Python for Data Analysis

Projet

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Introduction

Notre dataset est un jeu de données de 130 hôpitaux aux USA.

Ce dataset réunit les données de 1999 à 2008.

Présentation du dataset

Est-ce que la prise de médicaments permet de réduire les risques de réadmission des patients ?

US hôpitals (1999-2008)

Health and medicine

Classification, Clustering

Les étapes principales

preparation

- Exploration
- Nettoyage
- Mapping

Visualization

- Graphiques simples
- Graphiques ayant nécessité un mapping
- Résumé en histogrammes

Machine Learning

- Encodage
- Pipeline
- Entrainement

Exploration

```
df.head(5)
```

	race	gender	age	weight	admission_type_id	discharge_disposition_id	admission_source_id	time_in_hospital
0	Caucasian	Female	[0-10)	NaN	6	25	1	1
1	Caucasian	Female	[10-20)	NaN	1	1	7	3
2	AfricanAmerican	Female	[20-30)	NaN	1	1	7	2
3	Caucasian	Male	[30-40)	NaN	1	1	7	2
4	Caucasian	Male	[40-50)	NaN	1	1	7	1

5 rows × 48 columns

insulin	glyburide-metformin	glipizide-metformin	glimepiride-pioglitazone	metformin-rosiglitazone	metformin-pioglitazone	change	diabetesMed	readmitted
No	No	No	No	No	No	No	No	NO
Up	No	No	No	No	No	Ch	Yes	>30
No	No	No	No	No	No	No	Yes	NO
Up	No	No	No	No	No	Ch	Yes	NO
Steady	No	No	No	No	No	Ch	Yes	NO

Nettoyage

- Suppression des colonnes inexploitables
- Mise en forme des colonnes
- Vérification des données en double

```
Rate of Missing Values by Columns:
race                      2.233555
gender                    0.000000
age                       0.000000
weight                   96.858479
admission_type_id         0.000000
discharge_disposition_id  0.000000
admission_source_id       0.000000
time_in_hospital          0.000000
payer_code               39.557416
medical_specialty        49.082208
```

```
[ ]  df.drop(["weight", "medical_specialty", "payer_code"], axis=1, inplace=True)
```

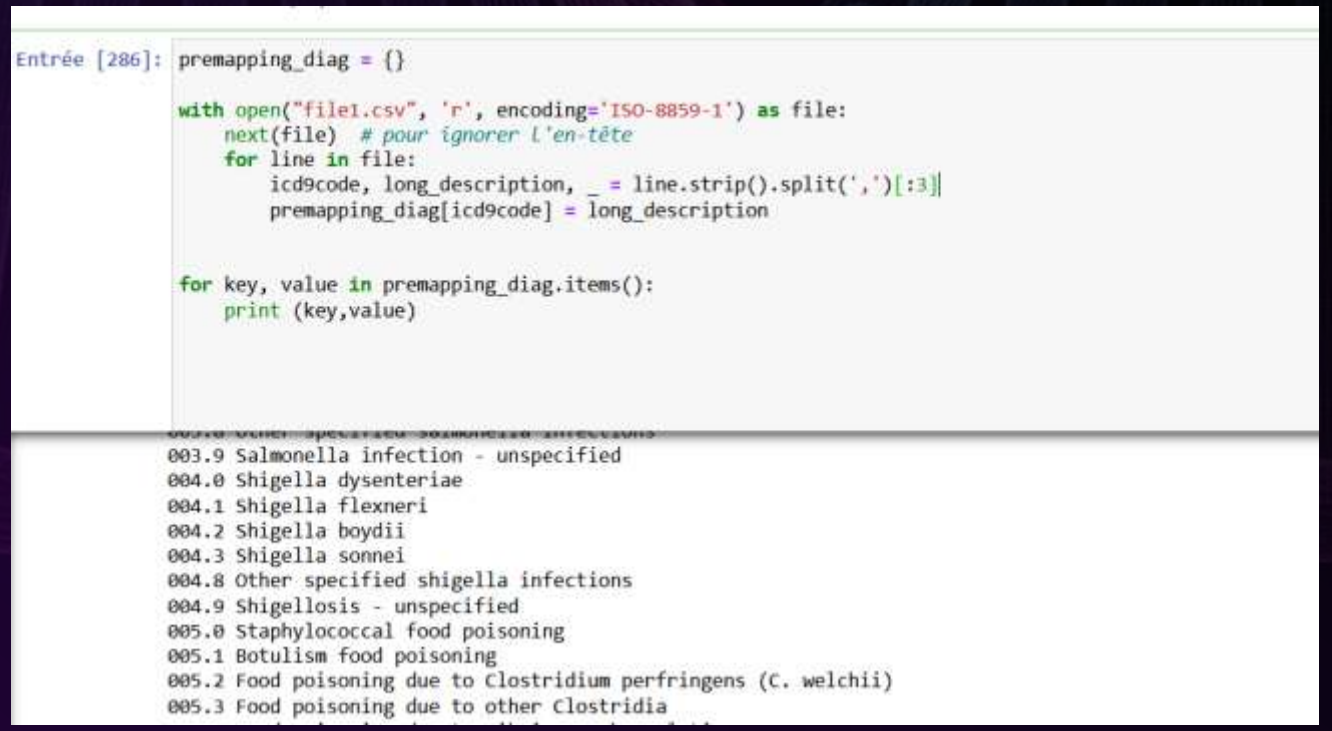
```
df['age']

0          [0-10)
1         [10-20)
2         [20-30)
3         [30-40)
4         [40-50)
           ...
101761    [70-80)
101762    [80-90)
101763    [70-80)
101764    [80-90)
101765    [70-80)
```

```
def tranche_age(texte):
    nombres = re.findall(r'\d+', texte)
    nombres = list(map(int, nombres))
    return (sum(nombres)/2)
```

```
df['age']

0          5
1         15
2         25
3         35
4         45
          ..
101761    75
101762    85
101763    75
101764    85
101765    75
```

Mapping 1

- Récupération d'un fichier.txt sur les codes IC9
- Enregistrement sous forme de pré-dictionnaire



Entrée [286]:

```
premapping_diag = {}

with open("file1.csv", 'r', encoding='ISO-8859-1') as file:
    next(file)  # pour ignorer l'en-tête
    for line in file:
        icd9code, long_description, _ = line.strip().split(',')[:3]
        premapping_diag[icd9code] = long_description


for key, value in premapping_diag.items():
    print (key,value)
```

```
003.9 Salmonella infection - unspecified
004.0 Shigella dysenteriae
004.1 Shigella flexneri
004.2 Shigella boydii
004.3 Shigella sonnei
004.8 Other specified shigella infections
004.9 Shigellosis - unspecified
005.0 Staphylococcal food poisoning
005.1 Botulism food poisoning
005.2 Food poisoning due to Clostridium perfringens (C. welchii)
005.3 Food poisoning due to other Clostridia
```

