utilisé ces informations pour remplir les valeurs "Not Available" dans les colonnes admission_source_id par rapport à admission_type_id. Par exemple, si admission_type_id est Emergency mais admission_source_id n'est pas disponible, nous pouvons remplir Emergency (mode) à cet endroit.
- Après l'avoir remplie, la colonne admission_type_id a été supprimée car elle donnait les mêmes informations que admission_source_id et était moins significative statistiquement.

In [28]:
```
df2 = df2.reset_index(drop = True )
```

In [29]:
```
# Avant
df2[df2['ADMISSION_TYPE']=='Emergency']['ADMISSION_SOURCE'].value_counts()
```

Out[29]:
```
Emergency                                         12395
Referral                                           2793
Transferred from another health care facility      2160
Not Available                                        39
Name: ADMISSION_SOURCE, dtype: int64
```

In [30]:
```
for i in range(df2.shape[0]):
    if df2.loc[i, 'ADMISSION_SOURCE'] == 'Not Available' and df2.loc[i, 'ADMISSION_TYPE'] == 'Emergency':
        df2.loc[i, 'ADMISSION_SOURCE'] = 'Emergency'
```

In [31]:
```
# Après
df2[df2['ADMISSION_TYPE']=='Emergency']['ADMISSION_SOURCE'].value_counts()
```

Out[31]:
```
Emergency                                         12434
Referral                                           2793
Transferred from another health care facility      2160
Name: ADMISSION_SOURCE, dtype: int64
```

In [32]:
```
# Avant
df2[df2['ADMISSION_TYPE']=='Elective']['ADMISSION_SOURCE'].value_counts()
```

Out[32]:
```
Referral                                           6806
Emergency                                           852
Transferred from another health care facility       252
Not Available                                         3
Name: ADMISSION_SOURCE, dtype: int64
```

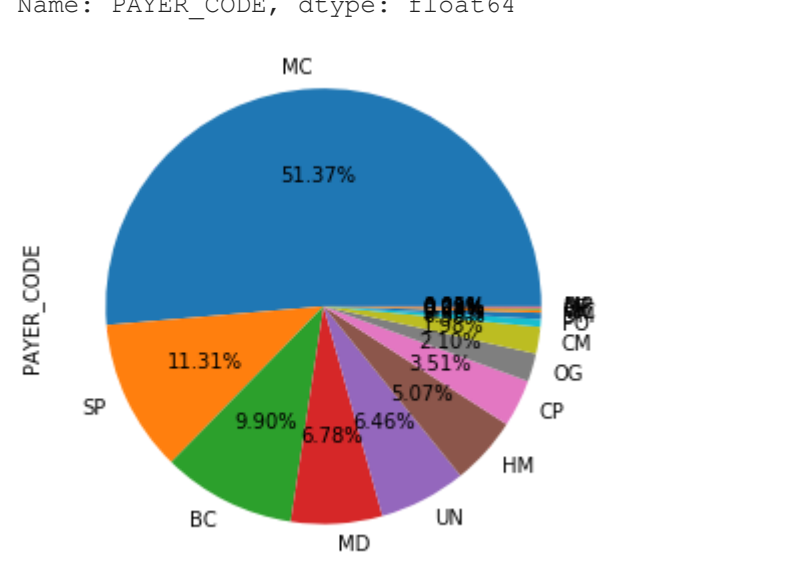
In [33]:
```
for i in range(df2.shape[0]):
    if df2.loc[i, 'ADMISSION_SOURCE'] == 'Not Available' and df2.loc[i, 'ADMISSION_TYPE'] == 'Elective':
        df2.loc[i, 'ADMISSION_SOURCE'] = 'Referral'
```

In [34]:
```
# Après
df2[df2['ADMISSION_TYPE']=='Elective']['ADMISSION_SOURCE'].value_counts()
```

Out[34]:
```
Referral                                           6809
Emergency                                           852
Transferred from another health care facility       252
Name: ADMISSION_SOURCE, dtype: int64
```

7. TIME_IN_HOSPITAL: Nombre entier de jours entre l'admission et la sortie

In [35]:
```
sns.countplot(df2.TIME_IN_HOSPITAL)
plt.show()
```

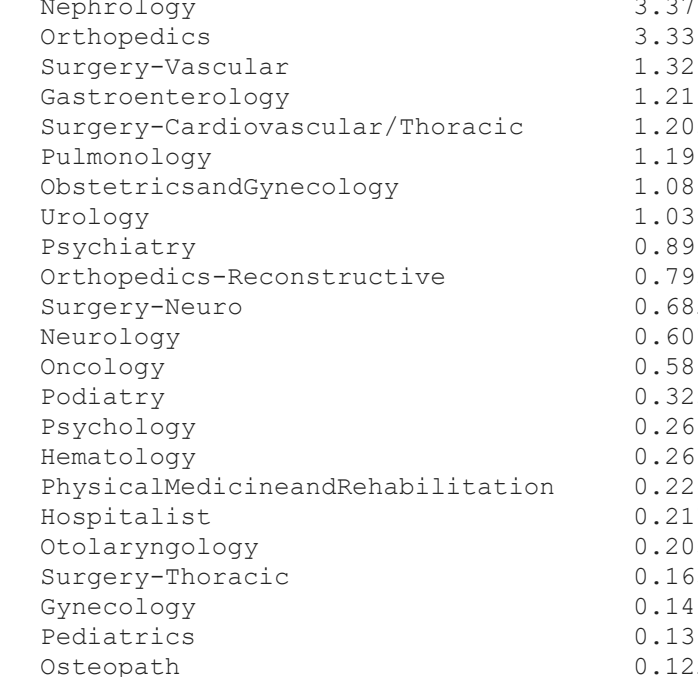


Le temps passé à l'hôpital varie de 1 jour à 14 jours.

