```
import numpy as np
import pandas as pd
import seaborn as sns

import matplotlib.pyplot as plt
```

```
df=pd.read_csv(r'/content/covid.csv')
```

```
df.head()
```

	id	sex	patient_type	entry_date	date_symptoms	date_died	intubed	pneumon
0	16169f	2.0	1.0	4/5/2020	2/5/2020	9999-99-99	97.0	2
1	1009bf	2.0	1.0	19-03-2020	17-03-2020	9999-99-99	97.0	2
2	167386	1.0	2.0	6/4/2020	1/4/2020	9999-99-99	2.0	2
3	0b5948	2.0	2.0	17-04-2020	10/4/2020	9999-99-99	2.0	1
4	0d01b5	1.0	2.0	13-04-2020	13-04-2020	22-04-2020	2.0	2

```
print(df.shape)
```

```
(566602, 23)
```

```
print(df.columns.size)
df.columns
```

```
23
Index(['id', 'sex', 'patient_type', 'entry_date', 'date_symptoms', 'date_died',
       'intubed', 'pneumonia', 'age', 'pregnancy', 'diabetes', 'copd',
       'asthma', 'inmsupr', 'hypertension', 'other_disease', 'cardiovascular',
       'obesity', 'renal_chronic', 'tobacco', 'contact_other_covid',
       'covid_res', 'icu'],
      dtype='object')
```

Data Pre-processing

1. Data Cleaning

```
for i in df.columns:
    if i in ['id','entry_date','date_symptoms','date_died','age']:
        continue
    else:
        print('unique values in '+ i +' column- ',end=' ')
        print(df[i].unique())
```

```
unique values in sex column-  [2 1]
unique values in patient_type column-  [1 2]
unique values in intubed column-  [97  2  1 99]
unique values in pneumonia column-  [ 2  1 99]
unique values in pregnancy column-  [97  2  1 98]
unique values in diabetes column-  [ 2  1 98]
unique values in copd column-  [ 2  1 98]
unique values in asthma column-  [ 2  1 98]
unique values in inmsupr column-  [ 2  1 98]
unique values in hypertension column-  [ 2  1 98]
unique values in other_disease column-  [ 2  1 98]
unique values in cardiovascular column-  [ 2  1 98]
unique values in obesity column-  [ 2  1 98]
unique values in renal_chronic column-  [ 2  1 98]
unique values in tobacco column-  [ 2  1 98]
unique values in contact_other_covid column-  [ 2 99  1]
unique values in covid_res column-  [1 2 3]
unique values in icu column-  [97  2  1 99]
```

1.1 Data Descriptors

These features are categorical so we convert them into different categories as follows:

(a) Sex:- Female (1), Male (2)

(b) Patient_type:- Outpatient (1), Inpatient (2)

(c) Columns with preconditions like pregnancy, diabetes, copd, asthma etc:- Yes (1), No (2)

(d) Covid result:- Positive (1), Negative (2), Results Awaited (3)

The values 97, 98, 99 indicate that the data is not available for these cells.

Okay great! Now that we have the available descriptors of each column, we can move forward with the cleaning and wrangling of the data.

```
df.info()
print('\nCovid Result positive-',len(df[df['covid_res']==1]))  #Covid Result positive
print('Covid Result negative-',len(df[df['covid_res']==2]))  #Covid Result negative
print('Covid result awaited-',len(df[df['covid_res']==3]))  #Covid result awaited
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 566602 entries, 0 to 566601
Data columns (total 23 columns):
 #   Column               Non-Null Count   Dtype 
---  ------               --------------   ----- 
 0   id                   566602 non-null  object
 1   sex                  566602 non-null  int64 
 2   patient_type         566602 non-null  int64 
 3   entry_date           566602 non-null  object
 4   date_symptoms        566602 non-null  object
 5   date_died            566602 non-null  object
 6   intubed              566602 non-null  int64
 7   pneumonia            566602 non-null  int64
 8   age                  566602 non-null  int64
 9   pregnancy            566602 non-null  int64
 10  diabetes             566602 non-null  int64
 11  copd                 566602 non-null  int64
 12  asthma               566602 non-null  int64
 13  inmsupr              566602 non-null  int64
 14  hypertension         566602 non-null  int64
 15  other_disease        566602 non-null  int64
 16  cardiovascular       566602 non-null  int64
 17  obesity              566602 non-null  int64
 18  renal_chronic        566602 non-null  int64
 19  tobacco              566602 non-null  int64
 20  contact_other_covid  566602 non-null  int64
 21  covid_res            566602 non-null  int64
 22  icu                  566602 non-null  int64
dtypes: int64(19), object(4)
memory usage: 99.4+ MB

Covid Result positive- 220657
Covid Result negative- 279035
Covid result awaited- 66910
```

No null values present in the data¶

```
date_cols=['entry_date','date_symptoms']
for dates in date_cols:
    df[dates]=pd.to_datetime(df[dates],infer_datetime_format=True)

# cleaning Date_died column
df['date_died'].replace('9999-99-99','NA',inplace=True)
date_cols.append('date_died')
#df[date_cols_2]
df[date_cols]
```

	entry_date	date_symptoms	date_died
0	2020-04-05	2020-02-05	NA
4	2020-04-13	2020-04-13	22-04-2020

```
df=df[['sex', 'patient_type', 'entry_date', 'date_symptoms', 'date_died', 'age',
       'intubed', 'pneumonia', 'pregnancy', 'diabetes', 'copd',
       'asthma', 'inmsupr', 'hypertension', 'other_disease', 'cardiovascular',
       'obesity', 'renal_chronic', 'tobacco', 'contact_other_covid',
       'covid_res', 'icu']]
```

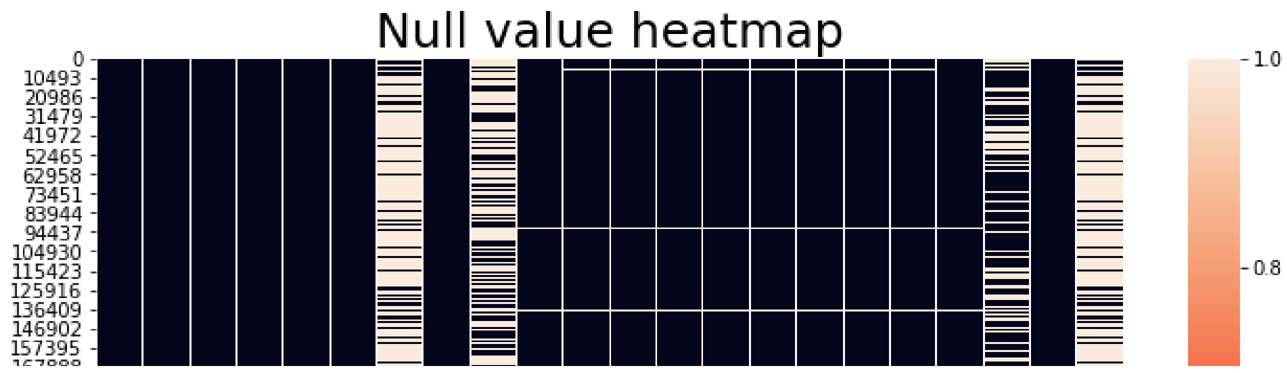
```
df.iloc[:,6:]=df.iloc[:,6:].replace([97,98,99],np.nan)
df.iloc[:,6:]=df.iloc[:,6:].replace(1,'Yes')
df.iloc[:,6:]=df.iloc[:,6:].replace(2,'No')

df.iloc[:,-2]=df.iloc[:,-2].replace('Yes','Positive')
df.iloc[:,-2]=df.iloc[:,-2].replace('No','Negative')
df.iloc[:,-2]=df.iloc[:,-2].replace(3,'Results awaited')
```