Mapping 1 (suite)

- Mise en forme des codes ICD9 dans un dictionnaire
- Rajout de valeurs manquantes
  -

```
mapping_diag = {}

for old_key, value in premapping_diag.items():
    new_key = old_key.lstrip("0")  # Supprime les zéros inutiles au début du nombre. exemple : 006 voudra 6
    nk_v2=re.sub(r'\.0$', '', new_key)# Supprime les '.0' inutiles en fin de chaîne. exemple : 120.0 voudra 120
    nk_v2=re.sub(r'\.00$', '', nk_v2)# Supprime les '.00' inutiles en fin de chaîne. exemple : 120.00 voudra 120
    nk_v2=re.sub(r'\.$', '', nk_v2)# Supprime les '.' en fin de chaîne.
    if '.' in nk_v2:
        nk_v2= nk_v2.rstrip("0") #supprime le dernier chiffre quand c'est un zéro si et seulement si le nombre est un nombre à
    mapping_diag[nk_v2] = value  # Ajoute la nouvelle clé et sa valeur correspondante dans le nouveau dictionnaire(if '.' in nk_

for key, value in mapping_diag.items():
    print (key,value)
```

```
1 Cholera due to vibrio cholerae
1.1 Cholera due to vibrio cholerae el tor
1.9 Cholera - unspecified
2 Typhoid fever
2.1 Paratyphoid fever A
2.2 Paratyphoid fever B
2.3 Paratyphoid fever C
2.9 Paratyphoid fever - unspecified
3 Salmonella gastroenteritis
3.1 Salmonella septicemia
3.2 Localized salmonella infection - unspecified
```

```
diags_lit = []
mauvaises_valeurs=[]
for value in df['diag_1']:
    if str(value) in mapping_diag.keys():
        diags_lit.append(mapping_diag[value])
    else:
        diags_lit.append(0)
        mauvaises_valeurs.append(value)



df['diag_lit_1'] = diags_lit

print((df['diag_lit_1'] == 0).sum())
valeurs_uniques = set(mauvaises_valeurs) #on convertit en set car il n'y a pas 2 fois la même valeur dans un set
print(valeurs_uniques)
```

```
4908
{'275', '558', '445', '584', '690', '444', '787', 'V71', 'V54', '350', '959', '58', 'V53', 'V25', '405', '?', '187', '323', '64
5', '799', '780', '362', '585', '790', '284'}
```

Mapping 2

- Extraction de données depuis le fichier IDS.csv

```
Entrée [301]: data = pd.read_csv('IDS_mapping.csv')

Entrée [302]: data.columns

  Out[302]: Index(['admission_type_id', 'description'], dtype='object')
```

on va d'abord récupérer les données pour l'admission (9 premières lignes)

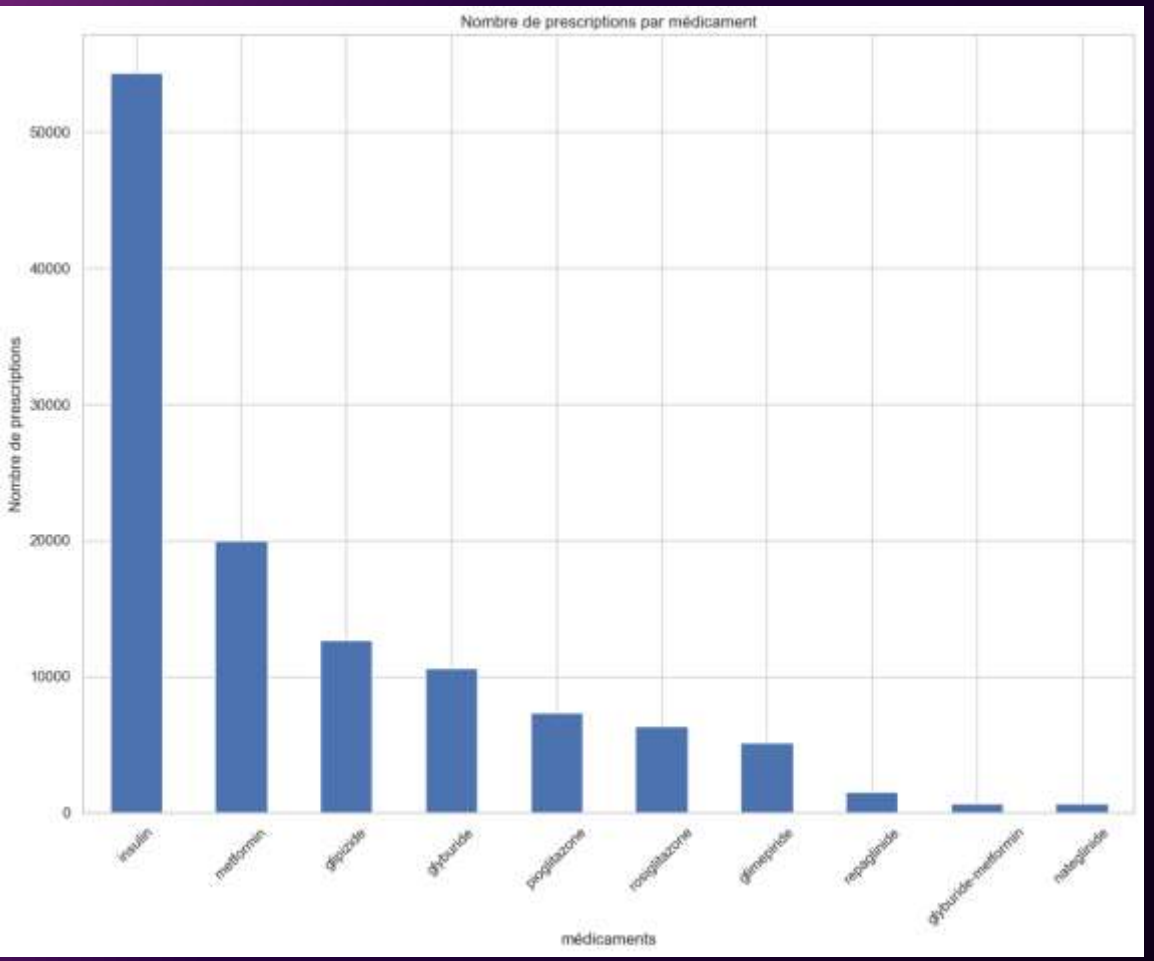
```
Entrée [303]: donnees = data.iloc[0:8]

              admission = {}
              for index, row in donnees.iterrows():
                  admission[row['admission_type_id']] = row['description']

              print(admission)

              {'1': 'Emergency', '2': 'Urgent', '3': 'Elective', '4': 'Newborn', '5': 'Not Available', '6': nan, '7': 'Trauma Center', '8': '
              Not Mapped'}
```

