1. About Dataset:

- COVID-19 Dataset --> https://www.kaggle.com/datasets/meirnizri/covid19-dataset

i. Problem Statement:

- The main goal of this project is to build a machine learning model that, given a Covid-19 patient's current symptom, status, and medical history, will **predict whether the patient is in high risk or not**.

ii. Features:

- The dataset was provided by the Mexican government.
- The raw dataset consists of **21 unique features** and **1,048,576 unique patients**.
- In the Boolean features, **1** means "**yes**" and **2** means "**no**".
- Values as 97 and 99 are **missing data**.
  - **Sex**: female(1) or male(2)
  - **Age**: of the patient.
  - **Classification**: covid test findings.
    - Values 1-3 mean that the patient was **diagnosed** with covid in different degrees.
    - 4 or higher means that the patient is **not a carrier** of covid or that the test is inconclusive.
  - **Patient type**: hospitalized(1) or not hospitalized(2).
  - **Pneumonia**: Whether the patient already have air sacs inflammation(1) or not(2).
  - **Pregnancy**: Whether the patient is pregnant(1) or not(2).
  - **Diabetes**: Whether the patient has diabetes(1) or not(2).
  - **Copd**: Indicates whether the patient has Chronic obstructive pulmonary disease(1) or not(2).
  - **Asthma**: Whether the patient has asthma(1) or not(2).
  - **Inmsupr**: Whether the patient is immunosuppressed(1) or not(2).
  - **Hypertension**: Whether the patient has hypertension(1) or not(2).
  - **Cardiovascular**: Whether the patient has heart or blood vessels related disease(1) or not(2).
  - **Renal chronic**: Whether the patient has chronic renal disease(1) or not(2).
  - **Other disease**: Whether the patient has other disease(1) or not(2).
  - **Obesity**: Whether the patient is obese(1) or not(2).
  - **Tobacco**: Whether the patient is a tobacco(1) user or not(2).
  - **usmr**: Indicates Whether the patient treated medical units of the first, second or third level.
  - **Medical unit**: Type of institution of the National Health System that provided the care.
  - **Intubed**: Whether the patient was connected to the ventilator(1) or not(2).
  - **ICU**: Indicates whether the patient had been admitted to an Intensive Care Unit(1) or not(2).
  - **Date Died**: Indicates when the patient has died.

2. Data Exploration:

In [1]:

```
#!pip install matplotlib
```

In [2]:

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

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

In [3]:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

pd.set_option('display.max_columns', None)
pd.set_option('display.max_rows', 200)
```

In [4]:

```
# Turn off warnings
import warnings
warnings.filterwarnings("ignore", category=FutureWarning)
```

In [5]:

```
df = pd.read_csv('/content/drive/MyDrive/Tech4Dev/Databases/5. Machine Learning (ML)/Covid_Data.csv')
df
```

Out[5]:

	USMER	MEDICAL_UNIT	SEX	PATIENT_TYPE	DATE_DIED	INTUBED	PNEUMONIA	AGE	PREGNANT	DIABETES	COPD	ASTHMA	INMSUPR	HIPERTENSION	OTHER_DISEASE	CARDIOVASCULA
0	2	1	1	1	03/05/2020	97	1	65	2	2	2	2	2	1	2	
1	2	1	2	1	03/06/2020	97	1	72	97	2	2	2	2	1	2	
2	2	1	2	2	09/06/2020	1	2	55	97	1	2	2	2	2	2	
3	2	1	1	1	12/06/2020	97	2	53	2	2	2	2	2	2	2	
4	2	1	2	1	21/06/2020	97	2	68	97	1	2	2	2	1	2	
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
1048570	2	13	2	1	9999-99-99	97	2	40	97	2	2	2	2	2	2	
1048571	1	13	2	2	9999-99-99	2	2	51	97	2	2	2	2	1	2	
1048572	2	13	2	1	9999-99-99	97	2	55	97	2	2	2	2	2	2	
1048573	2	13	2	1	9999-99-99	97	2	28	97	2	2	2	2	2	2	
1048574	2	13	2	1	9999-99-99	97	2	52	97	2	2	2	2	2	2	

1048575 rows × 21 columns

In [6]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1048575 entries, 0 to 1048574
Data columns (total 21 columns):
 #   Column                Non-Null Count    Dtype 
---  ------                --------------    ----- 
 0   USMER                 1048575 non-null  int64 
 1   MEDICAL_UNIT          1048575 non-null  int64 
 2   SEX                   1048575 non-null  int64 
 3   PATIENT_TYPE          1048575 non-null  int64 
 4   DATE_DIED             1048575 non-null  object
 5   INTUBED               1048575 non-null  int64 
 6   PNEUMONIA             1048575 non-null  int64 
 7   AGE                   1048575 non-null  int64 
 8   PREGNANT              1048575 non-null  int64 
 9   DIABETES              1048575 non-null  int64 
 10  COPD                  1048575 non-null  int64 
 11  ASTHMA                1048575 non-null  int64 
 12  INMSUPR               1048575 non-null  int64 
 13  HIPERTENSION          1048575 non-null  int64 
 14  OTHER_DISEASE         1048575 non-null  int64 
 15  CARDIOVASCULAR        1048575 non-null  int64 
 16  OBESITY               1048575 non-null  int64 
 17  RENAL_CHRONIC         1048575 non-null  int64 
 18  TOBACCO               1048575 non-null  int64 
 19  CLASIFFICATION_FINAL  1048575 non-null  int64 
 20  ICU                   1048575 non-null  int64 
dtypes: int64(20), object(1)
memory usage: 168.0+ MB
```

In [7]:

```
# From the description of dataset, null values are replaced with 97 or 99
# This is a double check
df.isnull().sum()
```

Out[7]:

```
USMER                   0
MEDICAL_UNIT            0
SEX                     0
PATIENT_TYPE            0
DATE_DIED               0
INTUBED                 0
PNEUMONIA               0
AGE                     0
PREGNANT                0
DIABETES                0
COPD                    0
ASTHMA                  0
INMSUPR                 0
HIPERTENSION            0
OTHER_DISEASE           0
CARDIOVASCULAR          0
OBESITY                 0
RENAL_CHRONIC           0
TOBACCO                 0
CLASIFFICATION_FINAL    0
ICU                     0
dtype: int64
```

In [8]:

```
# Check Cardinality in Categorical Features

selected_columns = df.columns.drop(['AGE','DATE_DIED'])

unique_dic = []

for col in selected_columns:

  unique_num = len(df[col].unique())
  unique_dic.append({'Total_Unique' : unique_num,
                     'Cardinality%': (unique_num/1048575)*100})

unique_df = pd.DataFrame(unique_dic, index = selected_columns).sort_values(by = 'Cardinality%', ascending = False)
unique_df
```

Out[8]:

	Total_Unique	Cardinality%
MEDICAL_UNIT	13	0.001240
CLASIFFICATION_FINAL	7	0.000668
ICU	4	0.000381
INTUBED	4	0.000381
PREGNANT	4	0.000381
HIPERTENSION	3	0.000286
TOBACCO	3	0.000286
RENAL_CHRONIC	3	0.000286
OBESITY	3	0.000286
CARDIOVASCULAR	3	0.000286
OTHER_DISEASE	3	0.000286
ASTHMA	3	0.000286
INMSUPR	3	0.000286
COPD	3	0.000286
DIABETES	3	0.000286
PNEUMONIA	3	0.000286
PATIENT_TYPE	2	0.000191
SEX	2	0.000191
USMER	2	0.000191

In [9]:

```
# Check unique values for each feature

selected_columns = df.columns.drop('AGE')

for column in selected_columns:
    print('\n*-*-*-*-*-*\n')
    print(pd.DataFrame(df[column].value_counts()))
```

```
*-*-*-*-*-*

    USMER
2  662903
1  385672

*-*-*-*-*-*

    MEDICAL_UNIT
12        602995
4         314405
6          40584
9          38116
3          19175
8          10399
10          7873
5           7244
11          5577
13           996
7            891
2            169
1            151

*-*-*-*-*-*

      SEX
1  525064
2  523511

*-*-*-*-*-*

   PATIENT_TYPE
1        848544
2        200031

*-*-*-*-*-*

            DATE_DIED
9999-99-99     971633
06/07/2020       1000
07/07/2020        996
13/07/2020        990
16/06/2020        979
...               ...
24/11/2020          1
17/12/2020          1
08/12/2020          1
16/03/2021          1
22/04/2021          1

[401 rows x 1 columns]

*-*-*-*-*-*

    INTUBED
97   848544
2    159050
1     33656
99     7325

*-*-*-*-*-*

    PNEUMONIA
2      892534
1      140038
99      16003

*-*-*-*-*-*

    PREGNANT
97    523511
2     513179
1       8131
98      3754

*-*-*-*-*-*

    DIABETES
2     920248
1     124989
98      3338

*-*-*-*-*-*

       COPD
2   1030510
1     15062
98     3003

*-*-*-*-*-*

     ASTHMA
2   1014024
1     31572
98     2979

*-*-*-*-*-*

    INMSUPR
2   1031001
1     14170
98     3404

*-*-*-*-*-*

    HIPERTENSION
2         882742
1         162729
98          3104

*-*-*-*-*-*

    OTHER_DISEASE
2         1015490
1           28040
98           5045
```

```
*_*_*_*_*_*

    CARDIOVASCULAR
2          1024730
1            20769
98            3076

*_*_*_*_*_*

    OBESITY
2    885727
1    159816
98     3032

*_*_*_*_*_*

    RENAL_CHRONIC
2         1026665
1           18904
98           3006

*_*_*_*_*_*

    TOBACCO
2    960979
1     84376
98     3220

*_*_*_*_*_*

   CLASIFFICATION_FINAL
7                499250
3                381527
6                128133
5                 26091
1                  8601
4                  3122
2                  1851

*_*_*_*_*_*

       ICU
97  848544
2   175685
1    16858
99    7488
```

In [10]:

```python
# Check age (continous data) description
# Minimum = 0, Maximum = 121, Median = 40
df.AGE.describe()
```

Out[10]:

```
count    1.048575e+06
mean     4.179410e+01
std      1.690739e+01
min      0.000000e+00
25%      3.000000e+01
50%      4.000000e+01
75%      5.300000e+01
max      1.210000e+02
Name: AGE, dtype: float64
```

In [11]:

```python
# We have 138 patient with age > 100 ie. 0.013% of our dataset

df[df.AGE > 100].AGE.count()
```

Out[11]:

```
138
```

- We have 138 patient with age > 100 ie. 0.013% of our dataset.
- Median (40) = Mean (41) wich means that age is normally distributed.
  - **So no need to drop it as outliers.**

- Features with no null values:

- Sex
- Age
- Classification
- Medical unit
- Patient type
- usmr

- Features with null values:

- Pneumonia: 99 = 16003
- Diabetes: 98 = 3338
- Copd: 98 = 3003
- Asthma: 98 = 2979
- Inmsupr: 98 = 3404
- Hypertension: 98 = 3104
- Cardiovascular: 98 = 3076
- Renal chronic: 98 = 3006
- Other disease: 98 = 5045
- Obesity: 98 = 3032
- Tobacco: 98 = 3220

- Null values ranges from 3000 - 16000 ie. (0.2 - 1.5 % of total dataset)
- The highest number (16000) in pneumonea may be explained by the shoratge of radiological investigations.
- Being a categorical features, we will replace these missed data with the (Mode).

- Features that show more than one type of null values:

- **Pregnancy: '97' = 523511, '98' = 3754**
  - We noticed that '97' count is = male count in our dataset
  - Sex: '2' = 523511
- **Intubed: '97' = 848544, '99' = 7325**
  - We noticed that '97' count is = hospitalized count in our dataset

    - Patient type: '1' = 848544
- **ICU: '97' = 848544, '99' = 7488**
    - We noticed that '97' count is = hospitalized count in our dataset
    - Patient type: '1' = 848544

- For pregnant category, males can't either be pregnant or not pregnant that why it appears like a null values, we will change the 97 values to 2 (non-pregnant), and fill the 98 with the mode.

- Applying the same concept to being in ICU or intubated, patient should be hospitalized. non hospitalized can't either be in ICU or not, or intubated or not.

- We think that the labeling of patient type is wrong, 1 should be for non hospitalized , 2 for hospitalized.

Visualization will confirm our opinion about these different null vlaues.