8. PAYER_CODE : Identifiant entier correspondant à 23 valeurs distinctes, par exemple, Blue Cross / Blue Shield, Medicare et Self-Pay Medical

In [36]:
```
print(df2['PAYER_CODE'].value_counts(1)*100)
df2['PAYER_CODE'].value_counts().plot(kind='pie',autopct='%.2f%%',figsize=(15,5))
plt.show()
```

```
MC    51.371512
SP    11.311521
BC     9.902514
MD     6.776651
UN     5.071634
HM     4.460907
CP     3.512649
CM     2.099696
OG     1.981292
PO     0.560445
DM     0.477562
WC     0.236808
CH     0.090776
OT     0.082883
MP     0.051308
SI     0.011840
Name: PAYER_CODE, dtype: float64
```



Payer_code n'est pas significatif pour la réadmission des patients, nous pouvons donc l'abandonner.

In [37]:
```
df2.drop(['PAYER_CODE'],axis=1,inplace=True)
```

9. MEDICAL_SPECIALTY: Identifiant entier d'une spécialité du médecin admettant, correspondant à 55 valeurs distinctes, par exemple, cardiologie, médecine interne, médecine familiale / médecine générale et chirurgien

In [38]:
```
df2.MEDICAL_SPECIALTY.nunique()
```

Out[38]: 55

In [39]:
```
df2.MEDICAL_SPECIALTY.value_counts(1)*100
```

Out[39]:
```
Emergency/Trauma                       27.035561
InternalMedicine                       22.465170
Family/GeneralPractice                 10.668193
Cardiology                              8.777677
Surgery-General                         6.709555
Radiologist                             4.033627
Nephrology                              3.378458
Orthopedics                             3.331097
Surgery-Vascular                        1.326124
Gastroenterology                        1.211667
Surgery-Cardiovascular/Thoracic         1.203773
Pulmonology                             1.191933
ObstetricsandGynecology                 1.089316
Urology                                 1.034061
Psychiatry                              0.891976
Orthopedics-Reconstructive              0.793306
Surgery-Neuro                           0.682796
Neurology                               0.607807
Oncology                                0.588073
Podiatry                                0.323637
Psychology                              0.264435
Hematology                              0.260489
PhysicalMedicineandRehabilitation       0.224967
Hospitalist                             0.217074
Otolaryngology                          0.205233
Surgery-Thoracic                        0.165765
Gynecology                              0.149978
Pediatrics                              0.138138
Osteopath                               0.122351
SurgicalSpecialty                       0.122351
Endocrinology                           0.118404
Ophthalmology                           0.094723
InfectiousDiseases                      0.086830
Obstetrics                              0.074989
Radiology                               0.063149
Surgeon                                 0.063149
Surgery-Cardiovascular                  0.051308
OutreachServices                        0.047362
Surgery-Plastic                         0.035521
Endocrinology-Metabolism                0.031574
Anesthesiology                          0.027628
DCPTEAM                                 0.019734
Rheumatology                            0.011840
Hematology/Oncology                     0.011840
PhysicianNotFound                       0.007894
Resident                                0.003947
Perinatology                            0.003947
Dentistry                               0.003947
Pediatrics-CriticalCare                 0.003947
Pediatrics-Pulmonology                  0.003947
Neurophysiology                         0.003947
Proctology                              0.003947
SportsMedicine                          0.003947
Dermatology                             0.003947
AllergyandImmunology                    0.003947
Name: MEDICAL_SPECIALTY, dtype: float64
```

10. NUM_LAB_PROCEDURES: Nombre de tests de laboratoire effectués pendant la rencontre

In [40]:
```
print('Le nombre de tests de laboratoire qu\'un patient a subi peut aller de',df2.NUM_LAB_PROCEDURES.min(),'
```

```
Le nombre de tests de laboratoire qu'un patient a subi peut aller de 1 à 132
```

11. NUM_PROCEDURES: Nombre de procédures (autres que les tests de laboratoire) effectuées pendant la rencontre

In [41]:
```
df2.NUM_PROCEDURES.value_counts()
```

Out[41]:
```
0    10273
1     5659
2     3426
3     2530
6     1471
4     1176
5      802
Name: NUM_PROCEDURES, dtype: int64
```

Le nombre de procédures va de 0 à 5

12. NUM_MEDICATIONS: Nombre de noms génériques distincts administrés pendant la rencontre

In [42]:
```
print('Le nombre de médicaments varie d\'un minimum de',df2.NUM_MEDICATIONS.min(),'à un maximum de',df2.NUM_
```

```
Le nombre de médicaments varie d'un minimum de 1 à un maximum de 81
```

13. NUMBER_OUTPATIENT: Nombre de visites ambulatoires du patient dans l'année précédant la rencontre

14. NUMBER_EMERGENCY : Nombre de visites d'urgence du patient dans l'année précédant la rencontre

15. NUMBER_INPATIENT: Nombre de visites hospitalières du patient dans l'année précédant la rencontre

16. DIAG_1: Le diagnostic principal (codé comme les trois premiers chiffres de la CIM9)

17. DIAG_2: Diagnostic secondaire (codé comme les trois premiers chiffres de la CIM9)

18. DIAG_3: Diagnostic secondaire supplémentaire (codé comme les trois premiers chiffres de la CIM9)

```
df2 = df2.reset_index(drop = True)
```

```
diag_cols = ['DIAG_1','DIAG_2','DIAG_3']
```

```
ord('E'), ord('V')
```