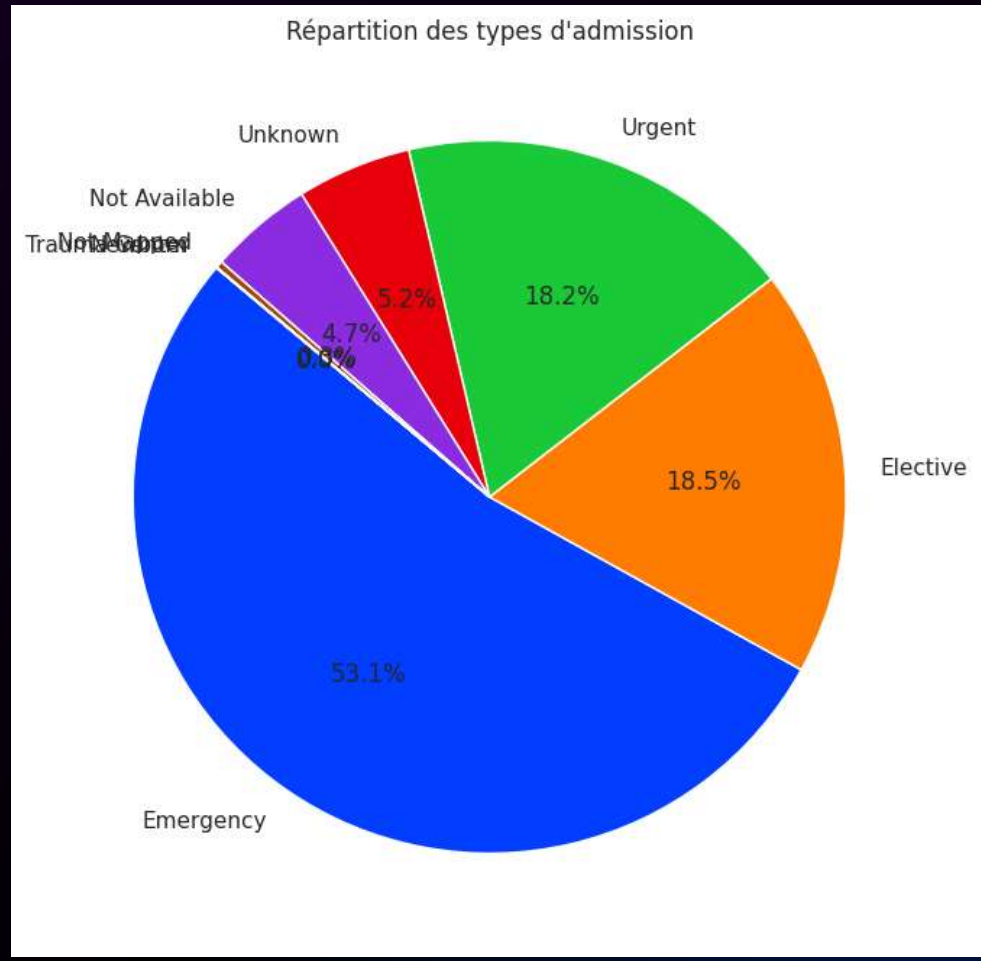
Mapping 2 (suite)

```
admissions_lit = []
mauvaises_valeurs=[]
for value in df['admission_type_id']:
    if str(value) in admission.keys():
        admissions_lit.append(admission[str(value)])
    else:
        admissions_lit.append(0)
        mauvaises_valeurs.append(value)



df['admission_type'] = admissions_lit

# on vérifie les valeurs manquantes
valeurs_uniques = set(mauvaises_valeurs) #on convertit en set car il n'y a pas 2 fois la même valeur dans un set
print(valeurs_uniques)
```