2. Data Visualization

Null value Heatmap

```
plt.figure(figsize=(12,10))
sns.heatmap(df.isnull())
plt.title('Null value heatmap',size=25)
```

```
Text(0.5, 1.0, 'Null value heatmap')
```



Since we are focusing on giving the chances of being affected by corona,so our main focus will be on either chance is positive or negative, hence we'll neglect awaiting chances.. Now here i am dropping all those rows which contains chance is awaiting i.e.3 value

```
df=df[df['covid_res']!='Results awaited']
```

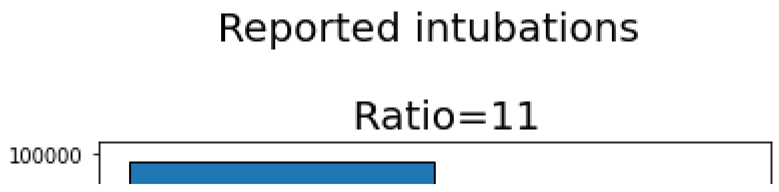
1. Intubation

```
df['intubed'].isna().value_counts()
# True indicates the NULL Values
```

```
True     392268
False    107424
Name: intubed, dtype: int64
```

```
#FROM THE REPORTED INTUBATION
%matplotlib inline
# plt.figure(figsize=(8,10))
ax=plt.hist(df['intubed'][df['intubed'].isna()==False],bins=2,edgecolor='black')
plt.xticks(size=10,)
plt.xlabel('Intubation \n \n Yes:{}  No:{}'.format(df['intubed'].value_counts()[1] , df['i
plt.ylabel('Count',size=10)
plt.title('Reported intubations \n \n  Ratio={0:.0f}'.format(df['intubed'].value_counts()[
          ,size=20)
```

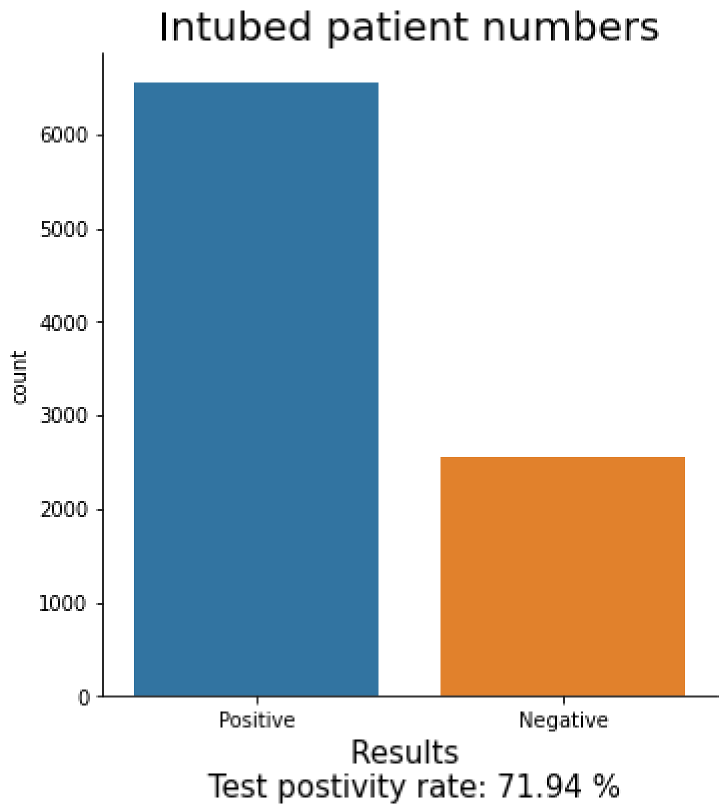
```
    Text(0.5, 1.0, 'Reported intubations \n \n  Ratio=11')
```



Intubation test positivity

```
df_intubed=df[df['intubed']=='Yes']
sns.catplot('covid_res',data=df_intubed,kind='count')
plt.title('Intubed patient numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_intubed['covid_res'].value_counts()[0]/df_intubed['covid_res'].size),size=15)
```

```
    /usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pas
      FutureWarning
    Text(0.5, 6.79999999999999, 'Results \n Test postivity rate: 71.94 %')
```



Intubation is a good indicator, so as to predict whether the person is Covid +ve or not

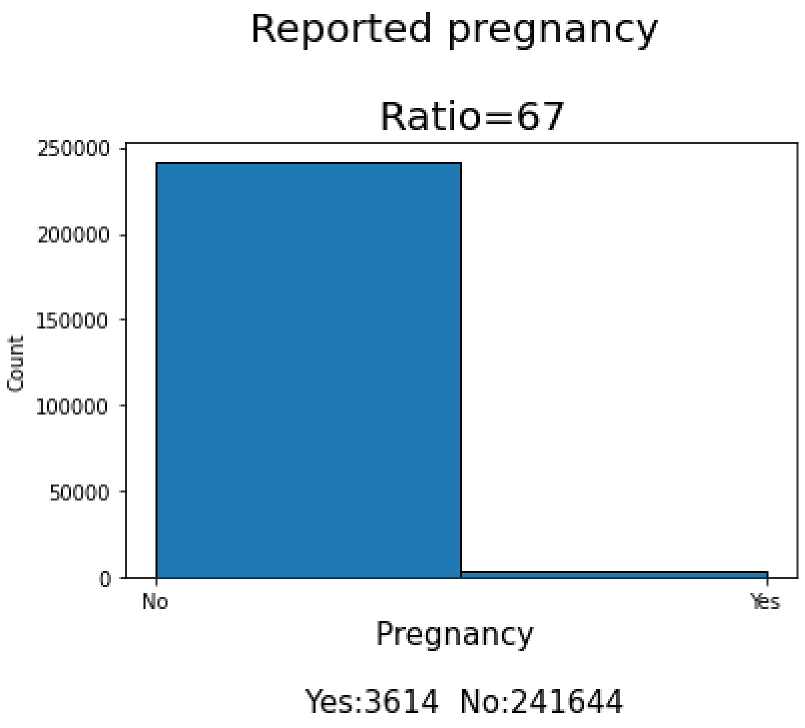
2. Pregnancy

```
df['pregnancy'].isna().value_counts()
# True indicates the NULL Values
# False indicates total reported pregnancy (might be yes or no)
```

```
    True     254434
    False    245258
    Name: pregnancy, dtype: int64
```

```
ax=plt.hist(df['pregnancy'][df['pregnancy'].isna()==False],bins=2,edgecolor='black')
plt.xticks(size=10,)
plt.xlabel('Pregnancy \n \n Yes:{}  No:{}'.format(df['pregnancy'].value_counts()[1] , df['
plt.ylabel('Count',size=10)
plt.title('Reported pregnancy \n \n  Ratio={0:.0f}'.format(df['pregnancy'].value_counts()[
          ,size=20)
```

```
     Text(0.5, 1.0, 'Reported pregnancy \n \n  Ratio=67')
```