(69, 86)

```
for i in diag_cols:
    for j in range(len(df2[i])):
        if str(df2.loc[j, i])[:3] == '250':
            df2.loc[j, i] = 'Diabetes'
        elif ord(str(df2.loc[j, i])[0]) in range(69, 87):
            df2.loc[j, i] = 'External causes of injury'
        elif str(df2.loc[j, i]) == '?':
            df2.loc[j, i] = 'Missing'
        else:
            x = float(df2.loc[j, i])
            if x in range(390, 460) or x == 785:
                df2.loc[j, i] = 'Circulatory'
            elif x in range(460, 520) or x == 786:
                df2.loc[j, i] = 'Respiratory'
            elif x in range(520, 580) or x == 787:
                df2.loc[j, i] = 'Digestive'
            elif x in range(800, 1000):
                df2.loc[j, i] = 'Injury and Poisoning'
            elif x in range(710, 740):
                df2.loc[j, i] = 'Musculoskeletal System and Connective Tissue'
            elif x in range(580, 630) or x == 788:
                df2.loc[j, i] = 'Genitourinary'
            elif x in range(140, 240):
                df2.loc[j, i] = 'Neoplasms'
            elif x in [780, 781, 784] or x in range(790, 800):
                df2.loc[j, i] = 'Other Symptoms'
            elif x in range(240, 280):
                df2.loc[j, i] = 'Endocrine, Nutritional, Metabolic, Immunity'
            elif x in range(680, 710) or x == 782:
                df2.loc[j, i] = 'Skin and Subcutaneous Tissue'
            elif x in range(1, 140):
                df2.loc[j, i] = 'Infectious and Parasitic'
            elif x in range(290, 320):
                df2.loc[j, i] = 'Mental Disorders'
            elif x in range(280, 290):
                df2.loc[j, i] = 'Blood and Blood-Forming Organs'
            elif x in range(320, 360):
                df2.loc[j, i] = 'Nervous'
            elif x in range(630, 680):
                df2.loc[j, i] = 'Pregnancy, Childbirth'
            elif x in range(360, 390):
                df2.loc[j, i] = 'Sense Organs'
            else:
                df2.loc[j, i] = 'Congenital Anomalies'
```

```
for i in range(len(df2['DIAG_2'])):
    if df2.loc[i, 'DIAG_2'] == 'Missing':
        if df2.loc[i, 'DIAG_1'] != 'Missing':
            df2.loc[i, 'DIAG_2'] = 'Not Required'
```

```
for i in range(len(df2['DIAG_3'])):
    if df2.loc[i, 'DIAG_3'] == 'Missing':
        if df2.loc[i, 'DIAG_1'] != 'Missing' or df2.loc[i, 'DIAG_2'] != 'Missing':
            df2.loc[i, 'DIAG_3'] = 'Not Required'
```

```
df3 = pd.DataFrame(df2['DIAG_1'].value_counts())
df4 = df3.merge(pd.DataFrame(df2['DIAG_2'].value_counts()), how = 'outer', left_index = True, right_index = 
df4.merge(pd.DataFrame(df2['DIAG_3'].value_counts()), how = 'outer', left_index = True, right_index = True)
```

	DIAG_1	DIAG_2	DIAG_3
Blood and Blood-Forming Organs	282	701	619
Circulatory	7623	8110	7647
Congenital Anomalies	210	146	110
Diabetes	2183	2918	4339
Digestive	2244	1090	951
Endocrine, Nutritional, Metabolic, Immunity	694	2120	2344
External causes of injury	243	660	1382
Genitourinary	1191	1804	1583
Infectious and Parasitic	557	472	433
Injury and Poisoning	1801	610	488
Mental Disorders	539	662	776
Musculoskeletal System and Connective Tissue	1613	553	560
Neoplasms	825	646	441
Nervous	240	323	385
Other Symptoms	680	638	621
Pregnancy, Childbirth	229	149	97
Respiratory	3441	2634	1802
Sense Organs	60	40	60
Skin and Subcutaneous Tissue	682	1061	699

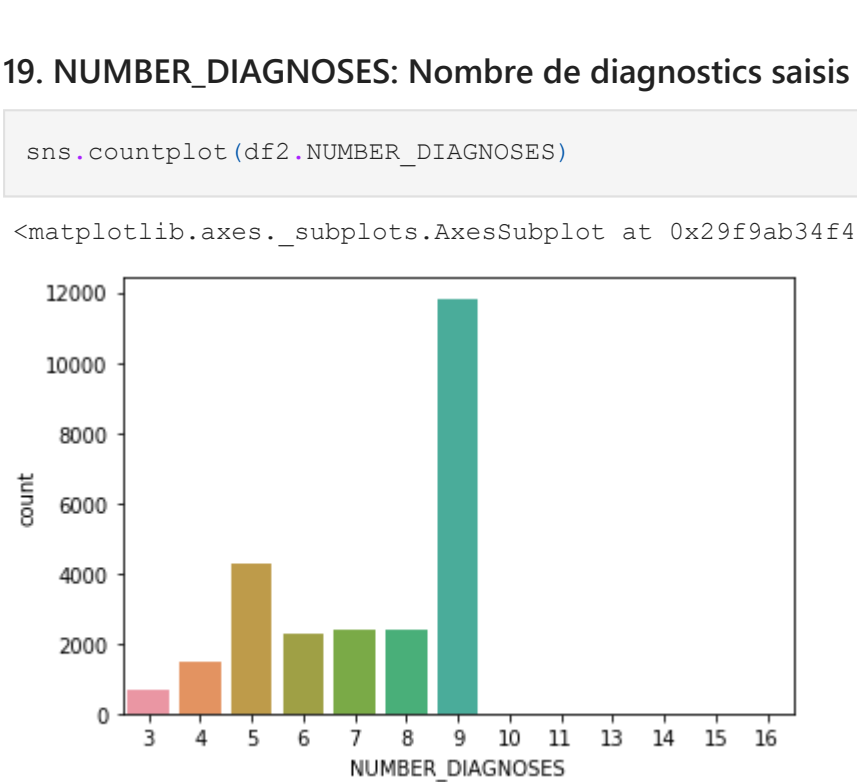
```
len(df2[df2['DIAG_1'] == 'Missing'])
```