- **Date Died:**

    - We can see that most of data are (9999-99-99), ie. having no death date, the count of this value = 971633 ie. 92% of dataset, it can't be just dropped.
    - So we considered this date as recovery ie. no death which is convinent as across the world, most patients recovered, this will be our label.
    - This also means that our dataset is imbalanced.
    - For **imbalance** we could use:
        - oversampling techniques, buy due to the very large dataset (1 Million), we can't use it.
        - Undersamping techniques resulted in very very low scores.
- **Classification:**

    - in our model, we will keep classes (1,2,3) as it is, cause it reflects the degree of infection, while changing all classes >= 4 into 0
    - We will make column of (covid Vs non covid) only for visualization

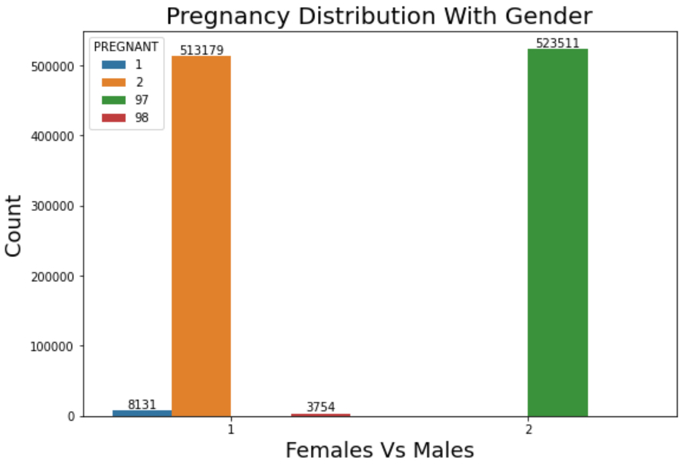
-Types of our Features/label:

- We will deal with all features as categorical data
- Except for classification, usmr --> Ordinal data
- Age --> Numerical data as it is
- For date, we will converted into Death(1) - no Death(2)

In [12]:
```
# Check gender type when pregnancy = 97
# Gender = 2 ie. male

pregnant_male = df[df.PREGNANT == 97]
pregnant_male.SEX.value_counts()
```

Out[12]:
```
2    523511
Name: SEX, dtype: int64
```

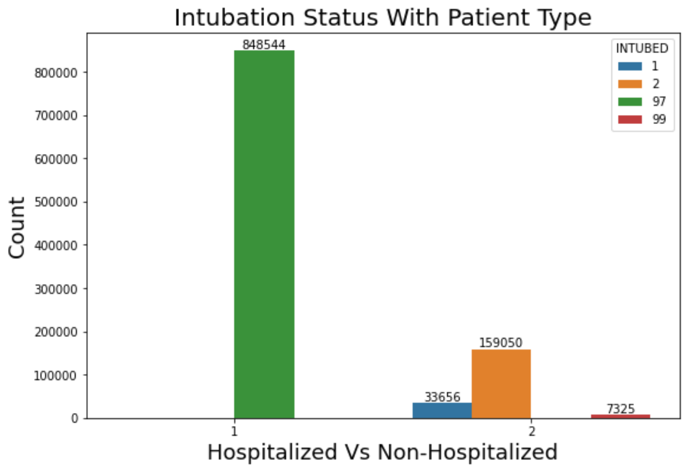
In [13]:
```
# Count plot to figure out the different categories of pregnancy across gender.

plt.figure(figsize = (9,6))
ax = sns.countplot(df.SEX, hue = df.PREGNANT)
for bars in ax.containers:
    ax.bar_label(bars)

plt.ylabel('Count', size = 18)
plt.xlabel('Females Vs Males', size = 18)
plt.title('Pregnancy Distribution With Gender', fontsize = 20);
```



In [14]:
```
# Check patient type when intubation = 97
# Patient type = 1 ie. (Hospitalized)

intubed_type = df[df.INTUBED == 97]
intubed_type.PATIENT_TYPE.value_counts()
```

Out[14]:
```
1    848544
Name: PATIENT_TYPE, dtype: int64
```

In [15]:
```
# Count plot to figure out intubation among differnt patients (Hospitalized Vs Non-hospitalized)

plt.figure(figsize = (9,6))
ax = sns.countplot(df.PATIENT_TYPE, hue = df.INTUBED)
for bars in ax.containers:
    ax.bar_label(bars)

plt.ylabel('Count', size = 18)
plt.xlabel('Hospitalized Vs Non-Hospitalized', size = 18)
plt.title('Intubation Status With Patient Type', fontsize = 20);
```



In [16]:

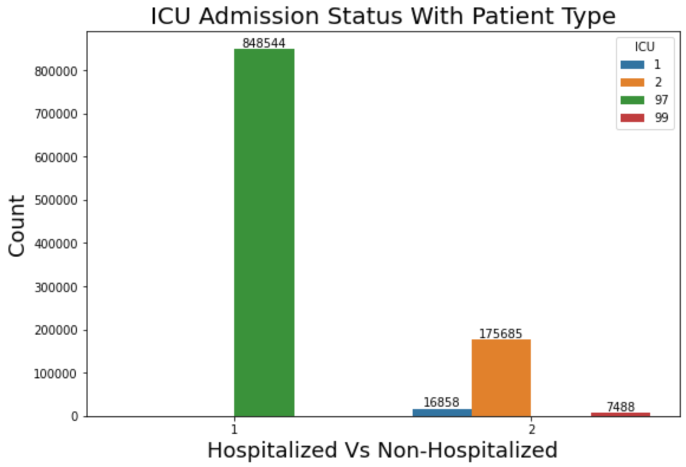
```
# Check patient type when ICU = 97
# Patient type = 1 ie. (Hospitalized)

icu_type = df[df.ICU == 97]
icu_type.PATIENT_TYPE.value_counts()
```

Out[16]:

```
1    848544
Name: PATIENT_TYPE, dtype: int64
```

In [17]:

```
# Count plot to figure out ICU admission among differnt patients (Hospitalized Vs Non-hospitalized)

plt.figure(figsize = (9,6))
ax = sns.countplot(df.PATIENT_TYPE, hue = df.ICU)
for bars in ax.containers:
    ax.bar_label(bars)

plt.ylabel('Count', size = 18)
plt.xlabel('Hospitalized Vs Non-Hospitalized', size = 18)
plt.title('ICU Admission Status With Patient Type', fontsize = 20);
```



These graphs confirms our insights that:

- Pregnant = 97 is when patient is male
- Intubed = 97 is when patient is hospitalized
- ICU = 97 is when patient is hospitalized

For 'INTUBED', 'ICU': It seems that the labeling of patient type in dataset description is wrong, as non hospitalized can't be in ICU or Intubated as shown in graph.

This means that datapoints where patient type = 1 is actually non-hospitalized patients and that's why their data is '97 ie. Null' as as non hospitalized can't be in ICU or Intubated as shown in graph.

This is further supported by the argument that most COVID-19 patients do not require an ICU.

--> will Create new column for patient type with the correct labeling.

3. Data Cleaning:

b. PREGNANT:

In [18]:

```
# Replace '97' in pregnant with '2' ie. when gender = male, pregnant = 2
# So that SEX and PREGNANT are independent variables.

df.PREGNANT = df.PREGNANT.replace(97, 2)
df.PREGNANT.value_counts()
```

Out[18]:

```
2     1036690
1        8131
98       3754
Name: PREGNANT, dtype: int64
```

c. PATIENT_TYPE:

In [19]:

```
# Creating new column (PATIENT_HOSP) to correct the definitions
# PATIENT_HOSP = 1 (Hospitalized)
# PATIENT_HOSP = 1 (Non_hospitalized)

def change_type(val):
    if val == 1:
        return 2
    elif val == 2 :
        return 1


df['PATIENT_HOSP'] = df['PATIENT_TYPE'].map(change_type)

df.head()
```

Out[19]:

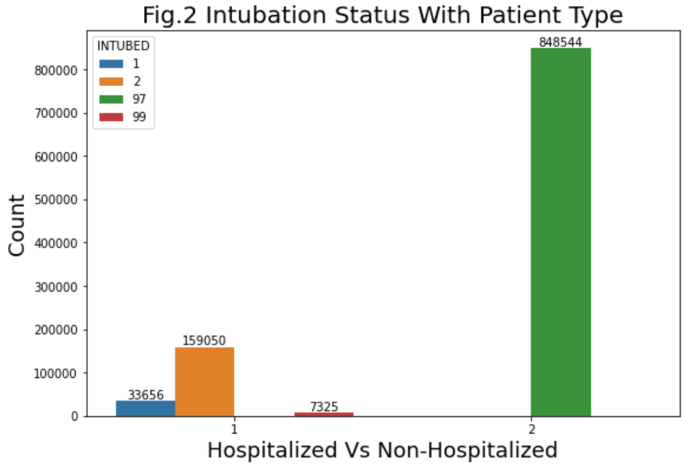
	USMER	MEDICAL_UNIT	SEX	PATIENT_TYPE	DATE_DIED	INTUBED	PNEUMONIA	AGE	PREGNANT	DIABETES	COPD	ASTHMA	INMSUPR	HIPERTENSION	OTHER_DISEASE	CARDIOVASCULAR	OBI
0	2	1	1	1	03/05/2020	97	1	65	2	2	2	2	2	1	2	2	
1	2	1	2	1	03/06/2020	97	1	72	2	2	2	2	2	1	2	2	
2	2	1	2	2	09/06/2020	1	2	55	2	1	2	2	2	2	2	2	
3	2	1	1	1	12/06/2020	97	2	53	2	2	2	2	2	2	2	2	
4	2	1	2	1	21/06/2020	97	2	68	2	1	2	2	2	1	2	2	

In [20]:

```
df = df.drop('PATIENT_TYPE', axis = 1)
```

In [21]:

```
# Ensure correct definnition of patient type

plt.figure(figsize = (9,6))
ax = sns.countplot(df.PATIENT_HOSP, hue = df.INTUBED)
for bars in ax.containers:
    ax.bar_label(bars)

plt.ylabel('Count', size = 18)
plt.xlabel('Hospitalized Vs Non-Hospitalized', size = 18)
plt.title('Fig.2 Intubation Status With Patient Type', fontsize = 20);
```



d. INTUBED:

In [22]:

```
# Replace '97' in Intubed with '2' ie. when patient not hospitalized, intubed = 2 (not-intubated)

df.INTUBED = df.INTUBED.replace(97, 2)
df.INTUBED.value_counts()
```

Out[22]:

```
2     1007594
1       33656
99       7325
Name: INTUBED, dtype: int64
```

e. ICU:

In [23]:

```
# Replace '97' in ICU with '2' ie. when patient not hospitalized, intubed = 2 (not in ICU)

df.ICU = df.ICU.replace(97, 2)
df.ICU.value_counts()
```

Out[23]:

```
2     1024229
1       16858
99       7488
Name: ICU, dtype: int64
```

f. CLASSIFICATION_FINAL:

- Classification: covid test findings.

- Values 1-3 mean that the patient was diagnosed with covid in different degrees.
- 4 or higher means that the patient is not a carrier of covid or that the test is inconclusive.

- We will convert classes of >= 4 to 0 (No-covid), keeping (1,2,3) as it is. (Ordinal Data)

In [24]:

```
df.CLASIFFICATION_FINAL.value_counts()
```

Out[24]:

```
7    499250
3    381527
6    128133
5     26091
1      8601
4      3122
2      1851
Name: CLASIFFICATION_FINAL, dtype: int64
```

In [25]:

```
# Replacing the non-covid patients with 0

df.CLASIFFICATION_FINAL = df.CLASIFFICATION_FINAL.replace([4,5,6,7], 0)
df.CLASIFFICATION_FINAL.value_counts()
```

Out[25]:

```
0    656596
3    381527
1      8601
2      1851
Name: CLASIFFICATION_FINAL, dtype: int64
```

In [26]:

```
# Creating new column for covid of Covid (1) , Non-covid (2) for visualization


def covid_diagnosis(val):
    if val == 0:
        return 2
    else :
        return 1


df['COVID'] = df['CLASIFFICATION_FINAL'].map(covid_diagnosis)

df.head()
```

Out[26]:

	USMER	MEDICAL_UNIT	SEX	DATE_DIED	INTUBED	PNEUMONIA	AGE	PREGNANT	DIABETES	COPD	ASTHMA	INMSUPR	HIPERTENSION	OTHER_DISEASE	CARDIOVASCULAR	OBESITY	RENAL_CI
0	2	1	1	03/05/2020	2	1	65	2	2	2	2	2	1	2	2	2	
1	2	1	2	03/06/2020	2	1	72	2	2	2	2	2	1	2	2	1	
2	2	1	2	09/06/2020	1	2	55	2	1	2	2	2	2	2	2	2	
3	2	1	1	12/06/2020	2	2	53	2	2	2	2	2	2	2	2	2	
4	2	1	2	21/06/2020	2	2	68	2	1	2	2	2	1	2	2	2	

In [27]:

```
df.COVID.value_counts()
```

Out[27]:

```
2    656596
1    391979
Name: COVID, dtype: int64
```

a. DATE_DIED:

In [28]:

```
# Creating new column for type of Death (1), Recovery (2) based on DATE_DIED


def death_numbers(val):
    if val == '9999-99-99':
        return 0
    else :
        return 1


df['DEATH'] = df['DATE_DIED'].map(death_numbers)

df.head()
```

Out[28]:

	USMER	MEDICAL_UNIT	SEX	DATE_DIED	INTUBED	PNEUMONIA	AGE	PREGNANT	DIABETES	COPD	ASTHMA	INMSUPR	HIPERTENSION	OTHER_DISEASE	CARDIOVASCULAR	OBESITY	RENAL_CI
0	2	1	1	03/05/2020	2	1	65	2	2	2	2	2	1	2	2	2	
1	2	1	2	03/06/2020	2	1	72	2	2	2	2	2	1	2	2	1	
2	2	1	2	09/06/2020	1	2	55	2	1	2	2	2	2	2	2	2	
3	2	1	1	12/06/2020	2	2	53	2	2	2	2	2	2	2	2	2	
4	2	1	2	21/06/2020	2	2	68	2	1	2	2	2	1	2	2	2	

In [29]:

```
# Creating dataframe for died patients for visualization and date/time extraction
df_death = df[df.DEATH == 1]
```

In [30]:

```
# Dropping DATE_DIED to avoid dealing with invalid values (9999-99-99)
df = df.drop('DATE_DIED', axis = 1)
```

In [31]:

```
# Checking type of DATE_DIED
df_death.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 76942 entries, 0 to 1047639
Data columns (total 23 columns):
 #   Column                Non-Null Count  Dtype 
---  ------                --------------  ----- 
 0   USMER                 76942 non-null  int64 
 1   MEDICAL_UNIT          76942 non-null  int64 
 2   SEX                   76942 non-null  int64 
 3   DATE_DIED             76942 non-null  object
 4   INTUBED               76942 non-null  int64 
 5   PNEUMONIA             76942 non-null  int64 
 6   AGE                   76942 non-null  int64 
 7   PREGNANT              76942 non-null  int64 
 8   DIABETES              76942 non-null  int64 
 9   COPD                  76942 non-null  int64 
 10  ASTHMA                76942 non-null  int64 
 11  INMSUPR               76942 non-null  int64 
 12  HIPERTENSION          76942 non-null  int64 
 13  OTHER_DISEASE         76942 non-null  int64 
 14  CARDIOVASCULAR        76942 non-null  int64 
 15  OBESITY               76942 non-null  int64 
 16  RENAL_CHRONIC         76942 non-null  int64 
 17  TOBACCO               76942 non-null  int64 
 18  CLASIFFICATION_FINAL  76942 non-null  int64 
 19  ICU                   76942 non-null  int64 
 20  PATIENT_HOSP          76942 non-null  int64 
 21  COVID                 76942 non-null  int64 
 22  DEATH                 76942 non-null  int64 
dtypes: int64(22), object(1)
memory usage: 14.1+ MB
```

In [32]:

```
# Convert it to datetime

time_col = 'DATE_DIED'
df_death['DATE_DIED'] = pd.to_datetime(df_death.DATE_DIED, dayfirst=True, yearfirst=True, format="%d/%m/%Y")
```

```
<ipython-input-32-7cdc7e8456bf>:4: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  df_death['DATE_DIED'] = pd.to_datetime(df_death.DATE_DIED, dayfirst=True, yearfirst=True, format="%d/%m/%Y")
```