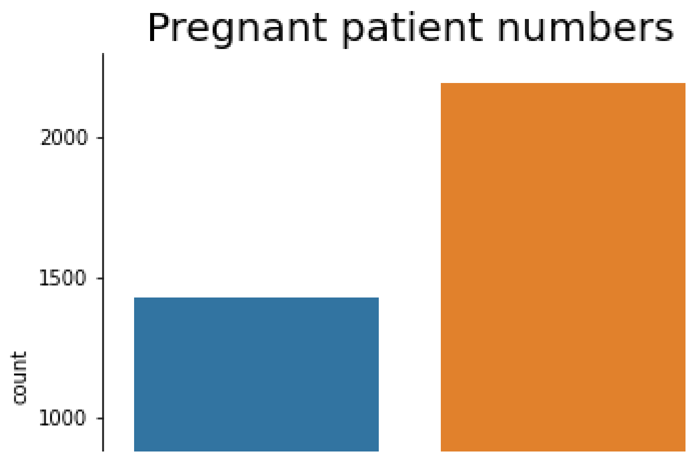


Pregnancy test positivity

Through this metric we try to understand what are the chances of a person being COVID +ve if she is pregnant.

```
df_pregnancy=df[df['pregnancy']=='Yes']
sns.catplot('covid_res',data=df_pregnancy,kind='count')
plt.title('Pregnant patient numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_pregnancy['covid_res'].value_counts()[1]/df_pregnancy['covid_res'].size),size=
plt.xticks(size=15)
```

```
/usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pas
  FutureWarning
(array([0, 1]), <a list of 2 Text major ticklabel objects>)
```



From the above charts, Most of the women's who are pregnant are found to be covid -ve. Although there is not much sifgnifiact difference in Covid positivity and negativity rates.

Pregnancy is not a good indicator to predict Covid positivity

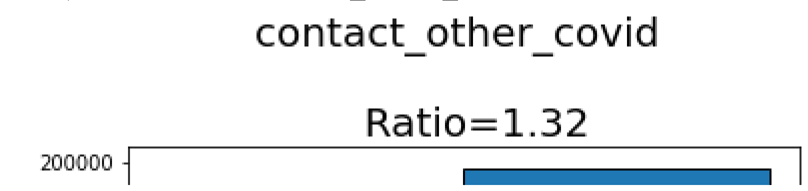
3. Contact with Other Covid +ve person

```
df['contact_other_covid'].isna().value_counts()
# True indicates the NULL Values
# False indicates total reported data (might be yes or no)
```

```
     False    346017
     True     153675
     Name: contact_other_covid, dtype: int64
```

```
ax=plt.hist(df['contact_other_covid'][df['contact_other_covid'].isna()==False],bins=2,edge
plt.xticks(size=10,)
plt.xlabel('contact_other_covid \n \n Yes:{}  No:{}'.format(df['contact_other_covid'].valu
plt.ylabel('Count',size=10)
plt.title('contact_other_covid \n \n  Ratio={0:.02f}'.format(df['contact_other_covid'].val
          ,size=20)
```

```
Text(0.5, 1.0, 'contact_other_covid \n \n  Ratio=1.32')
```

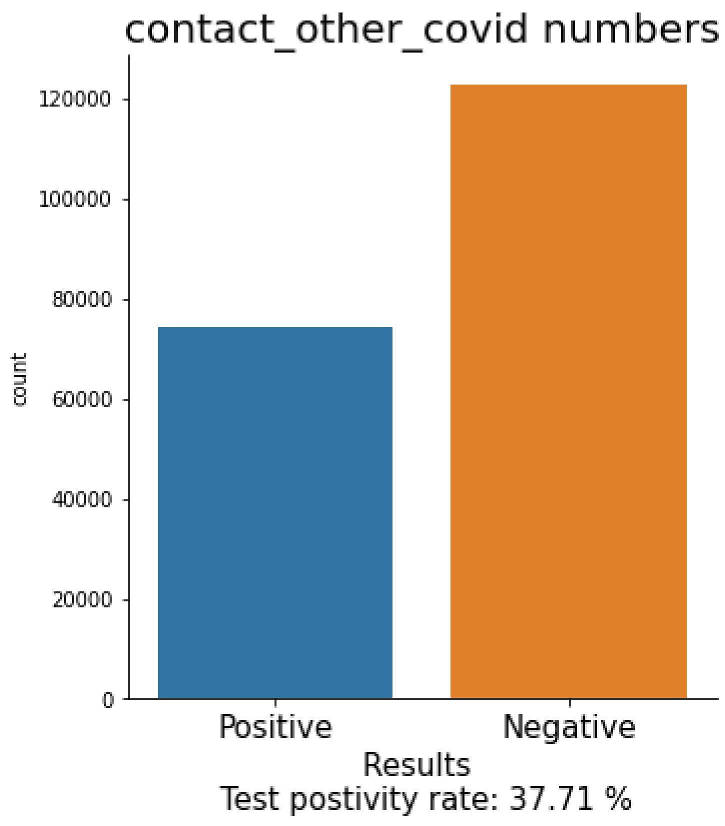


Contact Test positivity

Through this metric we try to understand what are the chances of a person being COVID +ve if he/she recently came in contact with other infected person.

```
# FROM THOSE WHO ARE REPORTED YES
df_contact_other_covid=df[df['contact_other_covid']=='Yes']
sns.catplot('covid_res',data=df_contact_other_covid,kind='count')
plt.title('contact_other_covid numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_contact_other_covid['covid_res'].value_counts()[1]/df_contact_other_covid['cov
plt.xticks(size=15)
```

```
/usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pas
  FutureWarning
(array([0, 1]), <a list of 2 Text major ticklabel objects>)
```



Just contacting other covid+ve person doesn't guarantee Covid positivity.