0

19. NUMBER_DIAGNOSES: Nombre de diagnostics saisis dans le système

```
sns.countplot(df2.NUMBER_DIAGNOSES)
```

<matplotlib.axes._subplots.AxesSubplot at 0x29f9ab34f48>



Le nombre de diagnostics saisis dans le système va de 1 à 16.

20. MAX_GLU_SERUM: Indique la plage du résultat ou si le test n'a pas été effectué.

Valeurs : "> 200", "> 300", "normal" et "None" si non mesuré

```
df2.MAX_GLU_SERUM.value_counts()
```

```
None    25335
Norm        2
Name: MAX_GLU_SERUM, dtype: int64
```

21. A1CRESULT: Indique la plage du résultat ou si le test n'a pas été effectué.

```
df2.A1CRESULT.value_counts()
```

```
None    21217
>8       1914
Norm     1122
>7       1084
Name: A1CRESULT, dtype: int64
```

Valeurs: "> 8" si le résultat est supérieur à 8%

```
«> 7» si le résultat est supérieur à 7% mais inférieur à 8%

«Normal» si le résultat est inférieur à 7%

«Aucun» s'il n'est pas mesuré.
```

22. caractéristiques pour les médicaments :

Pour les noms génériques : 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, et METFORMIN_PIOGLITAZONE

La fonction indique si le médicament a été prescrit ou s'il y a eu un changement de posologie.

Valeurs: «up» si la posologie a été augmentée pendant la rencontre

```
«Down» si le dosage a été diminué

«Stable» si la posologie n'a pas changé

«Non» si le médicament n'a pas été prescrit
```

```
meds = ['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']

for i in meds:
    print(i, df2[i].unique())
```

```
METFORMIN ['No' 'Steady' 'Up' 'Down']
REPAGLINIDE ['No' 'Steady' 'Down' 'Up']
NATEGLINIDE ['No' 'Steady' 'Down' 'Up']
CHLORPROPAMIDE ['No' 'Steady']
GLIMEPIRIDE ['No' 'Steady' 'Down' 'Up']
ACETOHEXAMIDE ['No']
GLIPIZIDE ['No' 'Steady' 'Down' 'Up']
GLYBURIDE ['No' 'Steady' 'Up' 'Down']
TOLBUTAMIDE ['No']
PIOGLITAZONE ['No' 'Up' 'Steady' 'Down']
ROSIGLITAZONE ['No' 'Steady' 'Up' 'Down']
ACARBOSE ['No' 'Steady' 'Up' 'Down']
MIGLITOL ['No' 'Steady' 'Down' 'Up']
TROGLITAZONE ['No' 'Steady']
TOLAZAMIDE ['No' 'Steady']
EXAMIDE ['No']
CITOGLIPTON ['No']
INSULIN ['Steady' 'No' 'Up' 'Down']
GLYBURIDE_METFORMIN ['No' 'Steady' 'Up' 'Down']
GLIPIZIDE_METFORMIN ['No' 'Steady']
GLIMEPIRIDE_PIOGLITAZONE ['No']
METFORMIN_ROSIGLITAZONE ['No']
METFORMIN_PIOGLITAZONE ['No' 'Steady']
```

Nous pouvons supprimer examide, citoglipton et metformin-rosiglitazone car ils ne sont pas prescrit à aucun patient.

```
df2.drop(['EXAMIDE', 'CITOGLIPTON','METFORMIN_ROSIGLITAZONE'], axis = 1, inplace = True)
```

```
meds = ['METFORMIN', 'REPAGLINIDE', 'NATEGLINIDE', 'CHLORPROPAMIDE',
        'GLIMEPIRIDE', 'ACETOHEXAMIDE', 'GLIPIZIDE', 'GLYBURIDE', 'TOLBUTAMIDE',
        'PIOGLITAZONE', 'ROSIGLITAZONE', 'ACARBOSE', 'MIGLITOL', 'TROGLITAZONE',
        'TOLAZAMIDE', 'INSULIN', 'GLYBURIDE_METFORMIN', 'GLIPIZIDE_METFORMIN',
        'GLIMEPIRIDE_PIOGLITAZONE', 'METFORMIN_PIOGLITAZONE']
```

```
# les médicaments peuvent être codés comme ci-dessous
for i in meds:
    df2[i] = df2[i].replace({'No' : -2,
                             'Down' : -1,
                             'Steady' : 0,
                             'Up' : 1})
```

```
for i in meds:
    df2[i] = df2[i].astype('int64')
```

23. CHANGE : Indique s'il y a eu un changement dans les médicaments diabétiques (soit la posologie, soit le nom générique)

```
df2.CHANGE.value_counts()
```

```
Ch    13823
No    11514
Name: CHANGE, dtype: int64
```

```
df2['CHANGE'] = df2['CHANGE'].replace({'No' : 0, 'Ch' : 1})
```

24. DIABETESMED : Indique si un médicament diabétique a été prescrit.

```
df2.DIABETESMED.value_counts()
```

```
Yes    20790
No      4547
Name: DIABETESMED, dtype: int64
```

```
df2['DIABETESMED'] = df2['DIABETESMED'].replace({'Yes' : 1, 'No' : 0})
```