In [33]:

```
df_death.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 76942 entries, 0 to 1047639
Data columns (total 23 columns):
 #   Column                Non-Null Count  Dtype
---  ------                --------------  -----
 0   USMER                 76942 non-null  int64
 1   MEDICAL_UNIT          76942 non-null  int64
 2   SEX                   76942 non-null  int64
 3   DATE_DIED             76942 non-null  datetime64[ns]
 4   INTUBED               76942 non-null  int64
 5   PNEUMONIA             76942 non-null  int64
 6   AGE                   76942 non-null  int64
 7   PREGNANT              76942 non-null  int64
 8   DIABETES              76942 non-null  int64
 9   COPD                  76942 non-null  int64
 10  ASTHMA                76942 non-null  int64
 11  INMSUPR               76942 non-null  int64
 12  HIPERTENSION          76942 non-null  int64
 13  OTHER_DISEASE         76942 non-null  int64
 14  CARDIOVASCULAR        76942 non-null  int64
 15  OBESITY               76942 non-null  int64
 16  RENAL_CHRONIC         76942 non-null  int64
 17  TOBACCO               76942 non-null  int64
 18  CLASIFFICATION_FINAL  76942 non-null  int64
 19  ICU                   76942 non-null  int64
 20  PATIENT_HOSP          76942 non-null  int64
 21  COVID                 76942 non-null  int64
 22  DEATH                 76942 non-null  int64
dtypes: datetime64[ns](1), int64(22)
memory usage: 14.1 MB
```

In [34]:

```
#extract the year, month, day for died patients

df_death['Year'] = df_death['DATE_DIED'].dt.year
df_death['Month'] = df_death['DATE_DIED'].dt.month
df_death['Day'] = df_death['DATE_DIED'].dt.day

df_death.head()
```

```
<ipython-input-34-5663f310d346>:3: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  df_death['Year'] = df_death['DATE_DIED'].dt.year
<ipython-input-34-5663f310d346>:4: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  df_death['Month'] = df_death['DATE_DIED'].dt.month
<ipython-input-34-5663f310d346>:5: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  df_death['Day'] = df_death['DATE_DIED'].dt.day
```

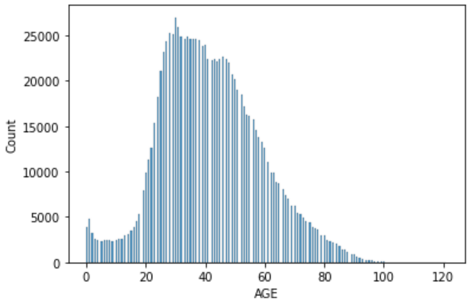
Out[34]:

	USMER	MEDICAL_UNIT	SEX	DATE_DIED	INTUBED	PNEUMONIA	AGE	PREGNANT	DIABETES	COPD	ASTHMA	INMSUPR	HIPERTENSION	OTHER_DISEASE	CARDIOVASCULAR	OBESITY	RENAL_CI
0	2	1	1	2020-05-03	2	1	65	2	2	2	2	2	1	2	2	2	
1	2	1	2	2020-06-03	2	1	72	2	2	2	2	2	1	2	2	1	
2	2	1	2	2020-06-09	1	2	55	2	1	2	2	2	2	2	2	2	
3	2	1	1	2020-06-12	2	2	53	2	2	2	2	2	2	2	2	2	
4	2	1	2	2020-06-21	2	2	68	2	1	2	2	2	1	2	2	2	

4. Data Visualization:

In [35]:

```
# AGE distribution
sns.histplot(df.AGE);
```



In [36]:

```
df.columns
```

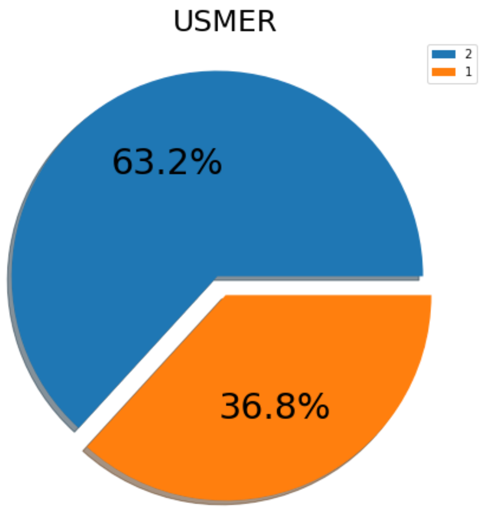
Out[36]:

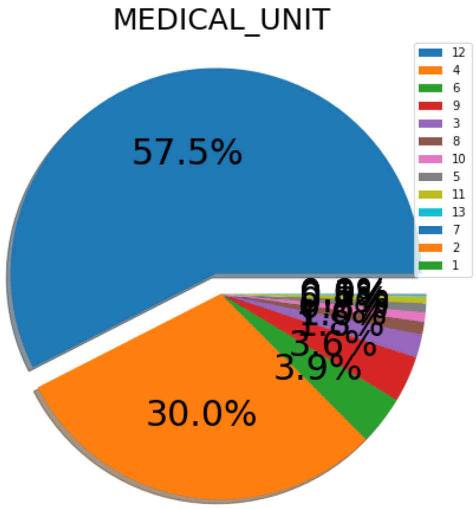
```
Index(['USMER', 'MEDICAL_UNIT', 'SEX', 'INTUBED', 'PNEUMONIA', 'AGE',
       'PREGNANT', 'DIABETES', 'COPD', 'ASTHMA', 'INMSUPR', 'HIPERTENSION',
       'OTHER_DISEASE', 'CARDIOVASCULAR', 'OBESITY', 'RENAL_CHRONIC',
       'TOBACCO', 'CLASIFFICATION_FINAL', 'ICU', 'PATIENT_HOSP', 'COVID',
       'DEATH'],
      dtype='object')
```

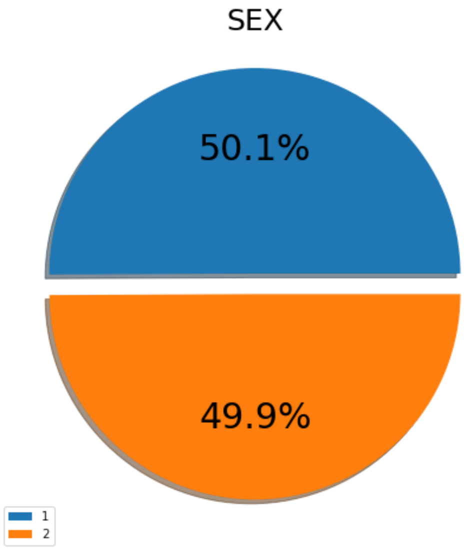
In [37]:

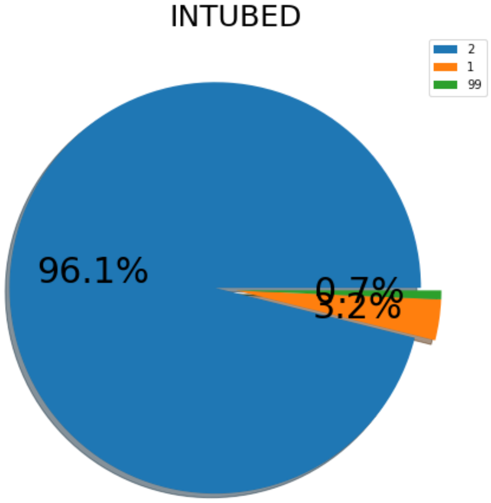
```
selected_columns = df.columns.drop('AGE','PREGNANT')
```

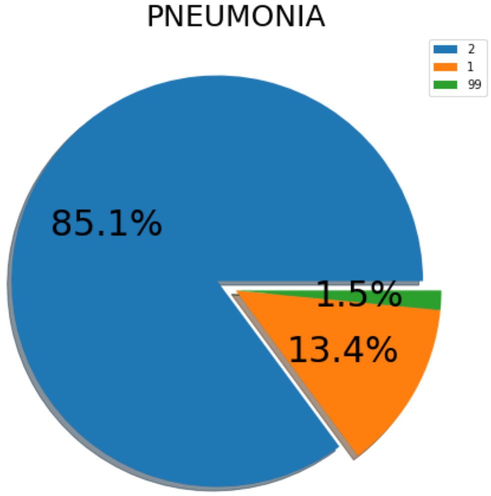
In [38]:
```
# Creating Pie Plots for Categorical Features

for column in selected_columns:

  df_column = df[column].value_counts().sort_values(ascending = False)

  explode = [0] * (len(df[column].unique()))
  explode[0] = 0.1


  df_column.plot(kind = 'pie', subplots = True, autopct = '%1.1f%%', explode = explode, labeldistance = None,
                 legend ='best', shadow=True, ylabel= '', xlabel = '', figsize = (8, 8), fontsize = 30)

  plt.title(str(column), size = 25)

  plt.show()
```