This might be the indicator if other attribute values are provided

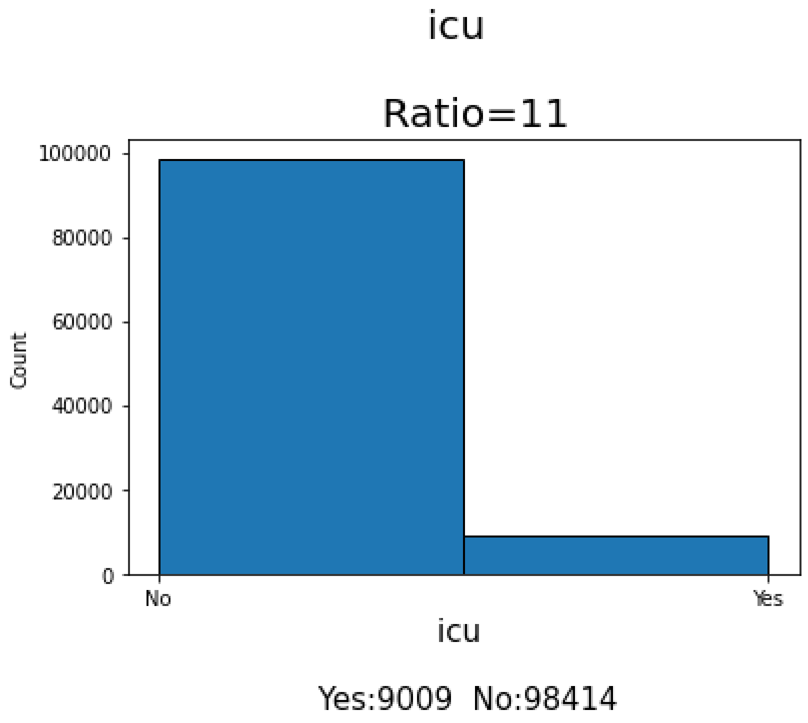
4. ICU reported patients

```
df['icu'].isna().value_counts()
# True indicates the NULL Values
# False indicates total reported data (might be yes or no)
```

```
     True     392269
     False    107423
     Name: icu, dtype: int64
```

```
ax=plt.hist(df['icu'][df['icu'].isna()==False],bins=2,edgecolor='black')
plt.xticks(size=10,)
plt.xlabel('icu \n \n Yes:{}  No:{}'.format(df['icu'].value_counts()[1] , df['icu'].value_
plt.ylabel('Count',size=10)
plt.title('icu \n \n  Ratio={0:.0f}'.format(df['icu'].value_counts()[0]/df['icu'].value_co
          ,size=20)
```

```
     Text(0.5, 1.0, 'icu \n \n  Ratio=11')
```

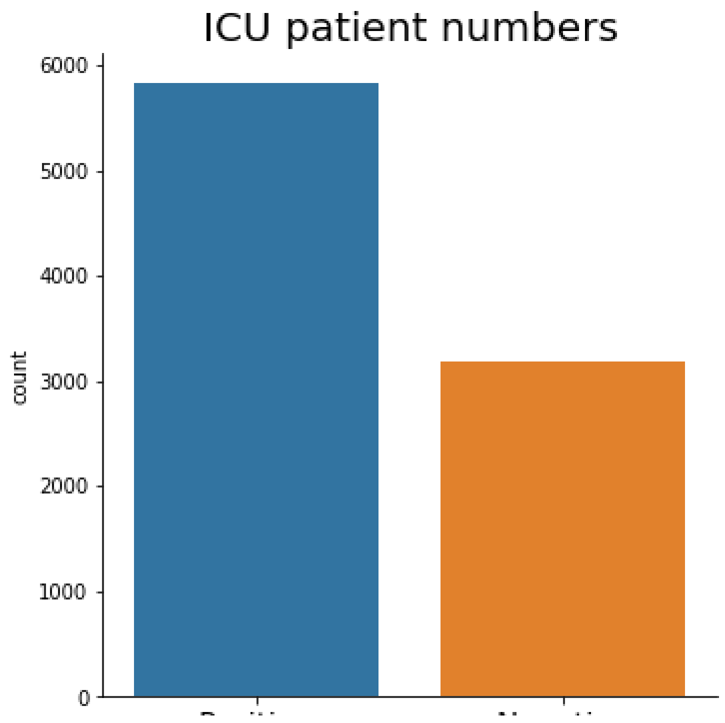


ICU patient's test positivity

Through this metric we try to understand what are the chances of a person being COVID +ve if he/she is in ICU.

```
df_icu=df[df['icu']=='Yes']
sns.catplot('covid_res',data=df_icu,kind='count')
plt.title('ICU patient numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_icu['covid_res'].value_counts()[0]/df_icu['covid_res'].size),size=15)
plt.xticks(size=15)
```

```
/usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pas
  FutureWarning
(array([0, 1]), <a list of 2 Text major ticklabel objects>)
```



here also Covid positivity rate is quite high.

ICU report is the good indicator to predict whether the person is Covid +ve or not