25. READMITTED: Outcome variable

Le résultat que nous examinons est de savoir si le patient est réadmis à l'hôpital dans les 30 jours ou non.

```
df2.READMITTED.value_counts()
```

```
NO     14044
>30     8539
<30     2754
Name: READMITTED, dtype: int64
```

Le résultat a en fait des catégories «<30 » 30 et Aucune réadmission. notre problème, nous allons le convertir en 2 catégories, c'est-à-dire pas de réadmission ou de réadmission dans 30 jours

```
df2['READMITTED'] = df2['READMITTED'].replace({'>30': 'NO'})
df2['READMITTED'] = df2['READMITTED'].replace({'NO': 0, '<30': 1}).astype(int)
```

```
df2.reset_index(drop = True, inplace = True)
```

(ADDITIONAL) Création de nouvelles fonctionnalités et suppression des fonctionnalités redondantes

1. Visites de l'année précédente:

'NUMBER_OUTPATIENT', 'NUMBER_EMERGENCY', 'NUMBER_INPATIENT' ont été combinés en les additionnant pour obtenir le nombre total de visites du patient au cours de l'année précédente, puis en supprimant les fonctionnalités de combinaison.

```
df2['preceding_year_visits']=df2['NUMBER_OUTPATIENT']+df2['NUMBER_EMERGENCY']+df2['NUMBER_INPATIENT']
```

```
# Dropping 'number_outpatient', 'number_emergency', 'number_inpatient'
df2 = df2.drop(columns=['NUMBER_OUTPATIENT','NUMBER_EMERGENCY','NUMBER_INPATIENT'])
```

2. Nombre de changements de médicaments

```
df2['number_changes'] = np.nan
for i in range(len(df2)):
    n = 0
    for j in meds:
        if df2.loc[i, j] == -1 or df2.loc[i, j] == 1:
            n += 1
    df2.loc[i, 'number_changes'] = n
```

```
df2['number_changes'].value_counts()
```

```
0.0    16388
1.0     8417
2.0      485
3.0       44
4.0        3
Name: number_changes, dtype: int64
```

3. Nombre de médicaments diabétiques

```
df2['number_diab_meds'] = np.nan
for i in range(len(df2)):
    n = 0
    for j in meds:
        if df2.loc[i, j] != -2:
            n += 1
    df2.loc[i, 'number_diab_meds'] = n
df2.number_diab_meds=df2.number_diab_meds.astype('int64')
df2['number_diab_meds'].value_counts()
```

```
1    11618
2     6017
0     4547
3     2597
4      535
5       22
6        1
Name: number_diab_meds, dtype: int64
```

4. Insulin_treatment

```
df2['insulin_treatment'] = np.nan
```

```
for i in range(len(df2)):
    if df2.loc[i, 'INSULIN'] != -2 and df2.loc[i, 'number_diab_meds'] == 1:
        df2.loc[i, 'insulin_treatment'] = 'insulin_only'
    elif df2.loc[i, 'INSULIN'] != -2 and df2.loc[i, 'number_diab_meds'] > 1:
        df2.loc[i, 'insulin_treatment'] = 'insulin_combo'
    elif df2.loc[i, 'INSULIN'] == -2 and df2.loc[i, 'number_diab_meds'] == 0:
        df2.loc[i, 'insulin_treatment'] = 'no_med'
    else:
        df2.loc[i, 'insulin_treatment'] = 'other_meds'
df2['insulin_treatment'].value_counts()
```

```
insulin_only     8128
insulin_combo    7511
other_meds       5151
no_med           4547
Name: insulin_treatment, dtype: int64
```

number_diab_meds a été créé pour faire le traitement de l'insuline de la colonne, par conséquent nous le déposons

```
df2=df2.drop('number_diab_meds',1)
df2.reset_index(drop = True, inplace = True)
```

Tests statistiques

```
# Caractéristiques numériques
num_cols = ['AGE_INT', 'TIME_IN_HOSPITAL', 'NUM_LAB_PROCEDURES', 'NUM_PROCEDURES', 'NUM_MEDICATIONS',
            'NUMBER_DIAGNOSES','preceding_year_visits', 'number_changes']
```

```
# Caractéristiques catégoriques
cat_cols = ['RACE', 'GENDER', 'ADMISSION_TYPE', 'DISCHARGE_DISPOSITION', 'ADMISSION_SOURCE',
            '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', 'INSULIN', 'GLYBURIDE_METFORMIN', 'GLIPIZIDE_METFORMIN',
            'GLIMEPIRIDE_PIOGLITAZONE', 'METFORMIN_ROSIGLITAZONE', 'METFORMIN_PIOGLITAZONE',
            'CHANGE', 'DIABETESMED', 'insulin_treatment']
```

```
df2.shape
```

(25337, 43)

```
len(num_cols)+len(cat_cols)
```

42

Chi-2 pour les catégoriques vs catégoriques et one way anova pour les catégoriques vs numériques