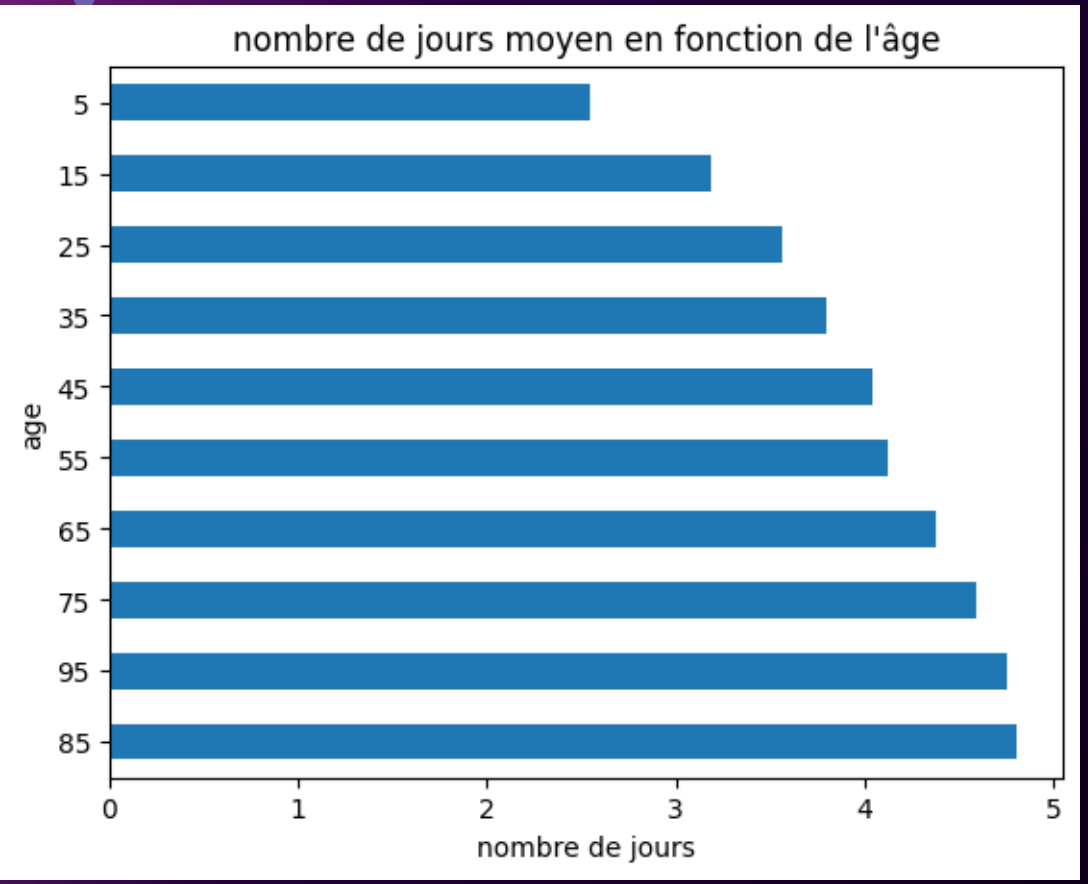
```
set()
```

Graphiques simples 1





Graphiques simples 2

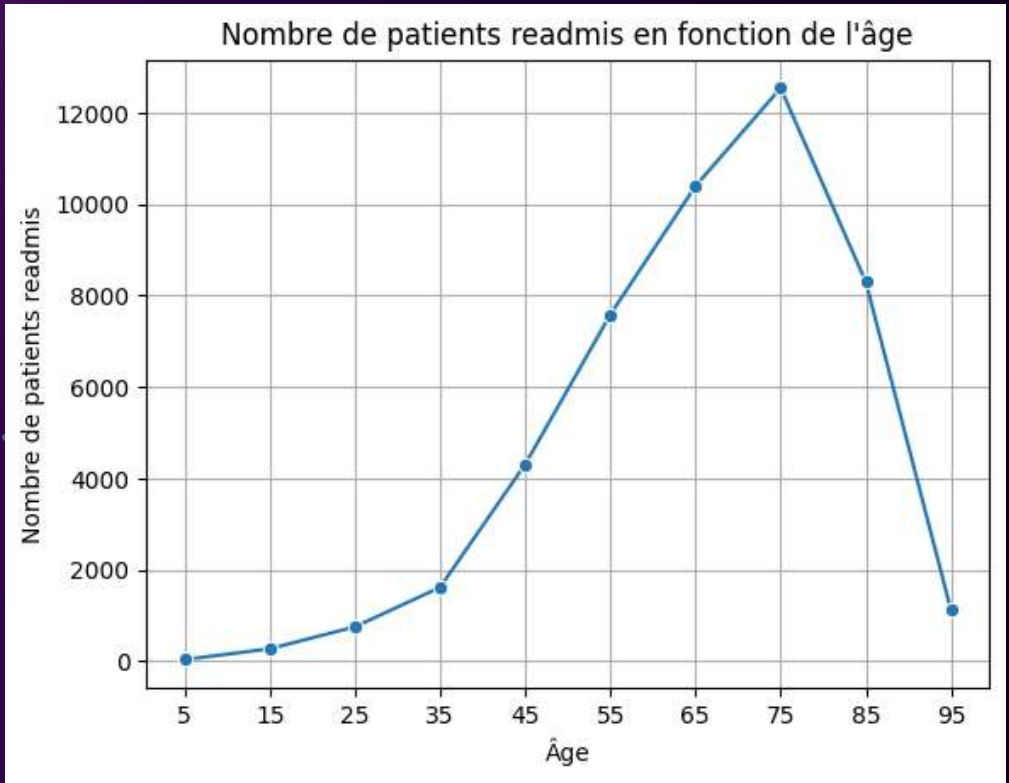


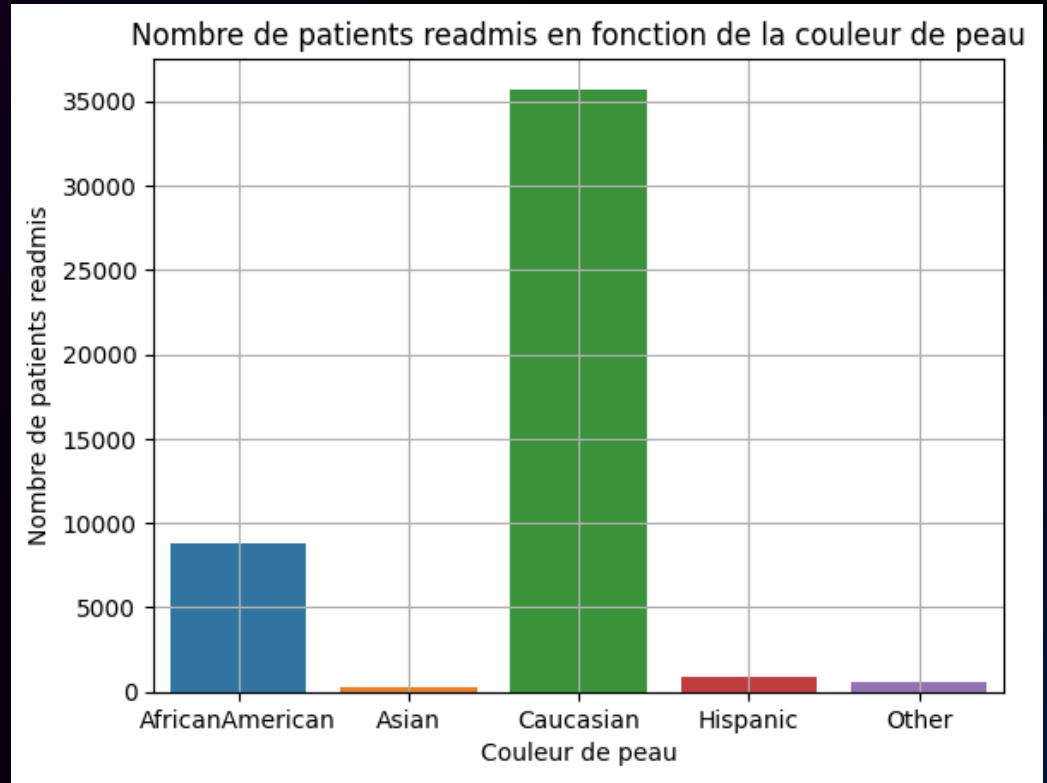

```
df_=df.copy()
df_['age']=df_['age'].apply(tranche_age).astype(int)
df_time_by_age = (df_.groupby('age')['time_in_hospital'].mean()).sort_values(ascending=False)
#print(df_time_by_age)
df_time_by_age.plot.barh()
plt.xlabel('nombre de jours')
plt.title("nombre de jours moyen en fonction de l'âge")
```