5. Other Disease reports analysis

```
df.columns
```

```
Index(['sex', 'patient_type', 'entry_date', 'date_symptoms', 'date_died',
       'age', 'intubed', 'pneumonia', 'pregnancy', 'diabetes', 'copd',
       'asthma', 'inmsupr', 'hypertension', 'other_disease', 'cardiovascular',
       'obesity', 'renal_chronic', 'tobacco', 'contact_other_covid',
       'covid_res', 'icu'],
      dtype='object')
```

```
fig2=plt.figure(figsize=(22,100))

# ax1=fig2.add_subplot(11,2,1)
df_pneumonia=df[df['pneumonia']=='Yes']
sns.catplot('covid_res',data=df_pneumonia,kind='count')
plt.title('pneumonia patient numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_pneumonia['covid_res'].value_counts()[0]/df_pneumonia['covid_res'].size),size=
plt.xticks(size=10,)

# ax2=fig2.add_subplot(11,2,2)


# ax3=fig2.add_subplot(11,2,3)
df_icu=df[df['diabetes']=='Yes']
sns.catplot('covid_res',data=df_icu,kind='count')
```

```
plt.title('diabetes patient numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_icu['covid_res'].value_counts()[0]/df_icu['covid_res'].size),size=15)
plt.xticks(size=10)

# ax4=fig2.add_subplot(11,2,4)


# ax5=fig2.add_subplot(11,2,5)
df_icu=df[df['copd']=='Yes']
sns.catplot('covid_res',data=df_icu,kind='count')
plt.title('copd patient numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_icu['covid_res'].value_counts()[1]/df_icu['covid_res'].size),size=15)
plt.xticks(size=10)


# ax7=fig2.add_subplot(11,2,7)
df_icu=df[df['asthma']=='Yes']
sns.catplot('covid_res',data=df_icu,kind='count')
plt.title('asthma patient numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_icu['covid_res'].value_counts()[1]/df_icu['covid_res'].size),size=15)
plt.xticks(size=10)

# ax9=fig2.add_subplot(11,2,9)
df_icu=df[df['inmsupr']=='Yes']
sns.catplot('covid_res',data=df_icu,kind='count')
plt.title('inmsupr patient numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_icu['covid_res'].value_counts()[1]/df_icu['covid_res'].size),size=15)
plt.xticks(size=10)

# ax10=fig2.add_subplot(11,2,10)

# ax11=fig2.add_subplot(11,2,11)
df_icu=df[df['hypertension']=='Yes']
sns.catplot('covid_res',data=df_icu,kind='count')
plt.title('hypertension patient numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_icu['covid_res'].value_counts()[0]/df_icu['covid_res'].size),size=15)
plt.xticks(size=10)