Pour voir si les fonctionnalités sont significatives par rapport à la variable cible (readmitted)

```
#Statistical Tests (Chi Square and Anova)

p_val = []
sig = []
for i in df2.columns:
    if i in num_cols:
        stat, p = stats.f_oneway(df2[df2['READMITTED'] == 0][i], df2[df2['READMITTED'] == 1][i])
    else:
        ct = pd.crosstab(df2[i], df2['READMITTED'])
        stat, p, dof, exp = stats.chi2_contingency(ct)
    p_val.append(p)
    if p < 0.05:
        sig.append('Significant')
    else:
        sig.append('Insignificant')
stats_df = pd.DataFrame({"columns" : df2.columns, "p_value" : p_val, "significance" : sig})

stats_df.sort_values(by="p_value",ascending = True)
```

	columns	p_value	significance
39	READMITTED	0.000000e+00	Significant
40	preceding_year_visits	9.387277e-128	Significant
4	DISCHARGE_DISPOSITION	1.277548e-29	Significant
32	INSULIN	2.382848e-22	Significant
14	NUMBER_DIAGNOSES	4.313655e-22	Significant
42	insulin_treatment	2.864962e-19	Significant
7	MEDICAL_SPECIALTY	3.399074e-17	Significant
41	number_changes	4.351799e-17	Significant
38	DIABETESMED	4.921855e-14	Significant
37	CHANGE	3.972180e-13	Significant
11	DIAG_1	5.830308e-13	Significant
13	DIAG_3	5.561852e-11	Significant
6	TIME_IN_HOSPITAL	3.560013e-08	Significant
10	NUM_MEDICATIONS	3.950003e-06	Significant
12	DIAG_2	3.845998e-05	Significant
5	ADMISSION_SOURCE	1.367425e-03	Significant
17	METFORMIN	1.004162e-02	Significant
29	MIGLITOL	2.402984e-02	Significant
16	A1CRESULT	2.851582e-02	Significant
26	PIOGLITAZONE	2.855366e-02	Significant
8	NUM_LAB_PROCEDURES	5.692811e-02	Insignificant
2	AGE_INT	6.031671e-02	Insignificant
18	REPAGLINIDE	8.278125e-02	Insignificant
24	GLYBURIDE	1.020866e-01	Insignificant
36	METFORMIN_PIOGLITAZONE	1.686771e-01	Insignificant
34	GLIPIZIDE_METFORMIN	2.086789e-01	Insignificant
23	GLIPIZIDE	5.069747e-01	Insignificant
21	GLIMEPIRIDE	5.101057e-01	Insignificant
15	MAX_GLU_SERUM	5.208370e-01	Insignificant
28	ACARBOSE	5.234767e-01	Insignificant
19	NATEGLINIDE	5.251118e-01	Insignificant
9	NUM_PROCEDURES	5.705998e-01	Insignificant
3	ADMISSION_TYPE	6.691503e-01	Insignificant
20	CHLORPROPAMIDE	7.680758e-01	Insignificant
31	TOLAZAMIDE	8.417851e-01	Insignificant
1	GENDER	8.508377e-01	Insignificant
0	RACE	8.786289e-01	Insignificant
27	ROSIGLITAZONE	8.966888e-01	Insignificant
33	GLYBURIDE_METFORMIN	9.191034e-01	Insignificant
25	TOLBUTAMIDE	1.000000e+00	Insignificant
30	TROGLITAZONE	1.000000e+00	Insignificant
22	ACETOHEXAMIDE	1.000000e+00	Insignificant
35	GLIMEPIRIDE_PIOGLITAZONE	1.000000e+00	Insignificant

```
sig_cols = stats_df[stats_df['significance'] == 'Significant']['columns'].reset_index(drop = True)
insig_cols = stats_df[stats_df['significance'] == 'Insignificant']['columns'].reset_index(drop = True)
print('Statistically significant features are :','\n')
print(sig_cols)
```

```
Statistically significant features are :

0     DISCHARGE_DISPOSITION
1          ADMISSION_SOURCE
2          TIME_IN_HOSPITAL
3         MEDICAL_SPECIALTY
4           NUM_MEDICATIONS
5                    DIAG_1
6                    DIAG_2
7                    DIAG_3
8          NUMBER_DIAGNOSES
9                 A1CRESULT
10                METFORMIN
11             PIOGLITAZONE
12                 MIGLITOL
13                  INSULIN
14                   CHANGE
15              DIABETESMED
16               READMITTED
17    preceding_year_visits
18           number_changes
19        insulin_treatment
Name: columns, dtype: object
```

Nous pouvons supprimer toutes les colonnes insignifiantes

```
df2 = df2.drop(['NATEGLINIDE','CHLORPROPAMIDE','ACETOHEXAMIDE', 'TOLBUTAMIDE',
                'ACARBOSE', 'MIGLITOL', 'TROGLITAZONE', 'TOLAZAMIDE',
                'GLYBURIDE_METFORMIN', 'GLIPIZIDE_METFORMIN',
                'GLIMEPIRIDE_PIOGLITAZONE', 'METFORMIN_PIOGLITAZONE'],axis=1)
```

CHANGE et number_change décrivent les mêmes informations et les deux sont significatives, nous en abandonnons une basée sur le fait que le nombre de changements est un peu plus significatif que le changement.

```
df2 = df2.drop(['CHANGE'],axis=1)
```

```
df2['ADMISSION_TYPE'].value_counts()
```

```
Emergency        17387
Elective          7913
Not Available       37
Name: ADMISSION_TYPE, dtype: int64
```

```
df2['ADMISSION_SOURCE'].value_counts()
```

```
Emergency                                        13287
Referral                                          9637
Transferred from another health care facility    2413
```

ADMISSION_SOURCE et ADMISSION_TYPE sont similaires car les détails de ADMISSION_TYPE sont présents dans l'identifiant de la source d'admission. Nous pouvons donc supprimer ADMISSION_TYPE et simplement conserver ADMISSION_SOURCE

```
df2 = df2.drop(['ADMISSION_TYPE'],axis=1)
```

```
df2.shape
```