Graphiques Mapping 1

Encoding : fonction tranche_age
Mapping

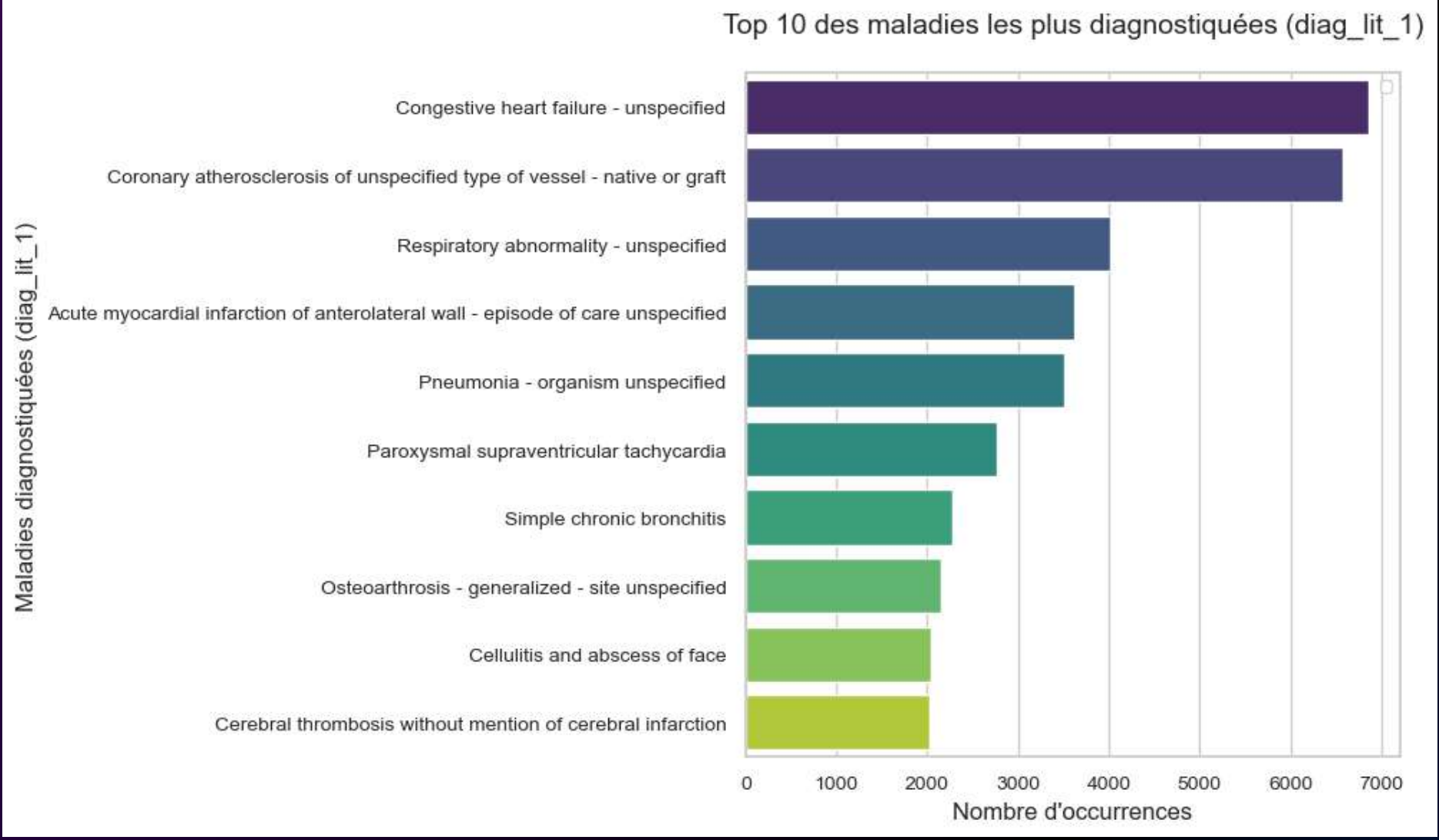
```
df_=df.copy()
mapping = {"<30":1,">30":1,"no":0}
df_['readmitted']=df_['readmitted'].map(mapping)
readmitted_by_race = df_.groupby('race')['readmitted'].sum().reset_index(name='count')
```