# ax12=fig2.add_subplot(11,2,12)

# ax13=fig2.add_subplot(11,2,13)
df_icu=df[df['other_disease']=='Yes']
sns.catplot('covid_res',data=df_icu,kind='count')
plt.title('other_disease patient numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_icu['covid_res'].value_counts()[1]/df_icu['covid_res'].size),size=15)
plt.xticks(size=10)

# ax14=fig2.add_subplot(11,2,14)
# ax15=fig2.add_subplot(11,2,15)
df_icu=df[df['cardiovascular']=='Yes']
sns.catplot('covid_res',data=df_icu,kind='count')
plt.title('cardiovascular patient numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_icu['covid_res'].value_counts()[1]/df_icu['covid_res'].size),size=15)
plt.xticks(size=10)

# ax16=fig2.add_subplot(11,2,16)

# ax17=fig2.add_subplot(11,2,17)
df_icu=df[df['obesity']=='Yes']
sns.catplot('covid_res',data=df_icu,kind='count')
plt.title('obesity patient numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_icu['covid_res'].value_counts()[0]/df_icu['covid_res'].size),size=15)
plt.xticks(size=10)

# ax18=fig2.add_subplot(11,2,18)

# ax19=fig2.add_subplot(11,2,19)
df_icu=df[df['renal_chronic']=='Yes']
sns.catplot('covid_res',data=df_icu,kind='count')
plt.title('renal_chronic patient numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_icu['covid_res'].value_counts()[1]/df_icu['covid_res'].size),size=15)
plt.xticks(size=10)

# ax20=fig2.add_subplot(11,2,20)

# ax21=fig2.add_subplot(11,2,21)
df_icu=df[df['tobacco']=='Yes']
sns.catplot('covid_res',data=df_icu,kind='count')
plt.title('tobacco patient numbers',size=20)
plt.xlabel('Results \n Test postivity rate: {0:.2f} %'.format(
    100* df_icu['covid_res'].value_counts()[1]/df_icu['covid_res'].size),size=15)
plt.xticks(size=10)

# ax22=fig2.add_subplot(11,2,22)
```

```
/usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pass
  FutureWarning
/usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pass
  FutureWarning
/usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pass
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  FutureWarning
/usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pass
  FutureWarning
(array([0, 1]), <a list of 2 Text major ticklabel objects>)
<Figure size 1584x7200 with 0 Axes>
```
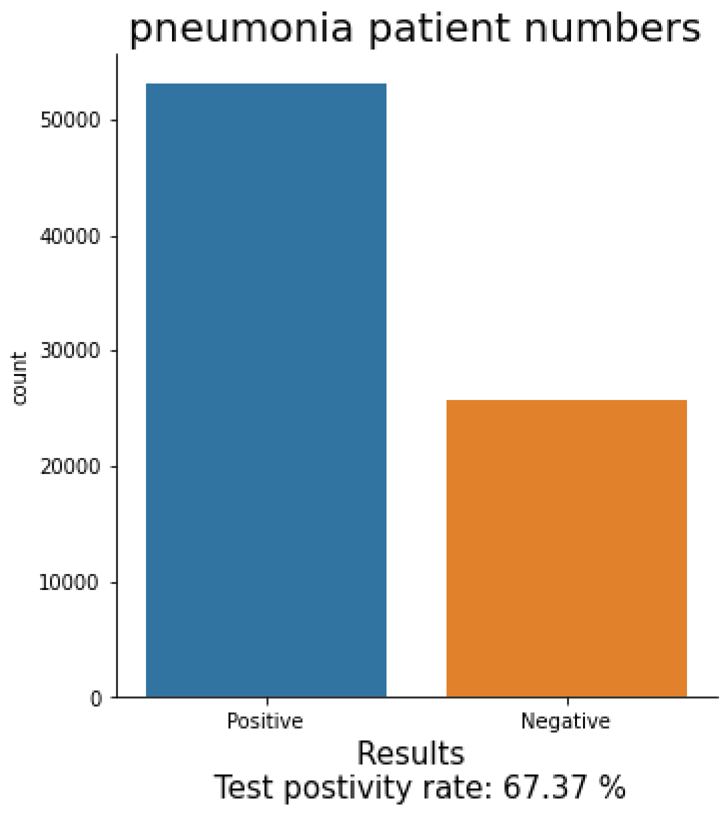
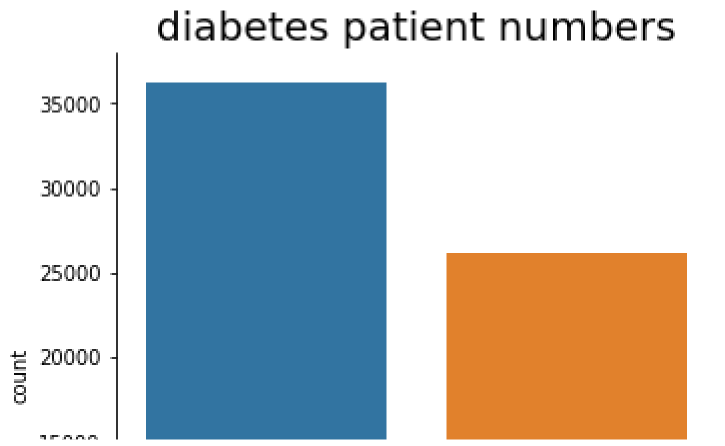
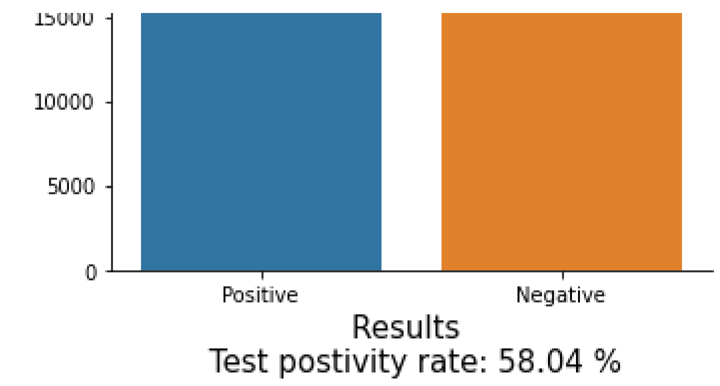
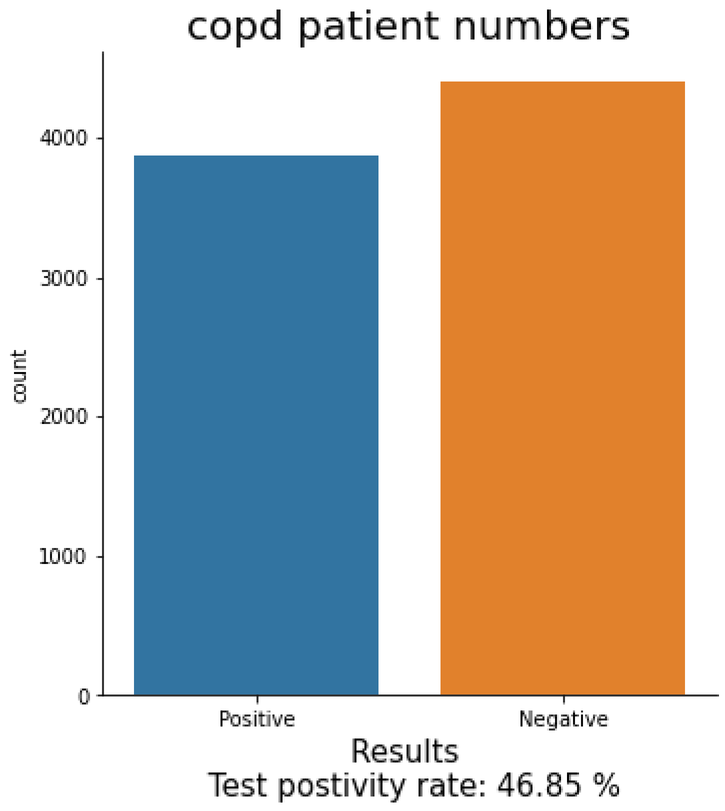
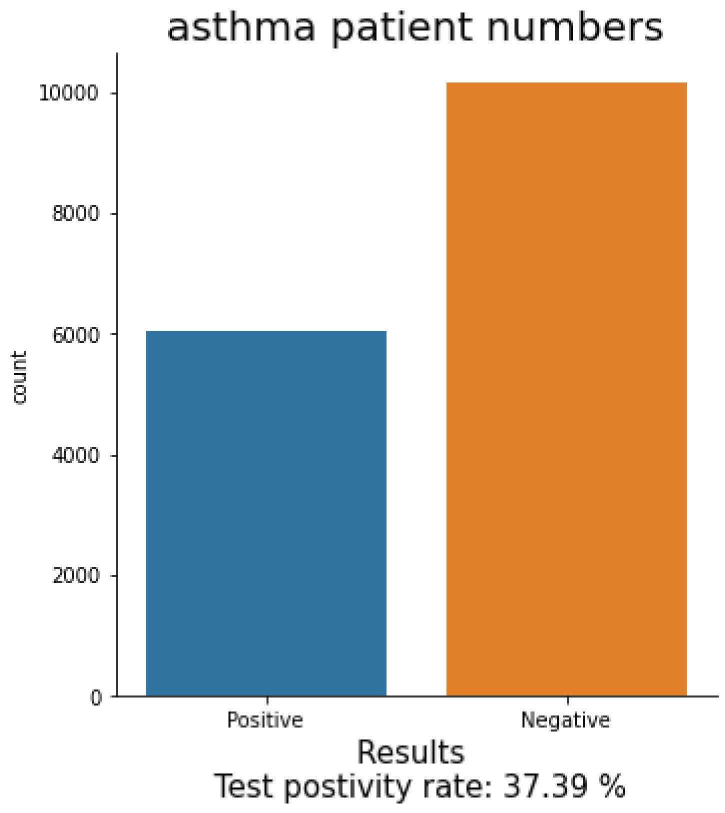