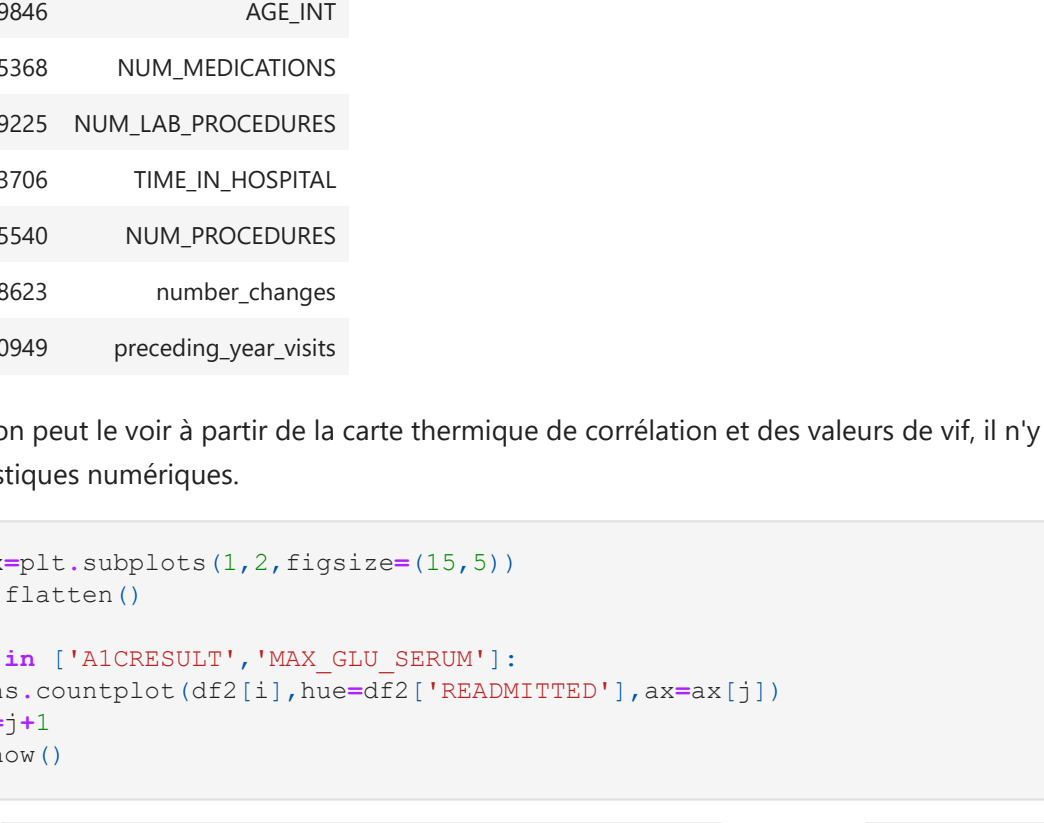
(25337, 29)

```
df2.columns
```

```
Index(['RACE', 'GENDER', 'AGE_INT', 'DISCHARGE_DISPOSITION',
       'ADMISSION_SOURCE', 'TIME_IN_HOSPITAL', 'MEDICAL_SPECIALTY',
       'NUM_LAB_PROCEDURES', 'NUM_PROCEDURES', 'NUM_MEDICATIONS', 'DIAG_1',
       'DIAG_2', 'DIAG_3', 'NUMBER_DIAGNOSES', 'MAX_GLU_SERUM', 'A1CRESULT',
       'METFORMIN', 'REPAGLINIDE', 'GLIMEPIRIDE', 'GLIPIZIDE', 'GLYBURIDE',
       'PIOGLITAZONE', 'ROSIGLITAZONE', 'INSULIN', 'DIABETESMED', 'READMITTED',
       'preceding_year_visits', 'number_changes', 'insulin_treatment'],
      dtype='object')
```

Multi-Collinearity

```
plt.figure(figsize=(8,5))
corr=df2[num_cols].corr()
sns.heatmap(corr,annot=True,cmap='YlGnBu')
b,t=plt.ylim()
plt.ylim(b+0.5,t-0.5)
plt.show()
```