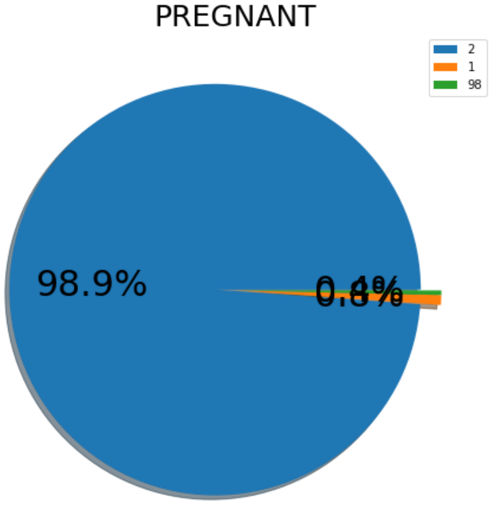


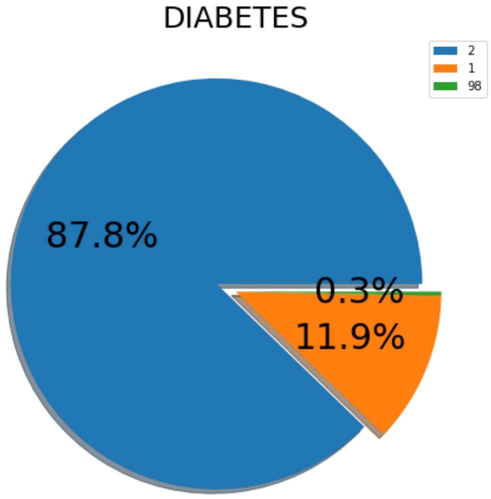


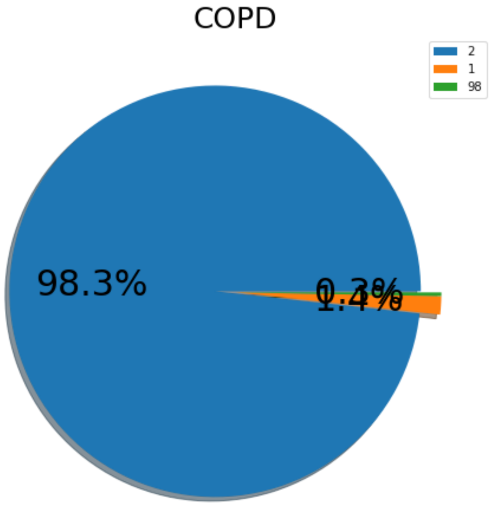


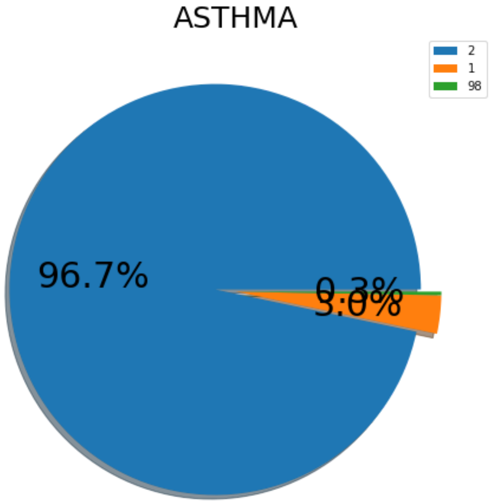

INTUBED
2
1
99
96.1%
0.7%
3.2%

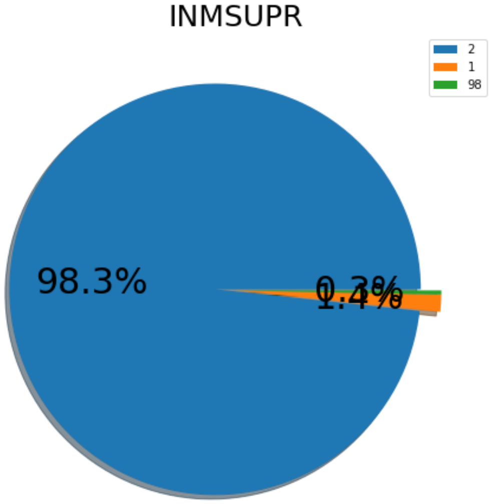

PNEUMONIA
2
1
99
85.1%
1.5%
13.4%

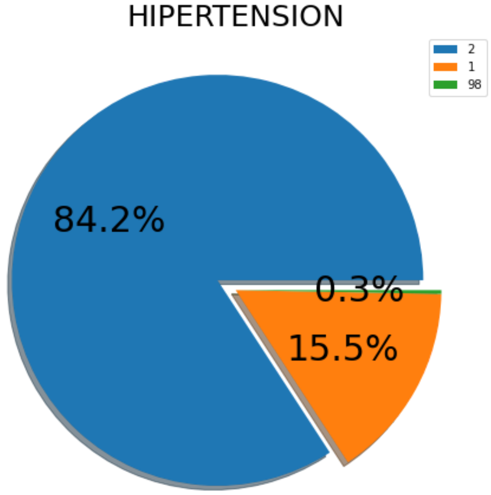

PREGNANT
2
1
98
98.9%
0.4%
0.8%

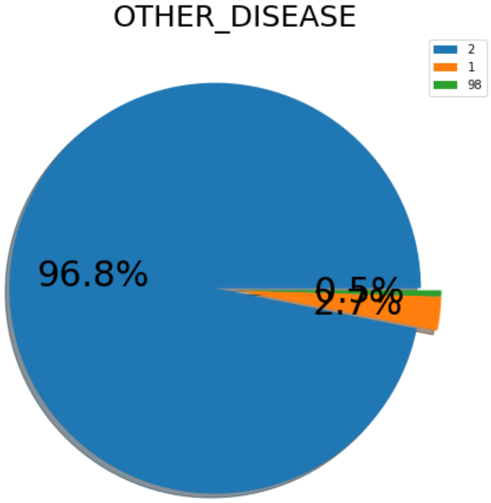

DIABETES
2
1
98
87.8%
0.3%
11.9%

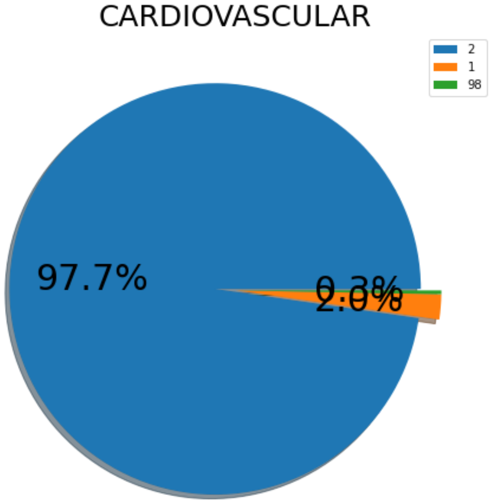

COPD
2
1
98
98.3%
0.3%
1.4%

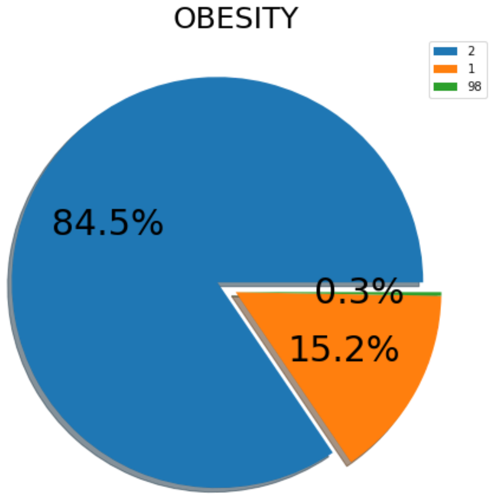

ASTHMA
2
1
98
96.7%
0.3%
3.0%

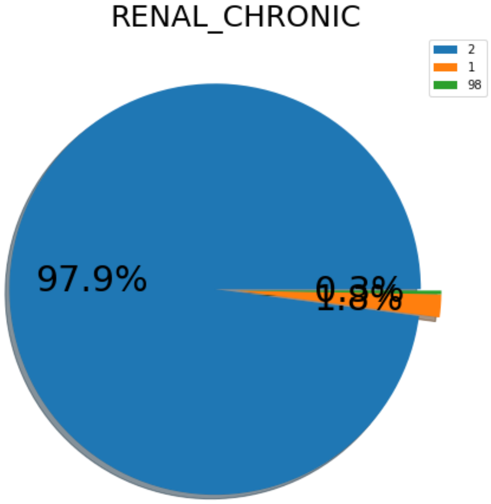

INMSUPR


HIPERTENSION

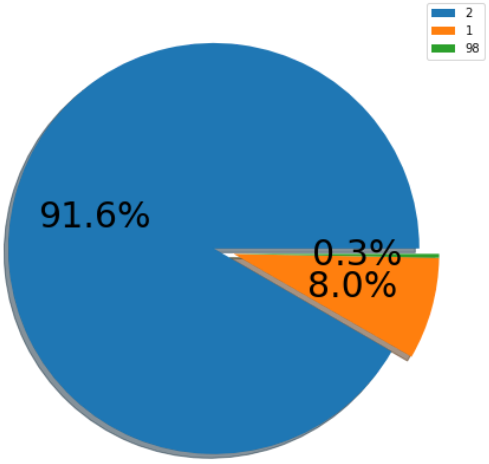

OTHER_DISEASE


CARDIOVASCULAR
2
1
98
97.7%
0.3%
2.0%

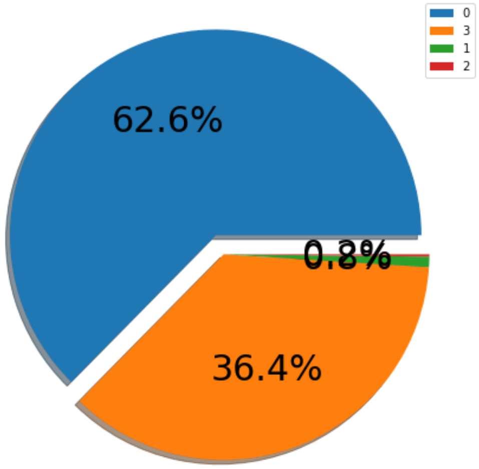

OBESITY
2
1
98
84.5%
0.3%
15.2%


RENAL_CHRONIC
2
1
98
97.9%
0.3%
1.8%

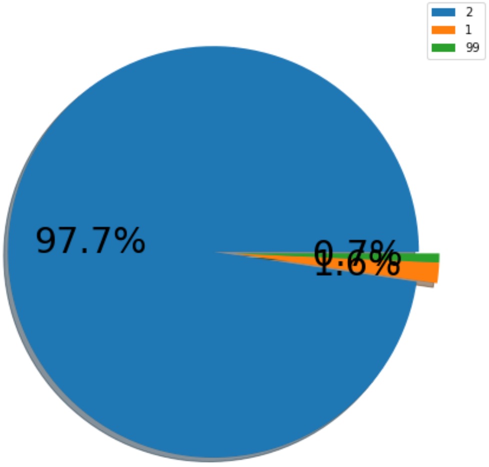
TOBACCO

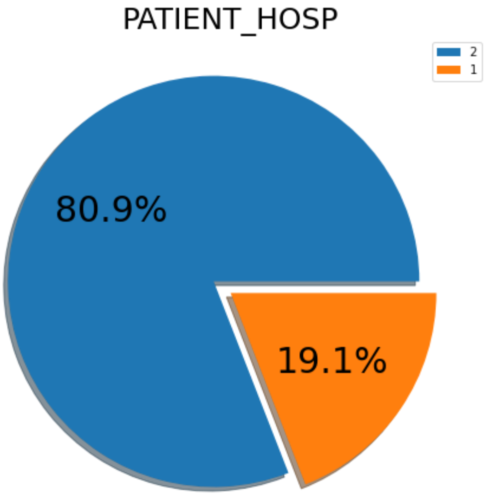


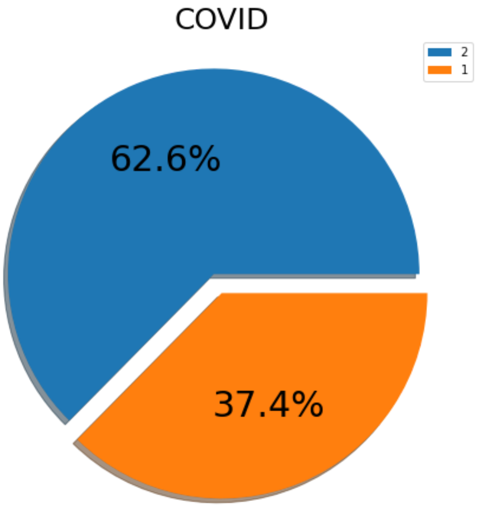
CLASIFFICATION_FINAL

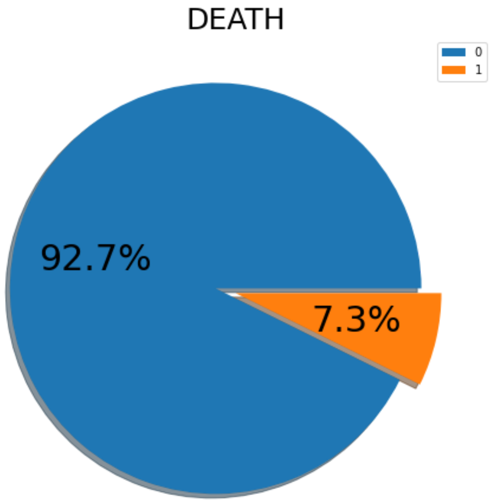


ICU



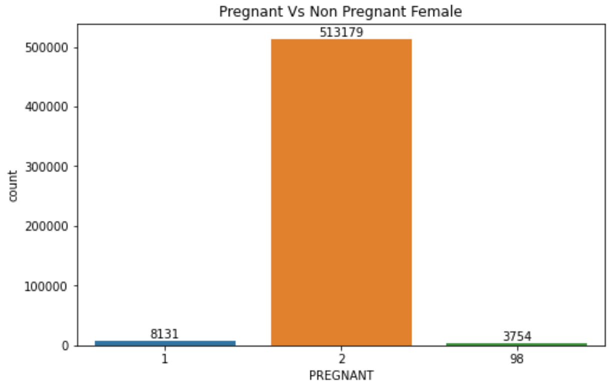




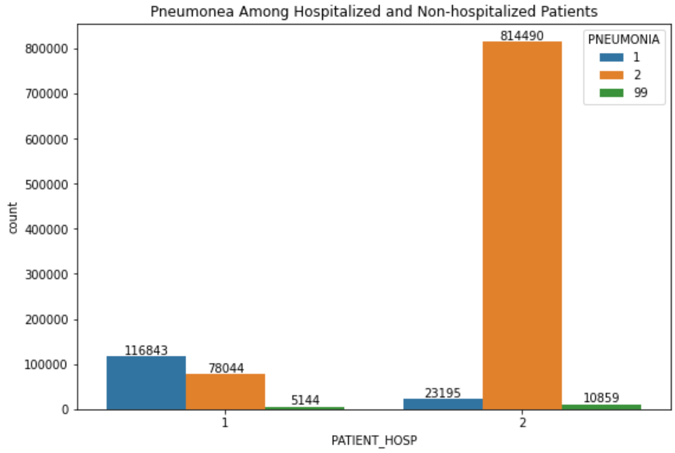


In [39]:

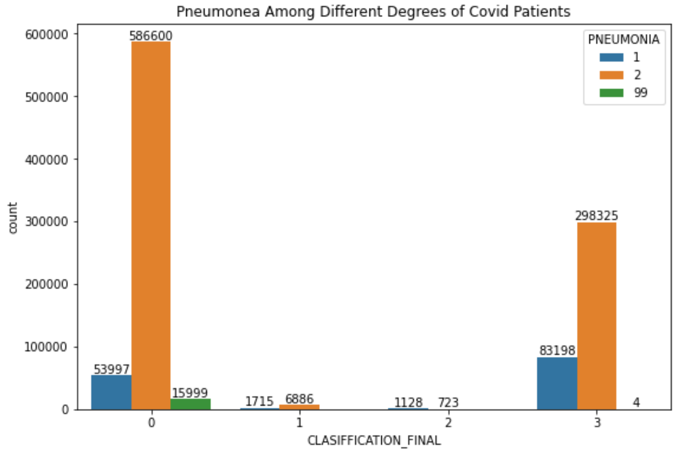
```
# Plotting distribution of pregnancies within FEMALE

df_female = df[df.SEX == 1]

plt.figure(figsize = (8,5))
ax = sns.countplot(df_female.PREGNANT)
for bars in ax.containers:
    ax.bar_label(bars)
plt.title("Pregnant Vs Non Pregnant Female", fontsize = 12);
```



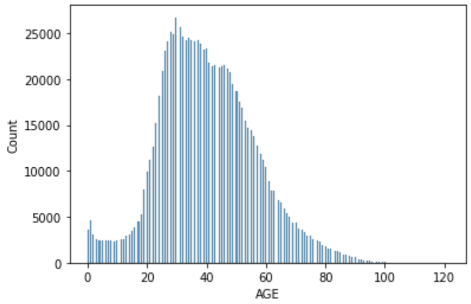
In [40]:
```
# Plotting the distribution of pneumonea among hospitalized and non-hospitalized patients

plt.figure(figsize = (9,6))
ax = sns.countplot(df.PATIENT_HOSP, hue = df.PNEUMONIA)
for bars in ax.containers:
    ax.bar_label(bars)
plt.title("Pneumonea Among Hospitalized and Non-hospitalized Patients");
```



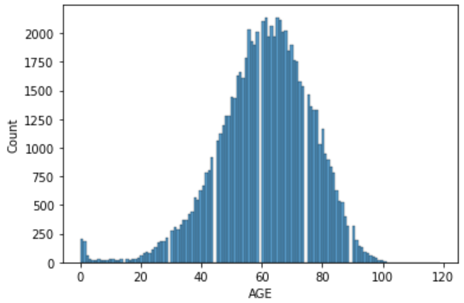
In [41]:
```
# Plotting the distribution of pneumonea across different degrees of covid

plt.figure(figsize = (9,6))
ax = sns.countplot(df.CLASIFFICATION_FINAL, hue = df.PNEUMONIA)
for bars in ax.containers:
    ax.bar_label(bars)

plt.title("Pneumonea Among Different Degrees of Covid Patients");
```



In [42]:
```
# Distribution of Age within the dead patients.
sns.histplot(df.AGE[df.DEATH == 0]);
```