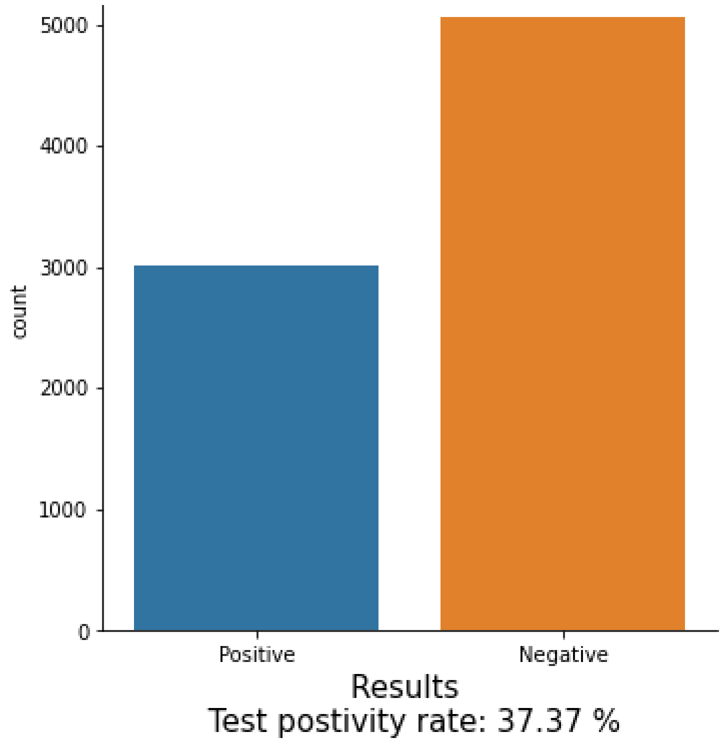


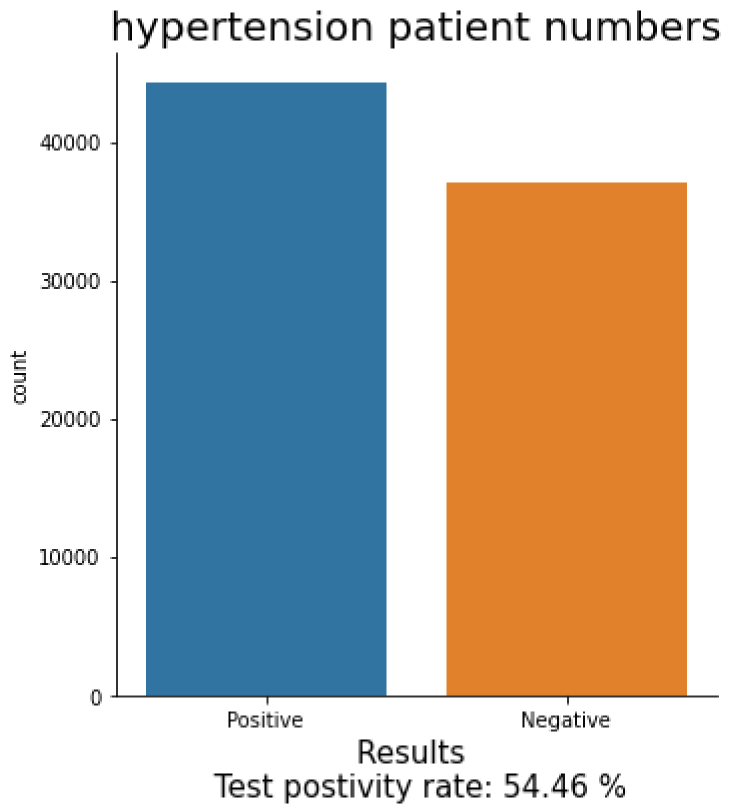


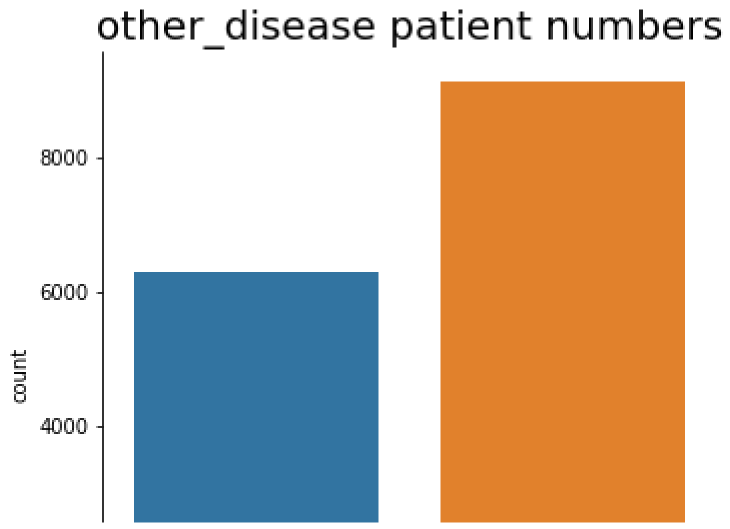


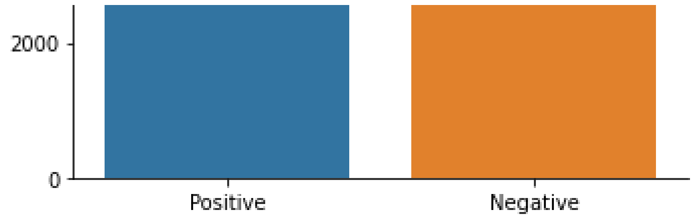


inmsupr patient numbers

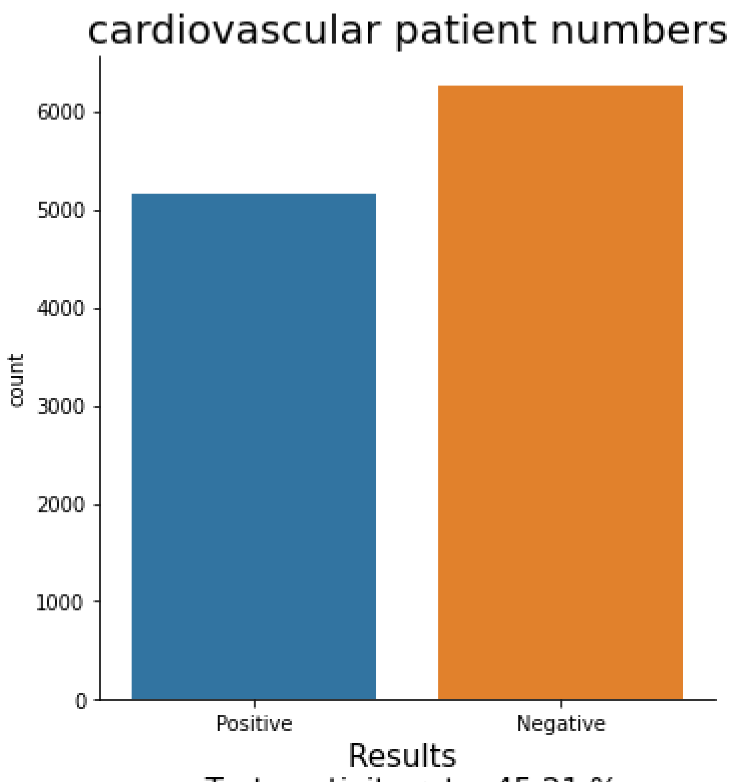

5000
4000
3000
2000
1000
0
count
Positive
Negative
Results
Test postivity rate: 37.37 %


hypertension patient numbers
40000
30000
20000
10000
0
count
Positive
Negative
Results
Test postivity rate: 54.46 %