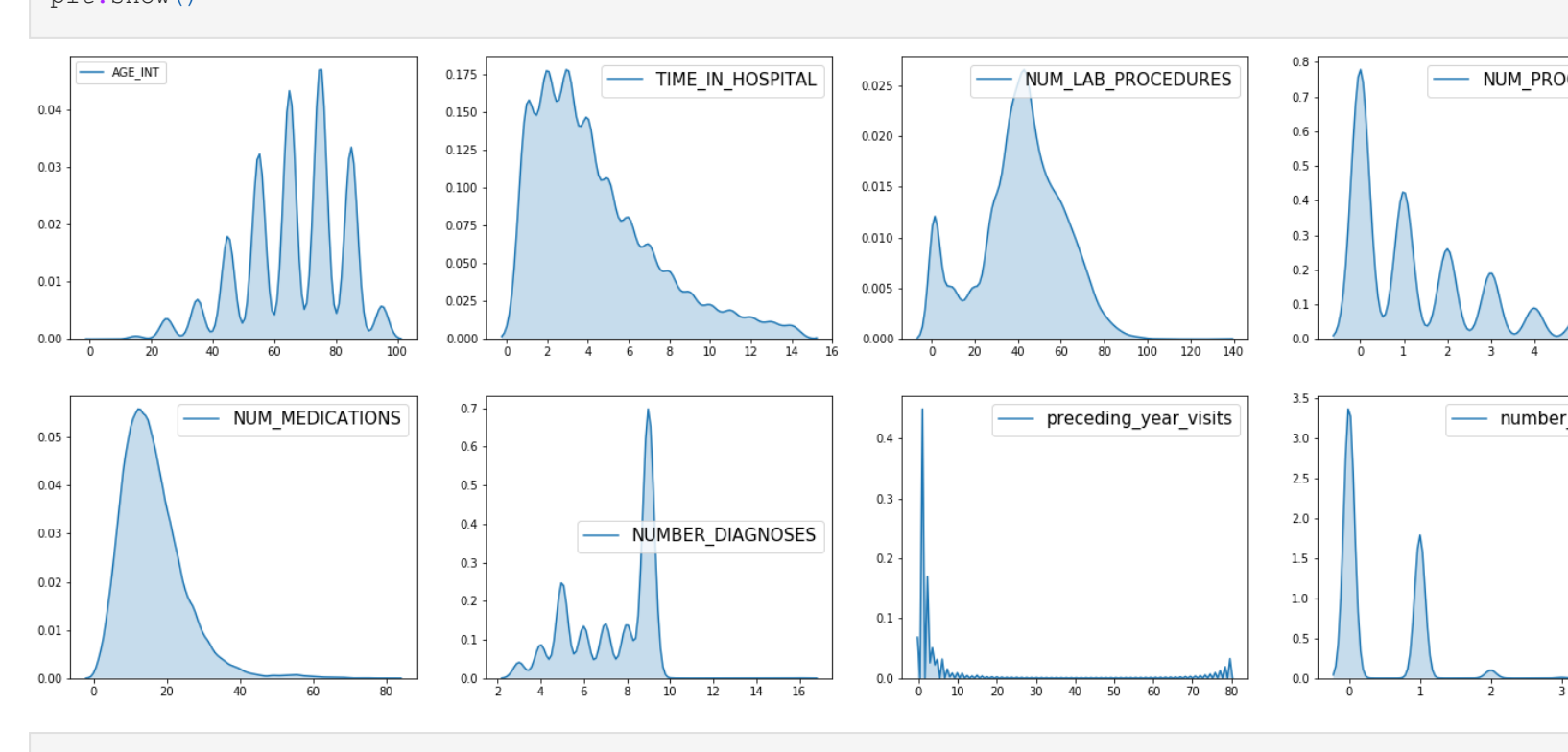


```
from statsmodels.stats.outliers_influence import variance_inflation_factor
vif=pd.DataFrame()
vif['VIF']=[variance_inflation_factor(df2[num_cols].values,i) for i in range(df2[num_cols].shape[1])]
vif['feature']=df2[num_cols].columns
vif=vif.sort_values('VIF',ascending=False)
vif
```

	VIF	feature
5	14.765046	NUMBER_DIAGNOSES
0	12.129846	AGE_INT
4	6.855368	NUM_MEDICATIONS
2	5.869225	NUM_LAB_PROCEDURES
1	4.273706	TIME_IN_HOSPITAL
3	1.935540	NUM_PROCEDURES
7	1.688623	number_changes
6	1.280949	preceding_year_visits

Comme on peut le voir à partir de la carte thermique de corrélation et des valeurs de vif, il n'y a pas de multi-colinéarité dans les caractéristiques numériques.

```
fig,ax=plt.subplots(1,2,figsize=(15,5))
ax=ax.flatten()
j=0
for i in ['A1CRESULT','MAX_GLU_SERUM']:
    sns.countplot(df2[i],hue=df2['READMITTED'],ax=ax[j])
    j=j+1
plt.show()
```



Nous pouvons voir que la majorité des patients réadmis n'ont pas subi de test A1C ni de test Max Glucose Serum.

Outliers et normalité

```
fig,ax=plt.subplots(2,4,figsize=(25,10))
ax=ax.flatten()
j=0
for i in num_cols:
    sns.kdeplot(df2[i],ax=ax[j],shade=True)
    plt.rc('legend', fontsize=15)
    j=j+1
plt.show()
```

```
#Number of outliers
for i in num_cols:
    q1 = df2[i].quantile(0.25)
    q3 = df2[i].quantile(0.75)
    iqr = q3-q1

    UL = q3 + (1.5 * iqr)
    LL = q1 - (1.5 * iqr)
    print(i,df2[(df2[i]>UL) | (df2[i]<LL)].count()[i])
    #print(K[(K[i]>UL) | (K[i]<LL)][i])
```

```
AGE_INT 69
TIME_IN_HOSPITAL 488
NUM_LAB_PROCEDURES 53
NUM_PROCEDURES 1471
NUM_MEDICATIONS 722
NUMBER_DIAGNOSES 9
preceding_year_visits 3778
number_changes 47
```

Les données ne sont pas normalement distribuées et ont peu de valeurs aberrantes, nous utilisons donc la transformation.

```
pt = PowerTransformer(method = 'yeo-johnson')
df_new=df2.copy()
df_new[num_cols]=pd.DataFrame(pt.fit_transform(df_new[num_cols]), columns = num_cols)
skew_df = pd.DataFrame({"Skew_Before" : df2[num_cols].skew(), "Skew_After" : df_new[num_cols].skew()})
skew_df
```

	Skew_Before	Skew_After
AGE_INT	-0.517891	-0.104587
TIME_IN_HOSPITAL	1.128727	0.012535
NUM_LAB_PROCEDURES	-0.290458	-0.283152
NUM_PROCEDURES	1.195864	0.131387
NUM_MEDICATIONS	1.496423	0.019794
NUMBER_DIAGNOSES	-0.592813	-0.189704
preceding_year_visits	7.121517	0.420725
number_changes	1.086956	0.619423

Scaling

```
mm=MinMaxScaler()
df_new[num_cols]=pd.DataFrame(mm.fit_transform(df_new[num_cols]), columns = num_cols)
```

```
df2.to_csv('CSV_Files/Diabetes_cleaned.csv', index = False)
```