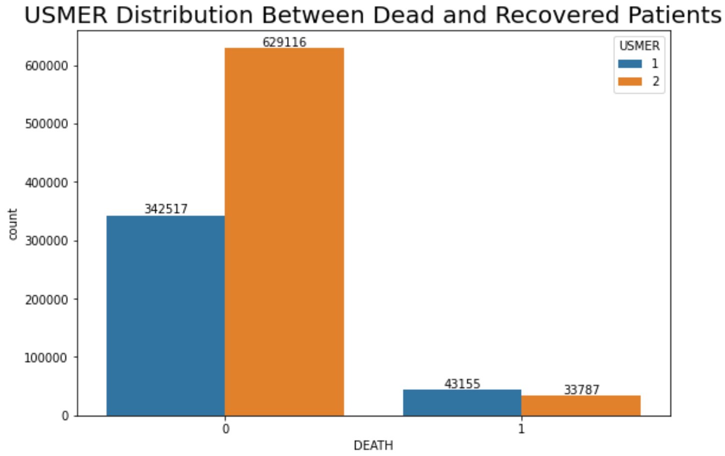


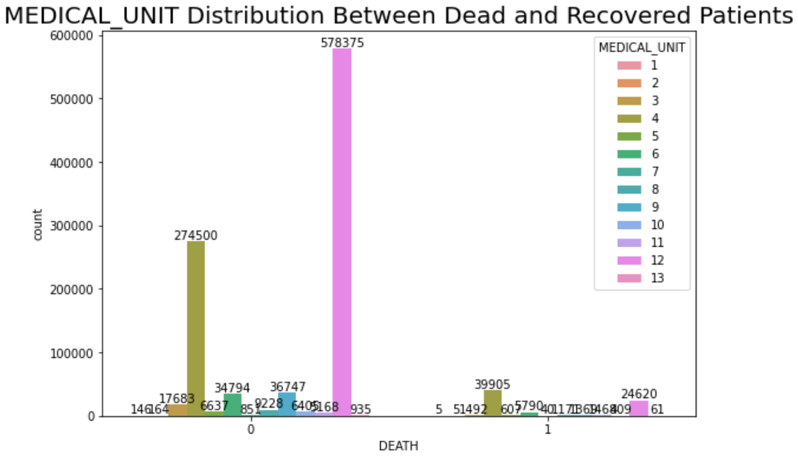
In [43]:
```
# Distribution of Age within the recovered patients.
sns.histplot(df.AGE[df.DEATH == 1]);
```

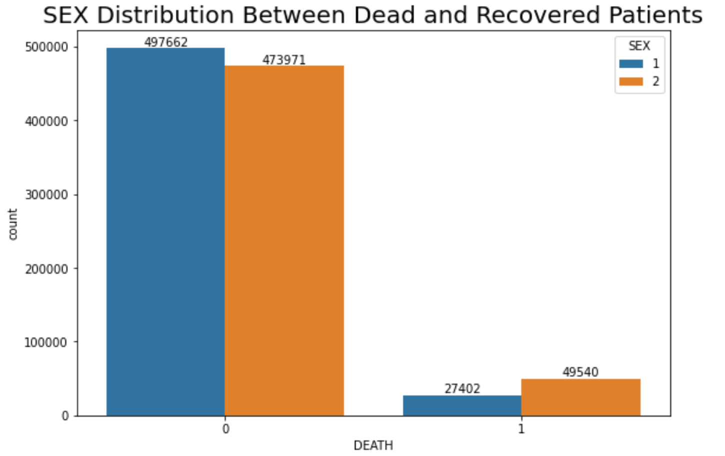


```
In [44]: selected_columns = df.columns.drop(['DEATH','PREGNANT','AGE'])
```

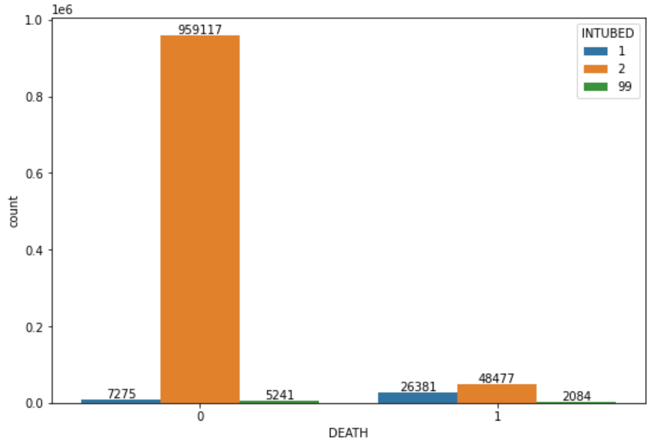
```
In [45]: # Show the distrubution of different features between dead and recovered patients.

         for column in selected_columns:

           plt.figure(figsize = (9,6))
           ax = sns.countplot(df.DEATH, hue = df[column])
           for bars in ax.containers:
               ax.bar_label(bars)


           plt.title(str(column) + ' Distribution Between Dead and Recovered Patients', fontsize = 20);
           plt.show()
```



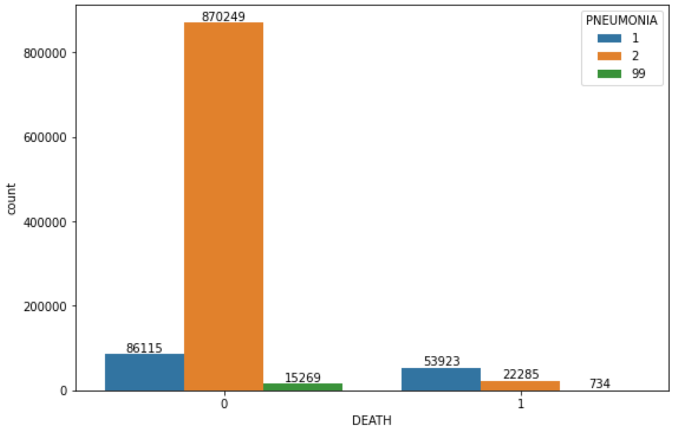




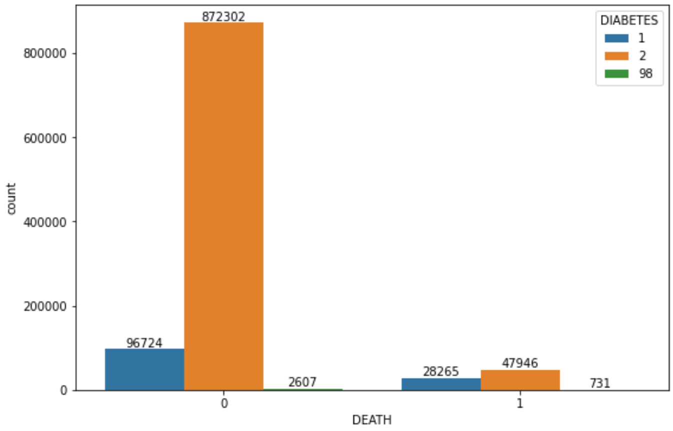
INTUBED Distribution Between Dead and Recovered Patients



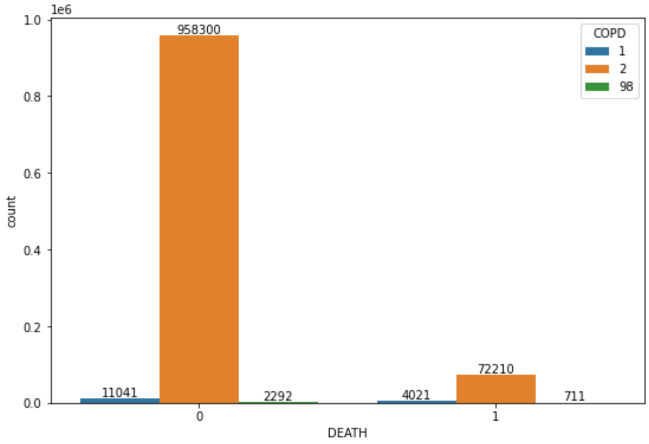
PNEUMONIA Distribution Between Dead and Recovered Patients



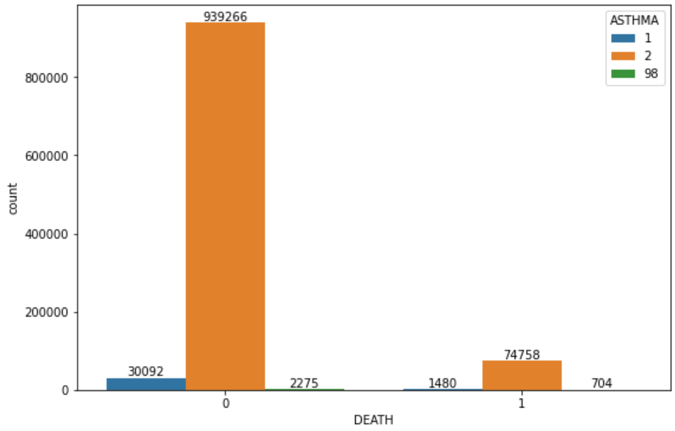
DIABETES Distribution Between Dead and Recovered Patients



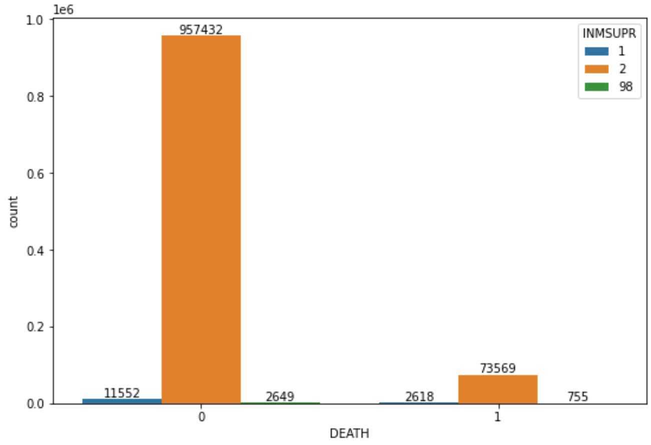
COPD Distribution Between Dead and Recovered Patients



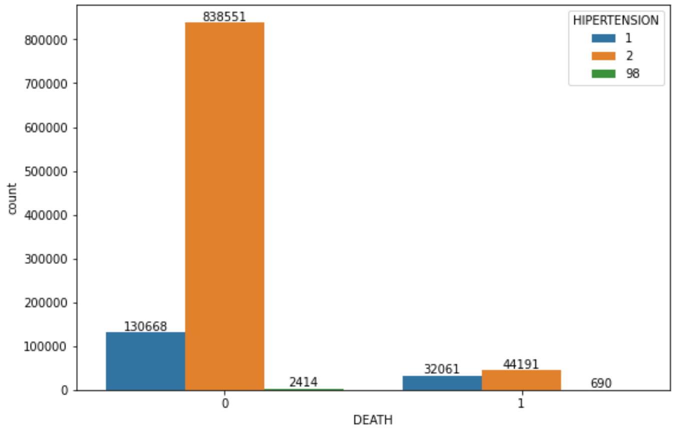
ASTHMA Distribution Between Dead and Recovered Patients



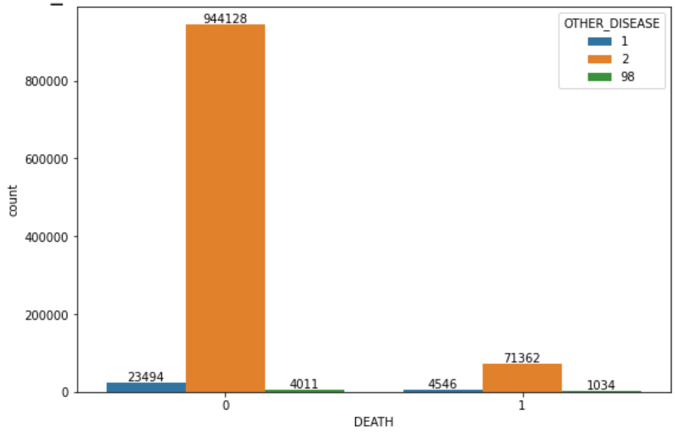
INMSUPR Distribution Between Dead and Recovered Patients



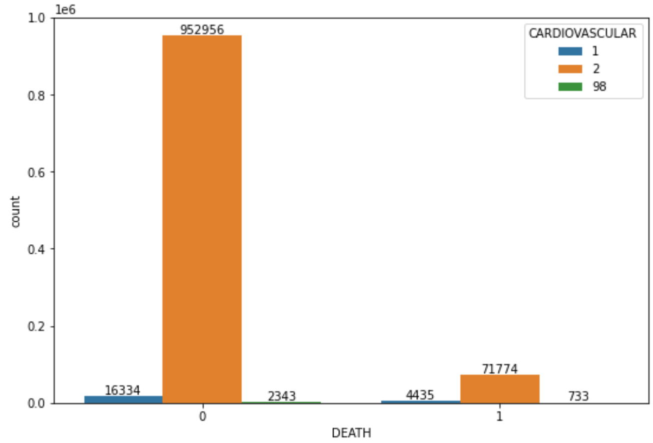
HIPERTENSION Distribution Between Dead and Recovered Patients



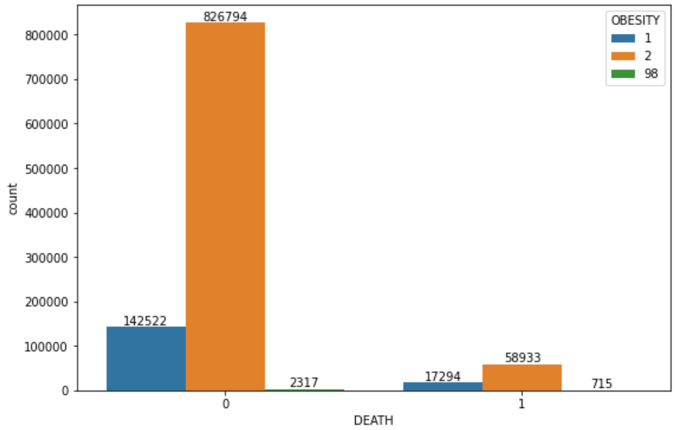
OTHER_DISEASE Distribution Between Dead and Recovered Patients



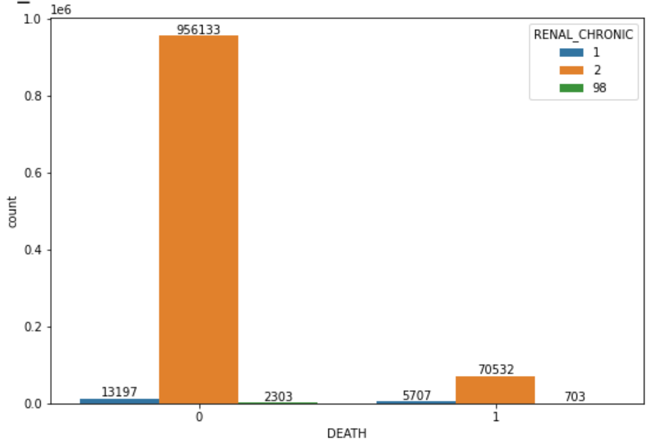
CARDIOVASCULAR Distribution Between Dead and Recovered Patients