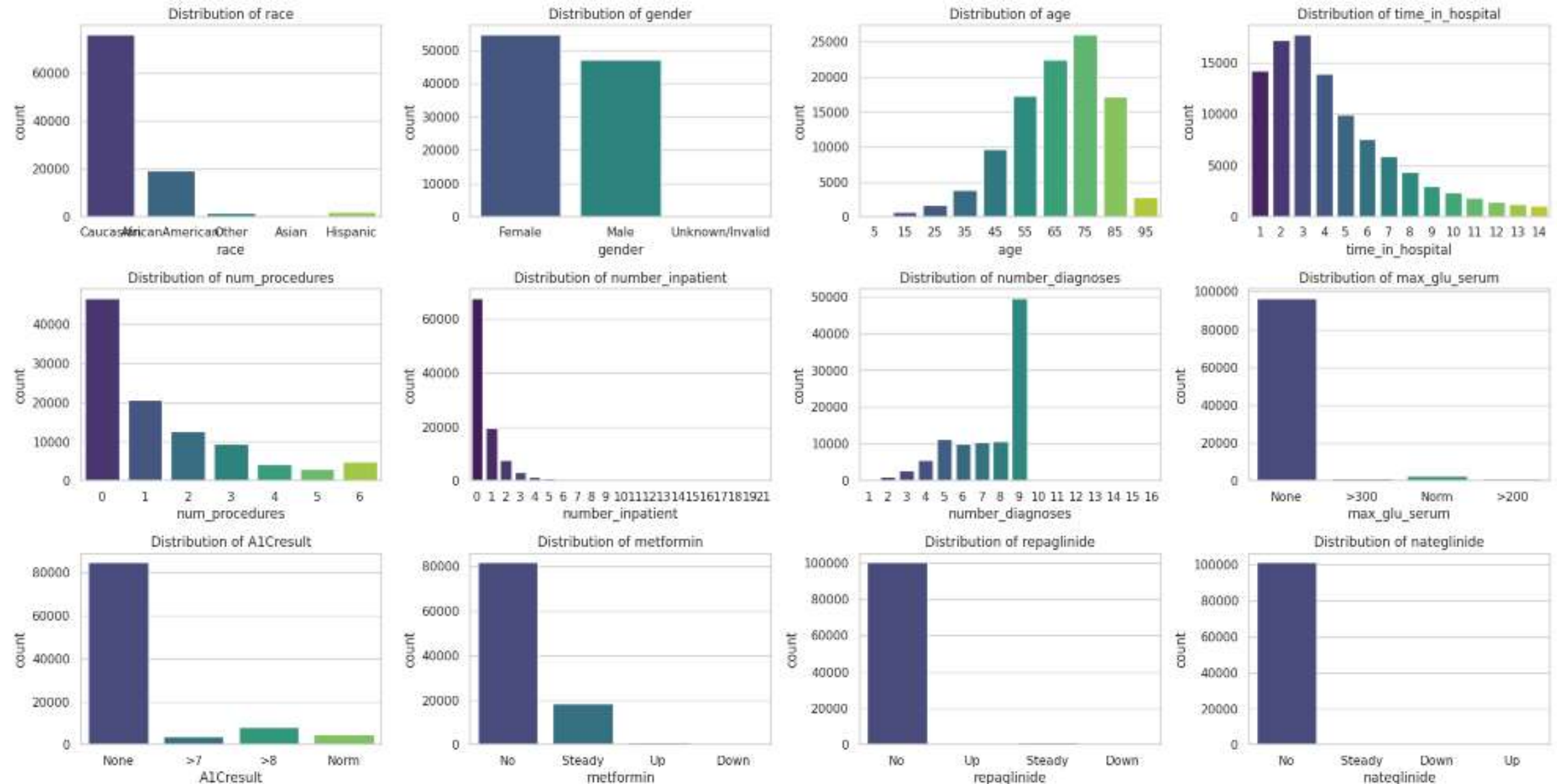


Graphiques Mapping 2

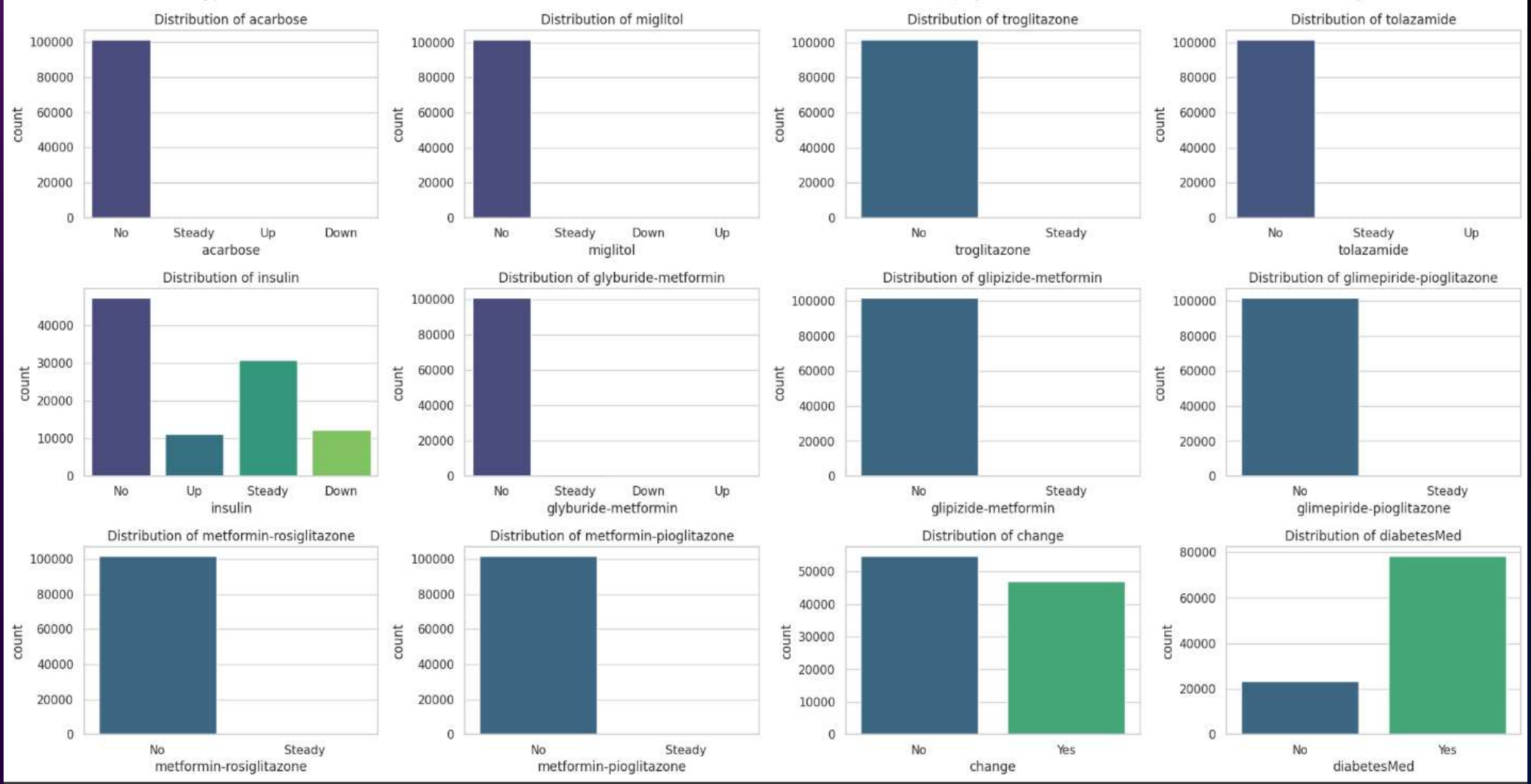
Mapping ICD9



Résumé graphiques 1



Résumé graphiques 2



Ordinal encoding vs onehot encoding

id	color
1	red
2	blue
3	green
4	blue

One Hot Encoding

id	color_red	color_blue	color_green