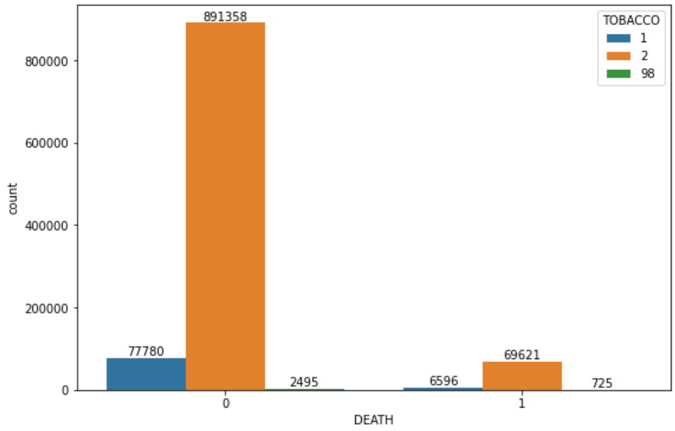
OBESITY Distribution Between Dead and Recovered Patients



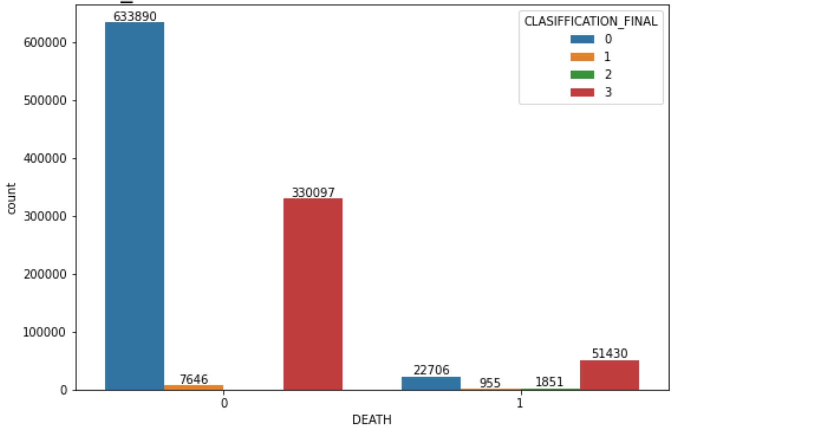
RENAL_CHRONIC Distribution Between Dead and Recovered Patients



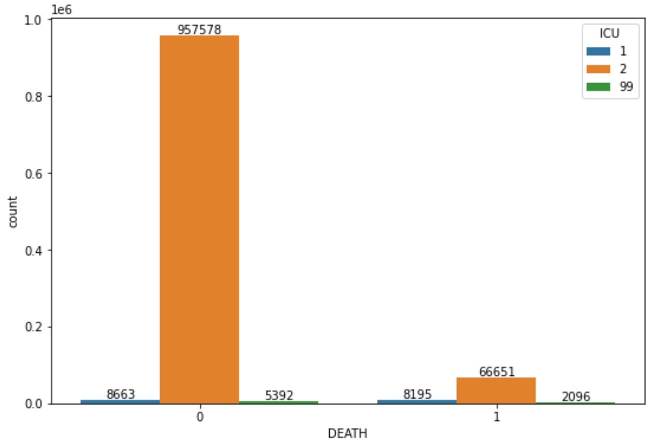
TOBACCO Distribution Between Dead and Recovered Patients



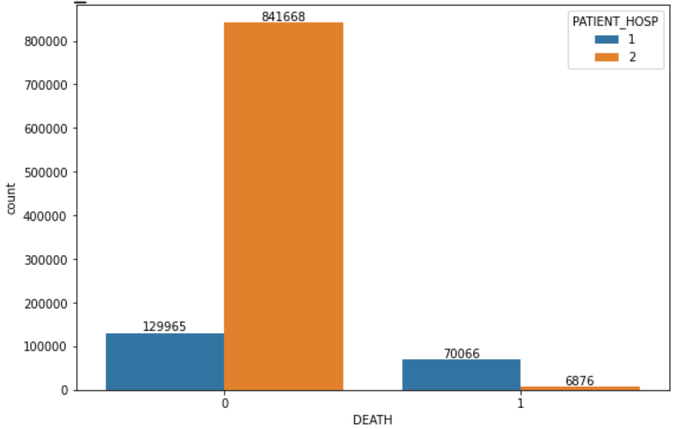
CLASIFFICATION_FINAL Distribution Between Dead and Recovered Patients



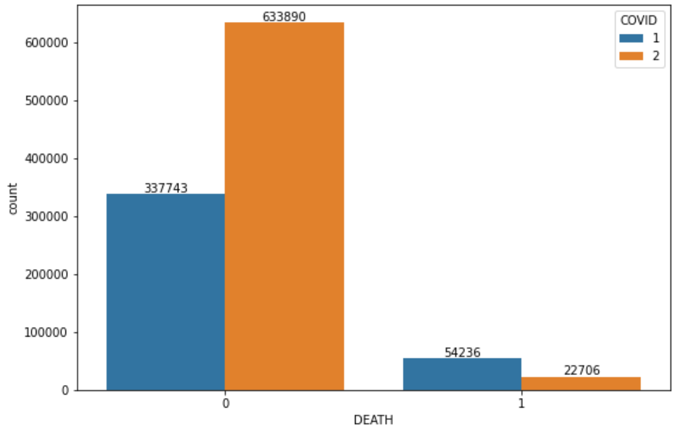
ICU Distribution Between Dead and Recovered Patients



PATIENT_HOSP Distribution Between Dead and Recovered Patients

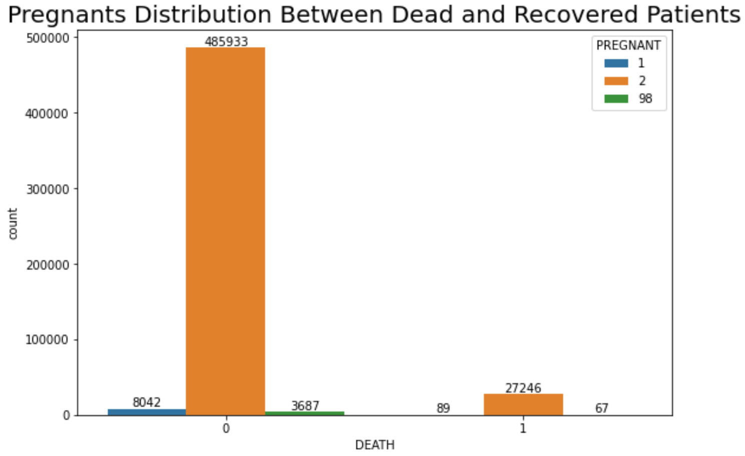


COVID Distribution Between Dead and Recovered Patients

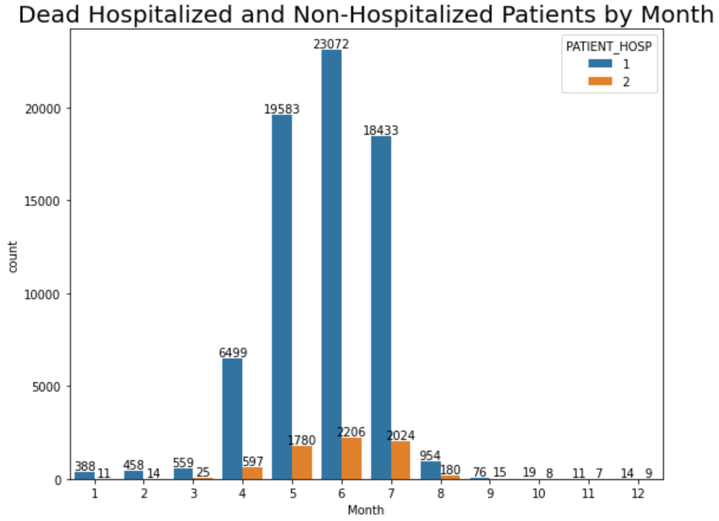


In [46]:

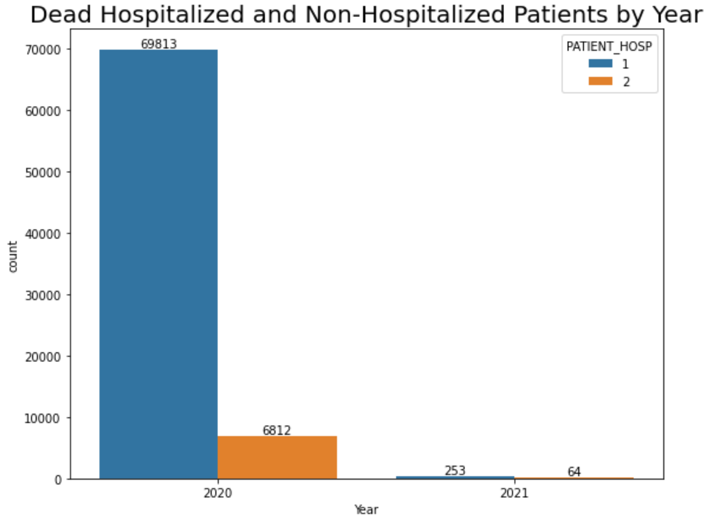
```
# Show the distrubution of pregnants and non-pregnants women between dead and recovered patient


plt.figure(figsize = (9,6))
ax = sns.countplot(df_female.DEATH, hue = df_female.PREGNANT)
for bars in ax.containers:
    ax.bar_label(bars)


plt.title( 'Pregnants Distribution Between Dead and Recovered Patients', fontsize = 20);
plt.show()
```



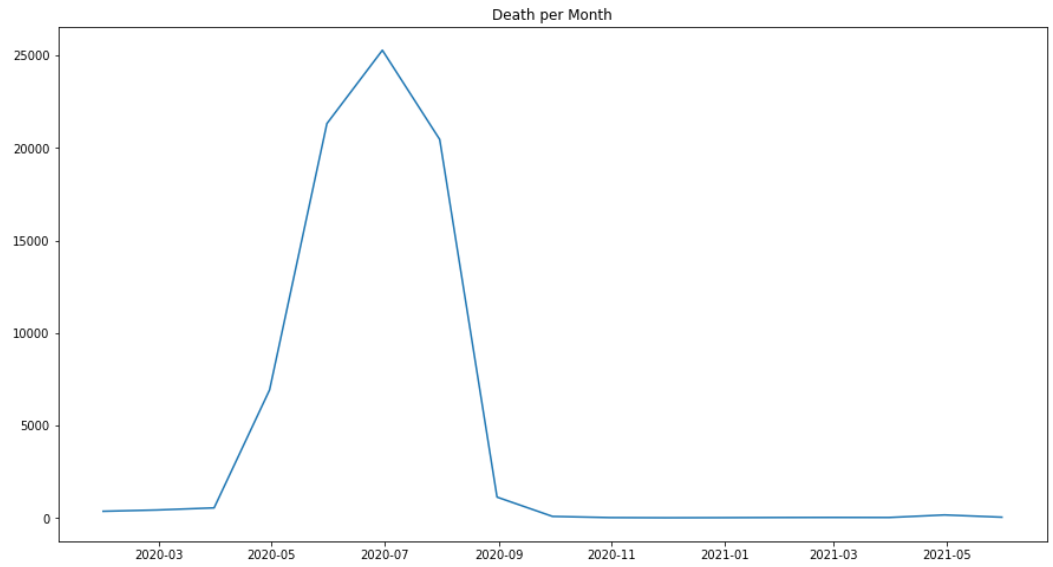
```
In [47]: # Plotting of Dead Hospitalized and Non-Hospitalized Patients by Month

         plt.figure(figsize = (9,7))
         ax = sns.countplot(x = "Month", hue = "PATIENT_HOSP", data = df_death)
         plt.title("Dead Hospitalized and Non-Hospitalized Patients by Month", fontsize = 20)
         for bars in ax.containers:
             ax.bar_label(bars)
```



```
In [48]: # Plotting of Dead Hospitalized and Non-Hospitalized Patients by Year

         plt.figure(figsize = (9,7))
         ax = sns.countplot(x = "Year", hue = "PATIENT_HOSP", data = df_death)
         plt.title("Dead Hospitalized and Non-Hospitalized Patients by Year", fontsize = 20)
         for bars in ax.containers:
             ax.bar_label(bars)
```



```
In [49]: # Death by time

         time_data = df_death.resample('M', on = time_col)['DEATH'].count().fillna(0)

         fig, ax = plt.subplots(figsize = (15,8))
         ax.plot(time_data)
         plt.title('Death per Month');
```



- Dealing with (Medical_UNIT) Feature:

- It seems that most people are in 12 or 4 type of medical units, may be they are the most available in Mexico.
- As long as we don't have any knowledge about these different types, we can't just combine them into 2 categories ex. (from 1 - 6) and from(7-13)
- We don't think it's of clinical importance in identifieng the patient risk.
- We also have data on (usmr) whivch indicates Whether the patient treated medical units of the first, second or third level.
- Having dummies for 13 extra columns of Medical Units for around 1 M data points makes our data unable to be processed.
- So we will drop medical unit

In [50]:
```
df.MEDICAL_UNIT.value_counts()
```

Out[50]:
```
12    602995
4     314405
6      40584
9      38116
3      19175
8      10399
10      7873
5       7244
11      5577
13       996
7        891
2        169
1        151
Name: MEDICAL_UNIT, dtype: int64
```

In [51]:
```
df.drop('MEDICAL_UNIT', axis = 1, inplace = True)
```

5. Pre-processing:

In [52]:
```
df.columns
```

Out[52]:
```
Index(['USMER', 'SEX', 'INTUBED', 'PNEUMONIA', 'AGE', 'PREGNANT', 'DIABETES',
       'COPD', 'ASTHMA', 'INMSUPR', 'HIPERTENSION', 'OTHER_DISEASE',
       'CARDIOVASCULAR', 'OBESITY', 'RENAL_CHRONIC', 'TOBACCO',
       'CLASIFFICATION_FINAL', 'ICU', 'PATIENT_HOSP', 'COVID', 'DEATH'],
      dtype='object')
```

In [53]:
```
# Specifying X and Y

X = df.drop(['DEATH','COVID'],axis =1)
y= df['DEATH']
```

In [54]:
```
# Split into test and train data

from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state= 1)
```

In [55]:
```
#check the shape

X_train.shape, X_test.shape
```

Out[55]:
```
((838860, 19), (209715, 19))
```

In [56]:
```
# Imputing missing data with mode
# Imputing test dataset with mode of train dataset to avoid overfitting
```

Features with null values:

- Pneumonia: 99 = 16003
- Diabetes: 98 = 3338
- Copd: 98 = 3003
- Asthma: 98 = 2979
- Inmsupr: 98 = 3404
- Hypertension: 98 = 3104
- Cardiovascular: 98 = 3076
- Renal chronic: 98 = 3006
- Other disease: 98 = 5045
- Obesity: 98 = 3032
- Tobacco: 98 = 3220
- Pregnancy: 98 = 3754
- Intubed: 99 = 7325

- ICU: 99 = 7488

In [57]:

```
# Check count values before and after imputation
X_train.PNEUMONIA.value_counts()
```

Out[57]:

```
2     714099
1     111975
99     12786
Name: PNEUMONIA, dtype: int64
```

In [58]:

```
# Imputation of train dataset (No null values in y (Death))
# Don't impute AGE beacause we don't want to drop age = 99 or 98 as this is not null in AGE


selected_columns = X_train.columns.drop('AGE')

for column in selected_columns:
    X_train[column].replace(98, np.nan, inplace = True)
    X_train[column].replace(99, np.nan, inplace = True)
    X_test[column].replace(98, np.nan, inplace = True)
    X_test[column].replace(99, np.nan, inplace = True)
```

In [59]:

```
X_train.isnull().sum()
```

Out[59]:

```
USMER                        0
SEX                          0
INTUBED                   5854
PNEUMONIA                12786
AGE                          0
PREGNANT                  2994
DIABETES                  2671
COPD                      2401
ASTHMA                    2389
INMSUPR                   2732
HIPERTENSION              2473
OTHER_DISEASE             4063
CARDIOVASCULAR            2468
OBESITY                   2417
RENAL_CHRONIC             2408
TOBACCO                   2577
CLASIFFICATION_FINAL         0
ICU                       5985
PATIENT_HOSP                 0
dtype: int64
```

In [60]:

```
X_test.isnull().sum()
```

Out[60]:

```
USMER                       0
SEX                         0
INTUBED                  1471
PNEUMONIA                3217
AGE                         0
PREGNANT                  760
DIABETES                  667
COPD                      602
ASTHMA                    590
INMSUPR                   672
HIPERTENSION              631
OTHER_DISEASE             982
CARDIOVASCULAR            608
OBESITY                   615
RENAL_CHRONIC             598
TOBACCO                   643
CLASIFFICATION_FINAL        0
ICU                      1503
PATIENT_HOSP                0
dtype: int64
```

In [61]:

```
#Imputation of train dataset (No null values in y (Death))

for column in X_train.columns:
  X_train[column].fillna(X_train[column].mode()[0], inplace=True)
```

In [62]:

```
#Imputation of test dataset (No null values in y (Death))

for column in X_test.columns:
  X_test[column].fillna(X_train[column].mode()[0], inplace=True)
```

In [63]:

```
X_train.isnull().sum()
```

Out[63]:

```
USMER                   0
SEX                     0
INTUBED                 0
PNEUMONIA               0
AGE                     0
PREGNANT                0
DIABETES                0
COPD                    0
ASTHMA                  0
INMSUPR                 0
HIPERTENSION            0
OTHER_DISEASE           0
CARDIOVASCULAR          0
OBESITY                 0
RENAL_CHRONIC           0
TOBACCO                 0
CLASIFFICATION_FINAL    0
ICU                     0
PATIENT_HOSP            0
dtype: int64
```

In [64]:

```
X_test.isnull().sum()
```

Out[64]:

```
USMER                   0
SEX                     0
INTUBED                 0
PNEUMONIA               0
AGE                     0
PREGNANT                0
DIABETES                0
COPD                    0
ASTHMA                  0
INMSUPR                 0
HIPERTENSION            0
OTHER_DISEASE           0
CARDIOVASCULAR          0
OBESITY                 0
RENAL_CHRONIC           0
TOBACCO                 0
CLASIFFICATION_FINAL    0
ICU                     0
PATIENT_HOSP            0
dtype: int64
```

In [65]:

```
# Check count values before and after imputation
X_train.PNEUMONIA.value_counts()
```

Out[65]:

```
2.0    726885
1.0    111975
Name: PNEUMONIA, dtype: int64
```

In [66]:

```
# Ensure imputation
# All categories must show 2 unique values except CLASSIFICATION_FINAL, MEDICAL_UNIT

# Check Cardinality in Categorical Features

selected_columns = X_train.columns.drop(['AGE'])

unique_dic = []

for col in selected_columns:

  unique_num_train = len(X_train[col].unique())
  unique_num_test = len(X_test[col].unique())
  unique_dic.append({'Total_Unique_Train' : unique_num_train,
                     'Total_Unique_Test' : unique_num_test })

unique_df = pd.DataFrame(unique_dic, index = selected_columns).sort_values(by = 'Total_Unique_Train', ascending = False)
unique_df
```

Out[66]:

	Total_Unique_Train	Total_Unique_Test
CLASIFFICATION_FINAL	4	4
USMER	2	2
SEX	2	2
ICU	2	2
TOBACCO	2	2
RENAL_CHRONIC	2	2
OBESITY	2	2
CARDIOVASCULAR	2	2
OTHER_DISEASE	2	2
HIPERTENSION	2	2
INMSUPR	2	2
ASTHMA	2	2
COPD	2	2
DIABETES	2	2
PREGNANT	2	2
PNEUMONIA	2	2
INTUBED	2	2
PATIENT_HOSP	2	2

In [67]:

```
# !pip install imblearn
```

In [68]:

```
# from imblearn.under_sampling import NearMiss
# nr = NearMiss()

# X_train, y_train = nr.fit_resample(X_train, y_train)
```

In [69]:

```
# Use  SMOTE (synthetic minority oversampling technique)

# from imblearn.over_sampling import SMOTE
# sm = SMOTE()
# X_train, y_train = sm.fit_resample(X_train, y_train)

# MemoryError: Unable to allocate 68.5 GiB for an array with shape (47277, 1554690) and data type uint8
```

In [70]:

```
# Get dummies dataframe for categorical data

numerical_train = X_train[['AGE']]
ordinal_train = X_train[['CLASIFFICATION_FINAL','USMER']]
categorical_train = X_train.drop(['AGE', 'CLASIFFICATION_FINAL','USMER'], axis = 1)
```

In [71]:

```
# Get dummies dataframe for categorical data

dummies_list = []

for column in categorical_train.columns:
  col_dummies = pd.get_dummies(X_train[column], drop_first = True)
  dummies_list.append(col_dummies)

dummies_df = pd.concat(dummies_list, axis=1)
```

In [72]:

```
dummies_df
```

Out[72]:

	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
656253	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	0
329191	0	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1
557768	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
93060	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
558339	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
491263	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
791624	0	1	1	1	1	1	1	1	0	1	1	0	1	1	1	1
470924	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
491755	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
128037	0	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1

838860 rows × 16 columns

In [73]:

```python
#Get dataframe for other features
num_ord_df = pd.concat([numerical_train, ordinal_train], axis =1)
```

In [74]:

```python
num_ord_df
```

Out[74]:

	AGE	CLASIFFICATION_FINAL	USMER
656253	59	3	1
329191	25	0	2
557768	37	3	1
93060	25	3	2
558339	34	3	2
...	...	...	...
491263	63	3	2
791624	46	0	2
470924	57	1	2
491755	30	3	2
128037	46	3	2

838860 rows × 3 columns

In [75]:

```python
# # Add all features back to X_train
X_train = pd.merge(num_ord_df, dummies_df, left_index=True, right_index=True)

X_train
```

Out[75]:

	AGE	CLASIFFICATION_FINAL	USMER	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
656253	59	3	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	0
329191	25	0	2	0	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1
557768	37	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
93060	25	3	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
558339	34	3	2	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
491263	63	3	2	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
791624	46	0	2	0	1	1	1	1	1	1	1	0	1	1	0	1	1	1	1
470924	57	1	2	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
491755	30	3	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
128037	46	3	2	0	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1

838860 rows × 19 columns

In [76]:

```python
# Same steps for X_test

numerical_test = X_test[['AGE']]
ordinal_test = X_test[['CLASIFFICATION_FINAL','USMER']]
categorical_test = X_test.drop(['AGE', 'CLASIFFICATION_FINAL','USMER'], axis = 1)
```

In [77]:

```python
# Get dummies dataframe for categorical data

dummies_list_test = []

for column in categorical_test.columns:
  col_dummies = pd.get_dummies(X_test[column], drop_first = True)
  dummies_list_test.append(col_dummies)

dummies_df_test = pd.concat(dummies_list_test, axis=1)
```

In [78]:

```python
# Get dataframe for other features
num_ord_df_test = pd.concat([numerical_test, ordinal_test], axis =1)
```

In [79]:

```python
# Add all features back to X_train
X_test = pd.merge(num_ord_df_test, dummies_df_test, left_index=True, right_index=True)

X_test
```

Out[79]:

	AGE	CLASIFFICATION_FINAL	USMER	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
1045953	46	0	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
358409	35	3	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
875012	36	0	2	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1
555046	27	3	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
272972	22	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
181305	30	0	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
672605	29	0	2	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
718823	68	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
1006146	54	0	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
23489	76	3	2	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0

209715 rows × 19 columns

6. Logistic Regression

i. Model Training

In [80]:

```
# Model training
# we will use solver = saga as we have a large dataset
from sklearn.linear_model import LogisticRegression

logreg = LogisticRegression(solver='saga', random_state=0)

logreg.fit(X_train, y_train)
```

```
/usr/local/lib/python3.8/dist-packages/sklearn/linear_model/_sag.py:352: ConvergenceWarning: The max_iter was reached which means the coef_ did not converge
  warnings.warn(
```

Out[80]:

```
LogisticRegression(random_state=0, solver='saga')
```

In [81]:

```
#test data
y_pred_test = logreg.predict(X_test)
y_pred_train = logreg.predict(X_train)
```

ii. Validation Metrics

a. Accuracy

In [82]:

```
#check for accuracy

from sklearn.metrics import accuracy_score

print('Model accuracy score(test): ', accuracy_score(y_test, y_pred_test))
print('Model accuracy score(train): ', accuracy_score(y_train, y_pred_train))
```

```
Model accuracy score(test):  0.9472951386405359
Model accuracy score(train):  0.9471890422716543
```

b. Null Accuracy

In [83]:

```
y_test.value_counts()
```

Out[83]:

```
0    194288
1     15427
Name: DEATH, dtype: int64
```

In [84]:

```
null_acuracy = 194288/(len(y_test))
null_acuracy
```

Out[84]:

```
0.9264382614500631
```

In [85]:

```
# null accuracy is less than our actual accuracy, hence, our model is not just predicting
# the most frequent value
```

c. Confusion Matrix

In [86]:

```
from sklearn.metrics import confusion_matrix
cm =confusion_matrix(y_test, y_pred_test)
```

In [87]:

```
print('True Negatives (TN) = ', cm[0,0])
print('False Positives (FP)= ', cm[0, 1])
print('False Negatives (FN)= ', cm[1, 0])
print('True Positives (TP))= ', cm[1, 1])
```

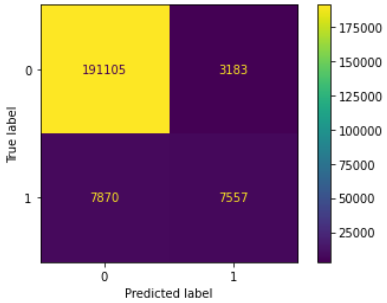
```
True Negatives (TN) =  191105
False positives (FP)=  3183
False Negatives (FN)=  7870
True Positives (TP))=  7557
```

In [88]:

```
# Visualze with heatmap
from sklearn.metrics import ConfusionMatrixDisplay
disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=logreg.classes_)
```

In [89]:

```
disp.plot();
```



d. Classification Report

In [90]:
```
from sklearn.metrics import classification_report
print(classification_report(y_test, y_pred_test))
```

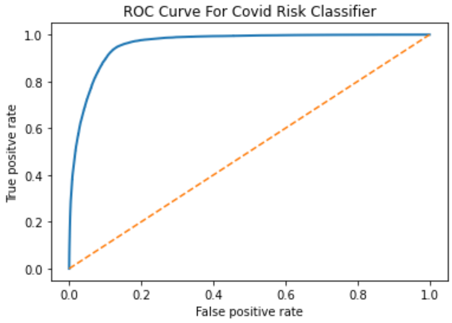
```
              precision    recall  f1-score   support

           0       0.96      0.98      0.97    194288
           1       0.70      0.49      0.58     15427

    accuracy                           0.95    209715
   macro avg       0.83      0.74      0.77    209715
weighted avg       0.94      0.95      0.94    209715
```

e. ROC, AUC

In [91]:
```
#probability of getting 0, i.e , Death
#probability of getting 1, i.e , Recovery

y_pred0 = logreg.predict_proba(X_test)[:,0]
y_pred1 = logreg.predict_proba(X_test)[:,1]
```

In [92]:
```
from sklearn.metrics import roc_curve

fpr, tpr, thresholds = roc_curve(y_test, y_pred1, pos_label=1)
```

In [93]:
```
plt.figure(figsize = (6,4))
plt.plot(fpr, tpr, linewidth=2)
plt.plot([0,1], [0,1], '--')
plt.title('ROC Curve For Covid Risk Classifier')
plt.xlabel('False positive rate')
plt.ylabel('True positve rate')
plt.show()
```



In [94]:
```
#computing AUC

from sklearn.metrics import roc_auc_score

ROC_AUC = roc_auc_score(y_test, y_pred1)

print(ROC_AUC)
```

```
0.9594526487596136
```

7. Random Forest Classifier:

i. Model Training

In [95]:
```
# importing random forest classifier from assemble module
from sklearn.ensemble import RandomForestClassifier
```

In [96]:
```
# creating a RF classifier
clf = RandomForestClassifier(n_estimators = 100)
# Training the model on the training dataset
# fit function is used to train the model using the training sets as parameters
clf.fit(X_train, y_train)
```