1	1	0	0
2	0	1	0
3	0	0	1
4	0	1	0

Ordinal Encoding

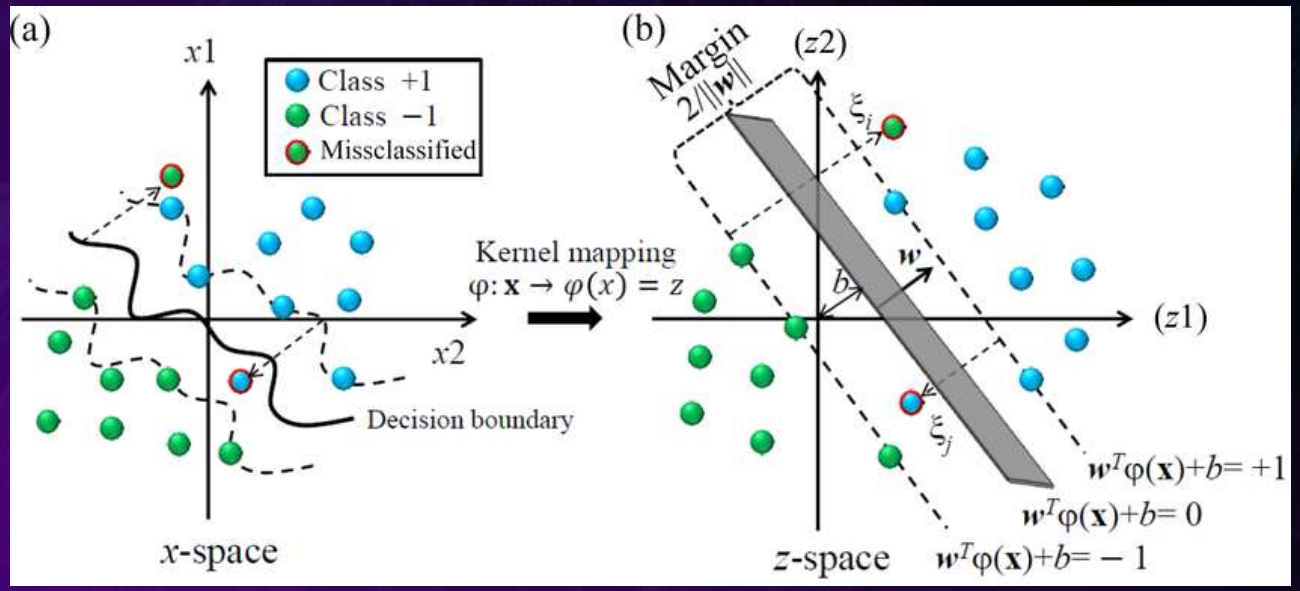
Grades
A
B
C
D
Fail

Grades	Encoded
A	4
B	3
C	2
D	1
Fail	0

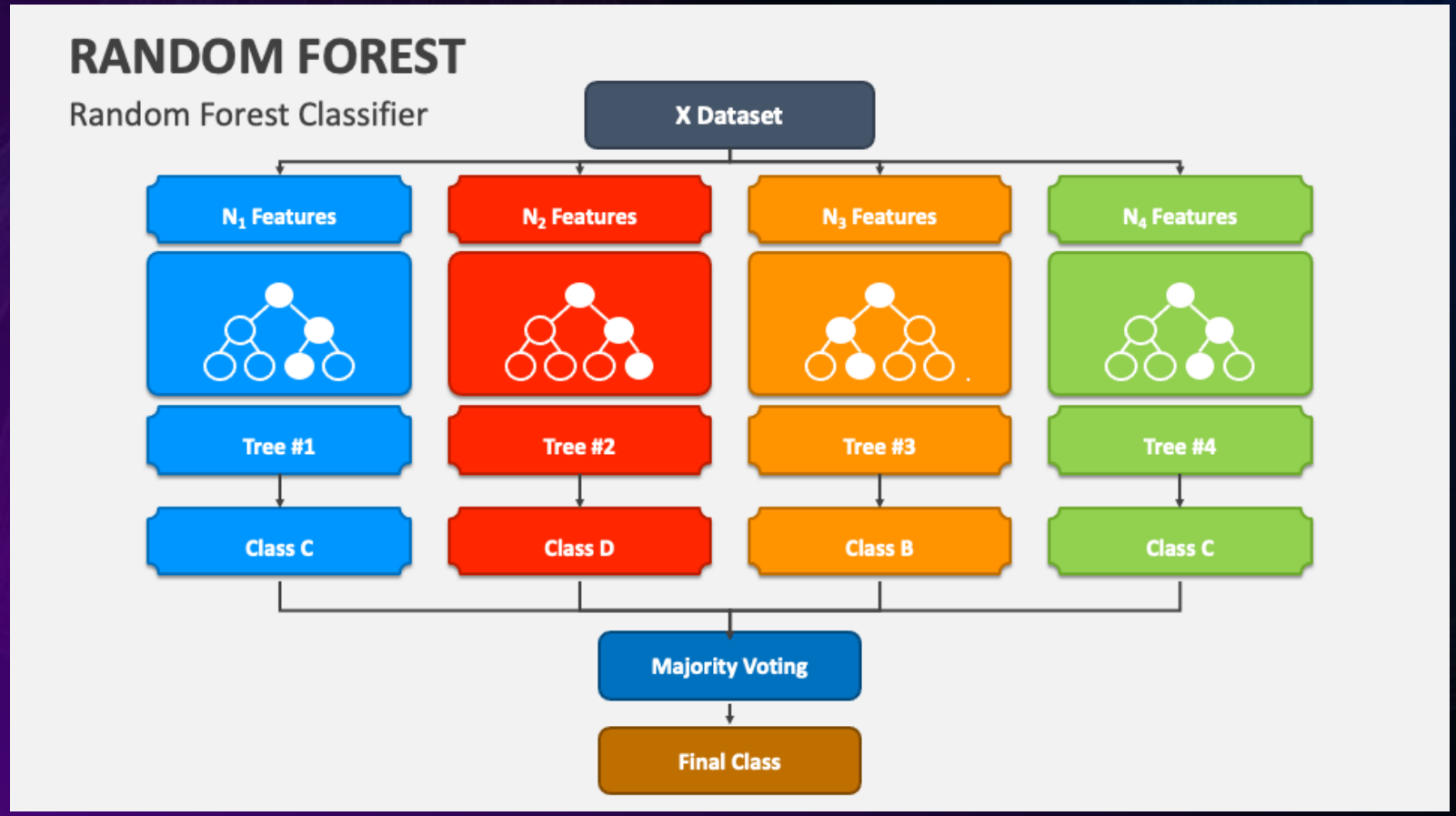
Algorithmes d'apprentissage supervisé

SMV vs Random Forest vs KNN