Out[96]:
```
RandomForestClassifier()
```

In [97]:
```
y_pred_test = clf.predict(X_test)
y_pred_train = clf.predict(X_train)
```

ii. Validation Metrics

a. Accuracy

In [98]:
```
#check for accuracy

from sklearn.metrics import accuracy_score
```

```
print('Model accuracy score(test): ', accuracy_score(y_test, y_pred_test))
print('Model accuracy score(train): ', accuracy_score(y_train, y_pred_train))
```

```
Model accuracy score(test):  0.943108504398827
Model accuracy score(train):  0.9651527072455476
```

b. Null Accuracy

In [99]:

```
y_test.value_counts()
```

Out[99]:

```
0    194288
1     15427
Name: DEATH, dtype: int64
```

In [100…

```
null_acuracy = 194288/(len(y_test))
null_acuracy
```

Out[100]:

```
0.9264382614500631
```

In [101…

```
# null accuracy is less than our actual accuracy, hence, our model is not just predicting
# the most frequent value
```

c. Confusion Matrix

In [102…

```
from sklearn.metrics import confusion_matrix
cm =confusion_matrix(y_test, y_pred_test)
```

In [103…

```
print('True Negatives (TN) = ', cm[0,0])
print('False positives (FP)= ', cm[0, 1])
print('False Negatives (FN)= ', cm[1, 0])
print('True Positives (TP))= ', cm[1, 1])
```

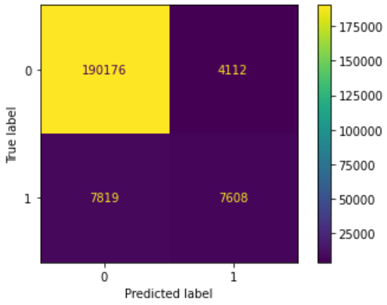
```
True Negatives (TN) =  190176
False positives (FP)=  4112
False Negatives (FN)=  7819
True Positives (TP))=  7608
```

In [104…

```
# Visualze with heatmap
from sklearn.metrics import ConfusionMatrixDisplay
disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=logreg.classes_)
```

In [105…

```
disp.plot();
```



d. Classification Report

In [106…

```
from sklearn.metrics import classification_report
print(classification_report(y_test, y_pred_test))
```

```
              precision    recall  f1-score   support

           0       0.96      0.98      0.97    194288
           1       0.65      0.49      0.56     15427

    accuracy                           0.94    209715
   macro avg       0.80      0.74      0.77    209715
weighted avg       0.94      0.94      0.94    209715
```

e. ROC, AUC

In [107…

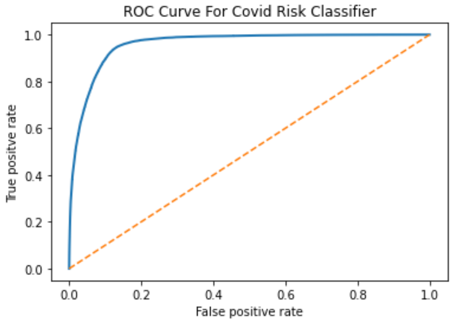
```
#probability of getting 0, i.e , Death
#probability of getting 1, i.e , Recovery

y_pred0 = logreg.predict_proba(X_test)[:,0]
y_pred1 = logreg.predict_proba(X_test)[:,1]
```

In [108…

```
from sklearn.metrics import roc_curve

fpr, tpr, thresholds = roc_curve(y_test, y_pred1, pos_label=1)
```

In [109…

```
plt.figure(figsize = (6,4))
plt.plot(fpr, tpr, linewidth=2)
plt.plot([0,1], [0,1], '--')
plt.title('ROC Curve For Covid Risk Classifier')
plt.xlabel('False positive rate')
plt.ylabel('True positve rate')
plt.show()
```



In [110…

```
#computing AUC

from sklearn.metrics import roc_auc_score

ROC_AUC = roc_auc_score(y_test, y_pred1)

print(ROC_AUC)
```

```
0.9594526487596136
```

8. Naive Bayes Classifiers:

i. Model Training

In [111…

```
# training the model on training set
from sklearn.naive_bayes import GaussianNB
gnb = GaussianNB()
gnb.fit(X_train, y_train)
```

Out[111]:

```
GaussianNB()
```

In [112…

```
# making predictions on the testing set

y_pred_test = gnb.predict(X_test)
y_pred_train = gnb.predict(X_train)
```

ii. Validation Metrics

a. Accuracy

In [113…

```
#check for accuracy

from sklearn.metrics import accuracy_score

print('Model accuracy score(test): ', accuracy_score(y_test, y_pred_test))
print('Model accuracy score(train): ', accuracy_score(y_train, y_pred_train))
```

```
Model accuracy score(test):  0.8975657439858856
Model accuracy score(train):  0.897655151038314
```

b. Null Accuracy

In [114…

```
y_test.value_counts()
```

Out[114]:

```
0    194288
1     15427
Name: DEATH, dtype: int64
```

In [115…

```
null_acuracy = 194288/(len(y_test))
null_acuracy
```

Out[115]:

```
0.9264382614500631
```

In [116…

```
# null accuracy is more than our actual accuracy, hence, our model may be just predicting
# the most frequent value
```

c. Confusion Matrix

In [117…

```
from sklearn.metrics import confusion_matrix
cm =confusion_matrix(y_test, y_pred_test)
```

In [118…

```
print('True Negatives (TN) = ', cm[0,0])
print('False positives (FP)= ', cm[0, 1])
print('False Negatives (FN)= ', cm[1, 0])
print('True Positives (TP))= ', cm[1, 1])
```

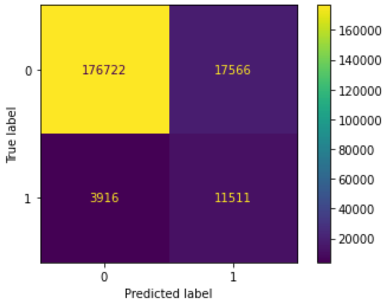
```
True Negatives (TN) =  176722
False positives (FP)=  17566
False Negatives (FN)=  3916
True Positives (TP))=  11511
```

In [119…

```
# Visualze with heatmap
from sklearn.metrics import ConfusionMatrixDisplay
disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=logreg.classes_)
```

In [120…

```
disp.plot();
```



d. Classification Report

In [121…

```
from sklearn.metrics import classification_report
print(classification_report(y_test, y_pred_test))
```

```
              precision    recall  f1-score   support

           0       0.98      0.91      0.94    194288
           1       0.40      0.75      0.52     15427

    accuracy                           0.90    209715
   macro avg       0.69      0.83      0.73    209715
weighted avg       0.94      0.90      0.91    209715
```

e. ROC, AUC

In [122…

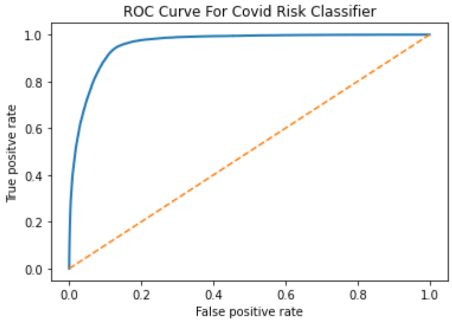
```
#probability of getting 0, i.e , Death
#probability of getting 1, i.e , Recovery

y_pred0 = logreg.predict_proba(X_test)[:,0]
y_pred1 = logreg.predict_proba(X_test)[:,1]
```

In [123…

```
from sklearn.metrics import roc_curve

fpr, tpr, thresholds = roc_curve(y_test, y_pred1, pos_label=1)
```

In [124…

```
plt.figure(figsize = (6,4))
plt.plot(fpr, tpr, linewidth=2)
plt.plot([0,1], [0,1], '--')
plt.title('ROC Curve For Covid Risk Classifier')
plt.xlabel('False positive rate')
plt.ylabel('True positve rate')
plt.show()
```



In [125…

```
#computing AUC

from sklearn.metrics import roc_auc_score

ROC_AUC = roc_auc_score(y_test, y_pred1)

print(ROC_AUC)
```

```
0.9594526487596136
```

9. SGD (Stochastic Gradient Descent) Classifier:

i. Model Training

In [ ]:

```
# training the model on training set

from sklearn.linear_model import SGDClassifier

clf = SGDClassifier(loss="perceptron", penalty="l2")
clf.fit(X_train, y_train)
```

In [ ]:

```
X_train
```

In [ ]:

```
# making predictions on the testing set

y_pred_test = clf.predict(X_test)
y_pred_train = clf.predict(X_train)
```

ii. Validation Metrics

a. Accuracy

In [ ]:

```
#check for accuracy

from sklearn.metrics import accuracy_score
```

```
print('Model accuracy score(test): ', accuracy_score(y_test, y_pred_test))
print('Model accuracy score(train): ', accuracy_score(y_train, y_pred_train))
```

b. Null Accuracy

In [ ]:

```
y_test.value_counts()
```

In [ ]:

```
null_acuracy = 194288/(len(y_test))
null_acuracy
```

In [ ]:

```
# null accuracy is less than our actual accuracy, hence, our model is not just predicting
# the most frequent value
```

c. Confusion Matrix

In [ ]:

```
from sklearn.metrics import confusion_matrix
cm =confusion_matrix(y_test, y_pred_test)
```

In [134…

```
print('True Negatives (TN) = ', cm[0,0])
print('False positives (FP)= ', cm[0, 1])
print('False Negatives (FN)= ', cm[1, 0])
print('True Positives (TP))= ', cm[1, 1])
```

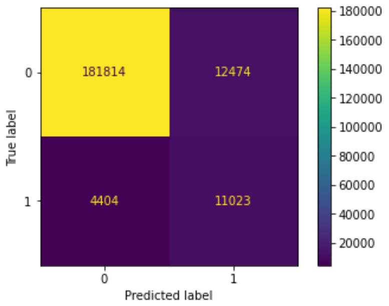
```
True Negatives (TN) =  181814
False positives (FP)=  12474
False Negatives (FN)=  4404
True Positives (TP))=  11023
```

In [135…

```
# Visualze with heatmap
from sklearn.metrics import ConfusionMatrixDisplay
disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=logreg.classes_)
```

In [136…

```
disp.plot();
```



d. Classification Report

In [137…

```
from sklearn.metrics import classification_report
print(classification_report(y_test, y_pred_test))
```

```
              precision    recall  f1-score   support

           0       0.98      0.94      0.96    194288
           1       0.47      0.71      0.57     15427

    accuracy                           0.92    209715
   macro avg       0.72      0.83      0.76    209715
weighted avg       0.94      0.92      0.93    209715
```

e. ROC, AUC

In [138…

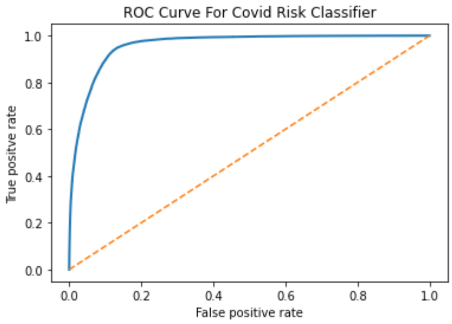
```
#probability of getting 0, i.e , Death
#probability of getting 1, i.e , Recovery

y_pred0 = logreg.predict_proba(X_test)[:,0]
y_pred1 = logreg.predict_proba(X_test)[:,1]
```

In [139…

```
from sklearn.metrics import roc_curve

fpr, tpr, thresholds = roc_curve(y_test, y_pred1, pos_label=1)
```

In [140…

```
plt.figure(figsize = (6,4))
plt.plot(fpr, tpr, linewidth=2)
plt.plot([0,1], [0,1], '--')
plt.title('ROC Curve For Covid Risk Classifier')
plt.xlabel('False positive rate')
plt.ylabel('True positve rate')
plt.show()
```



In [141…

```
#computing AUC

from sklearn.metrics import roc_auc_score

ROC_AUC = roc_auc_score(y_test, y_pred1)
```

```
print(ROC_AUC)
```

```
0.9594526487596136
```

10. Support Vector Machine (SVM):

i. Model Training

In [ ]:
```
from sklearn.svm import SVC
svc_model= SVC(kernel = 'linear')
svc_model.fit(X_train, y_train)
prediction= svc_model.predict(X_test)
```

In [ ]:
```
print(svc_model.score(X_train, y_train))
print(svc_model.score(X_test, y_test))
```

In [ ]:
```
print('Confusion Matrix: \n',
     confusion_matrix(prediction, y_test))
```

ii. Validation Metrics

a. Accuracy

In [ ]:
```
#check for accuracy

from sklearn.metrics import accuracy_score

print('Model accuracy score(test): ', accuracy_score(y_test, y_pred_test))
print('Model accuracy score(train): ', accuracy_score(y_train, y_pred_train))
```

b. Null Accuracy

In [ ]:
```
y_test.value_counts()
```

In [ ]:
```
null_acuracy = 194288/(len(y_test))
null_acuracy
```

In [ ]:
```
# null accuracy is less than our actual accuracy, hence, our model is not just predicting
# the most frequent value
```

c. Confusion Matrix

In [ ]:
```
from sklearn.metrics import confusion_matrix
cm =confusion_matrix(y_test, y_pred_test)
```

In [ ]:
```
print('True Negatives (TN) = ', cm[0,0])
print('False positives (FP)= ', cm[0, 1])
print('False Negatives (FN)= ', cm[1, 0])
print('True Positives (TP))= ', cm[1, 1])
```

In [ ]:
```
# Visualze with heatmap
from sklearn.metrics import ConfusionMatrixDisplay
disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=logreg.classes_)
```

In [ ]:
```
disp.plot();
```

d. Classification Report

In [ ]:
```
from sklearn.metrics import classification_report
print(classification_report(y_test, y_pred_test))
```

e. ROC, AUC

In [ ]:
```
#probability of getting 0, i.e , Death
#probability of getting 1, i.e , Recovery

y_pred0 = logreg.predict_proba(X_test)[:,0]
y_pred1 = logreg.predict_proba(X_test)[:,1]
```

In [ ]:
```
from sklearn.metrics import roc_curve

fpr, tpr, thresholds = roc_curve(y_test, y_pred1, pos_label=1)
```

In [ ]:
```
plt.figure(figsize = (6,4))
plt.plot(fpr, tpr, linewidth=2)
plt.plot([0,1], [0,1], '--')
plt.title('ROC Curve For Covid Risk Classifier')
plt.xlabel('False positive rate')
plt.ylabel('True positve rate')
plt.show()
```

In [ ]:
```
#computing AUC

from sklearn.metrics import roc_auc_score

ROC_AUC = roc_auc_score(y_test, y_pred1)

print(ROC_AUC)
```

In [ ]:
```

```