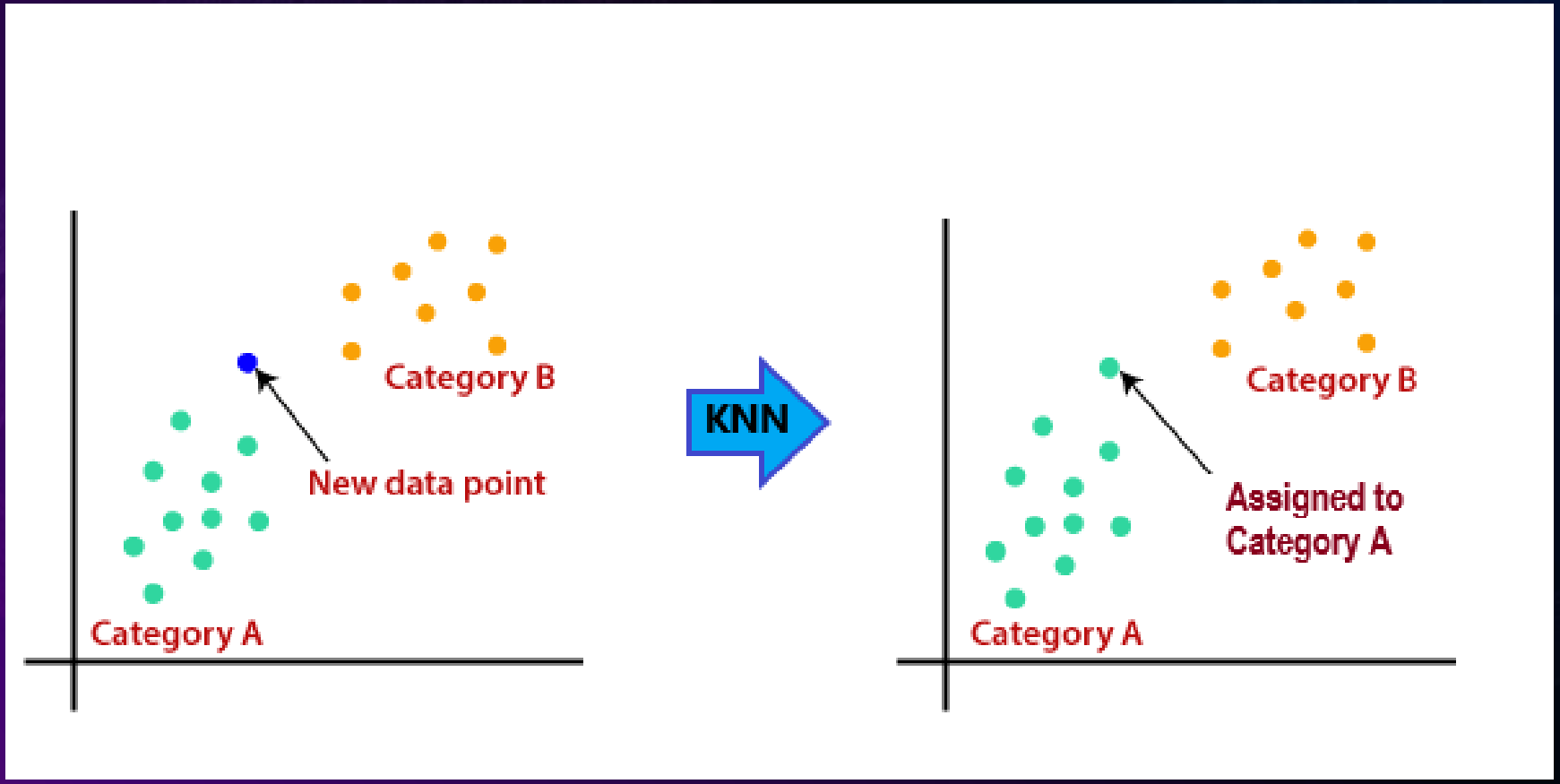
Support Vector Machine (SVM)



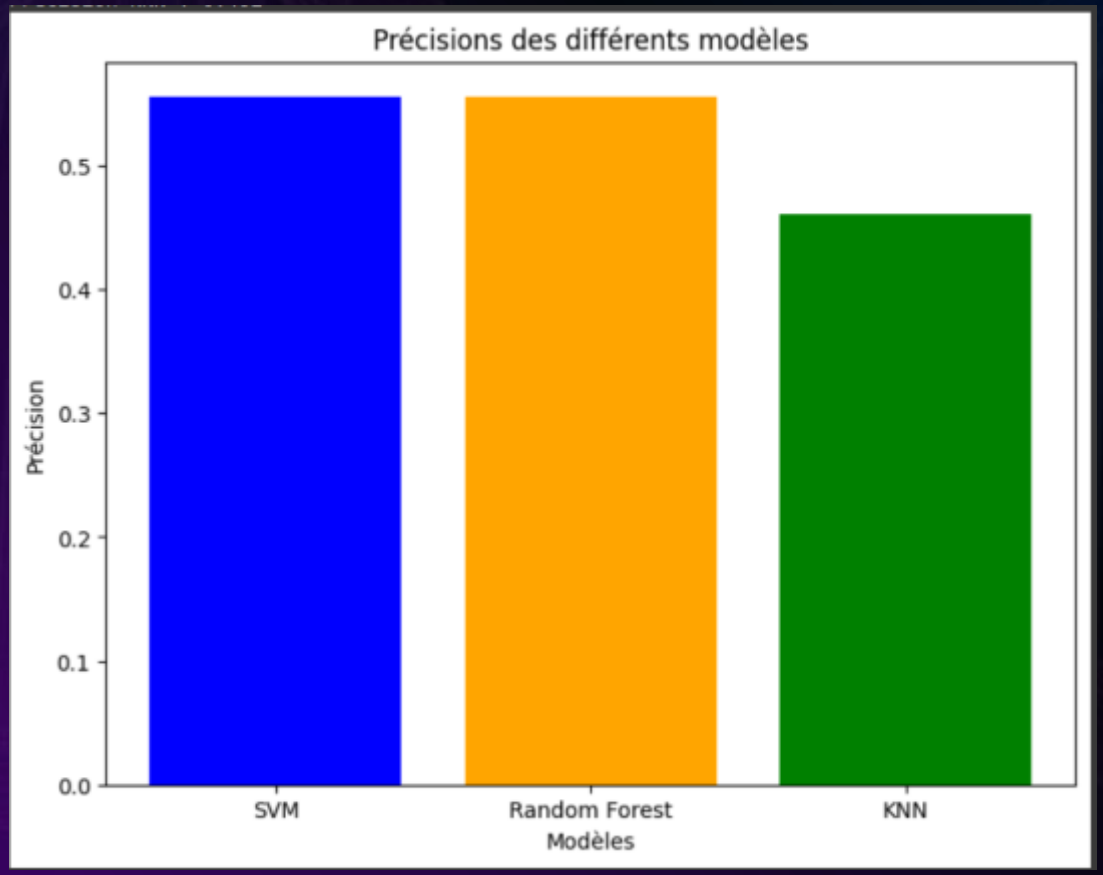
Random Forest



K-Nearest Neighbors (KNN)



Résultats


Précisions des différents modèles
Précision
0.0
0.1
0.2
0.3
0.4
0.5
SVM
Random Forest
KNN
Modèles

Conclusion

Merci