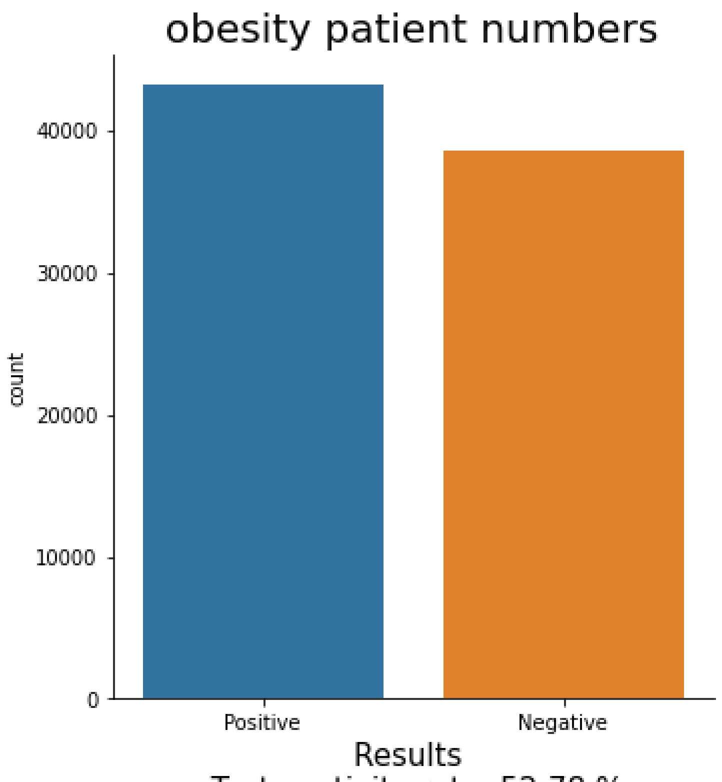

other_disease patient numbers
8000
6000
4000
count



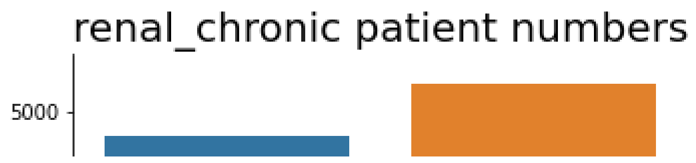
Test postivity rate: 40.82 %

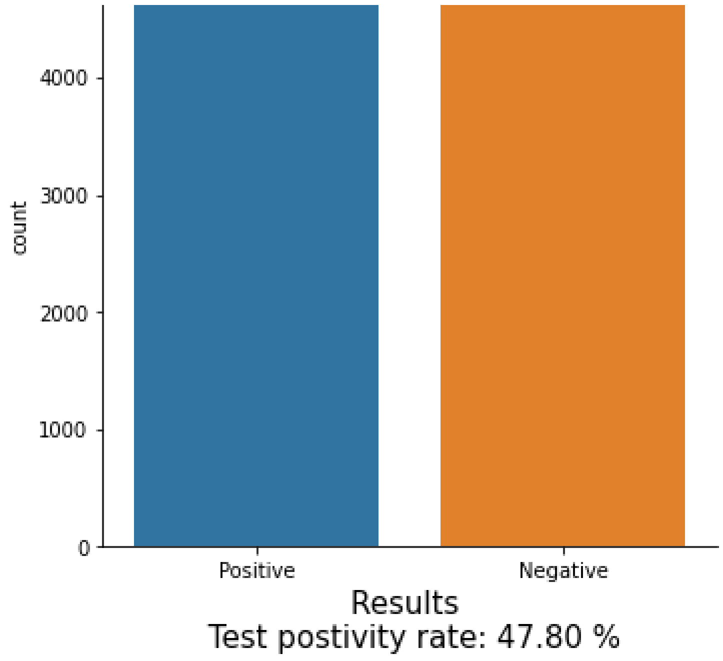


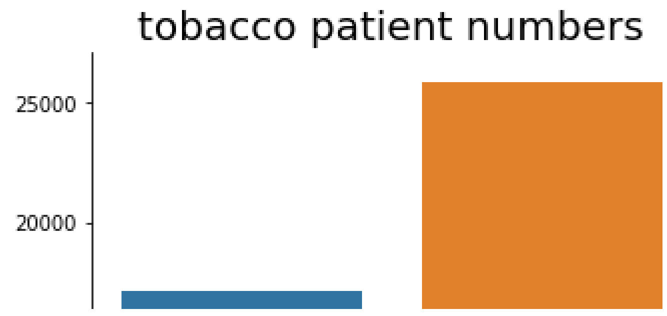
Test postivity rate: 45.21 %



Test postivity rate: 52.78 %







Observations

There is a high chance of a person being affected by Covid 19, if he/she is a pneumonia patient (67.37 %)

Those patient who are diabetic, have high chance of being covid positive (58.04 %)

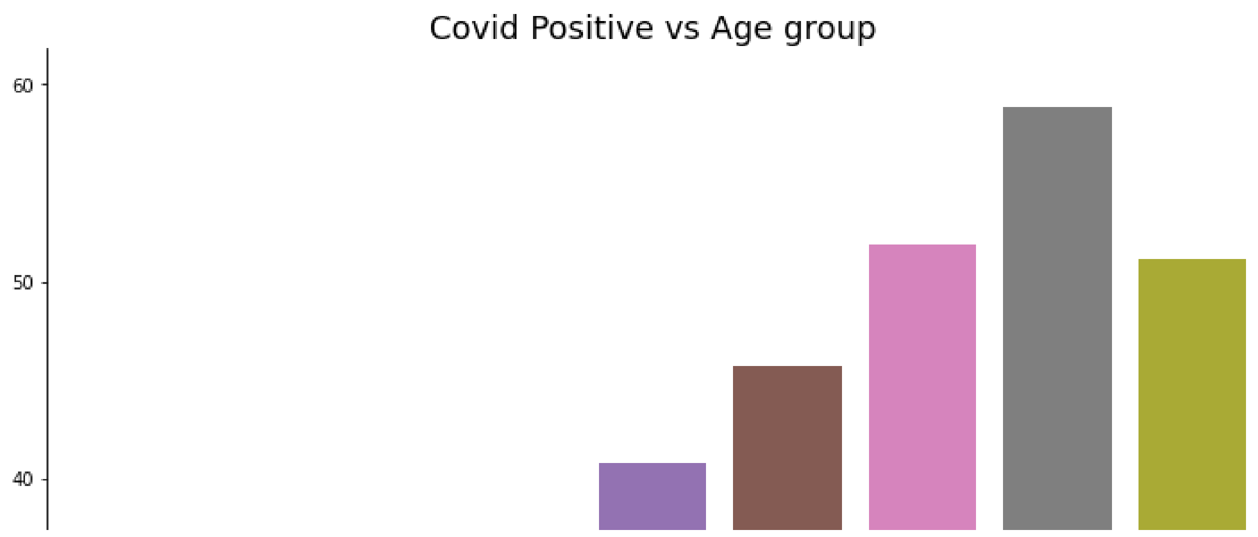
Hypertensed and obese patients have decent 50 % probability of being Covid positive (54 % and 52 % respectively)

Let's analyse now, how people of different age groups relates with Covid positivity

6. Age band

```
df1=df
df1
df1.iloc[:,-2]=df.iloc[:,-2].replace('Positive',1)
df1.iloc[:,-2]=df.iloc[:,-2].replace('Negative',0)
# df1.iloc[:,-2]=df.iloc[:,-2].replace('Results awaited',3)
df1
df1 = df1[df1['covid_res']!=3]


def age_band(age):

    if age<2:
        return '0-2'
    elif (age>1) and (age<11):
        return '2-10'
    elif (age>10 and age<21):
        return '10-20'
    elif (age>20 and age<31):
        return '20-30'
    elif (age>30 and age<41):
        return '30-40'
    elif (age>40 and age<51):
        return '40-50'
    elif (age>50 and age<61):
        return '50-60'
    elif (age>60 and age<81):
        return '60-80'
    else:
        return 'Above 80'


# df_pos=df1[df1['covid_res']=='Positive']
df1['Age_band']=df1['age'].apply(age_band)
df1['Count']=1
df_Age_Band = df1.groupby('Age_band')['covid_res','Count'].sum().reset_index()
df_Age_Band['Percentage_covid_positive']=100*df_Age_Band.covid_res/df_Age_Band.Count
#df_Age_Band.sort_values(by='covid_res',ascending=False).reset_index(drop=True)
df_Age_Band.sort_values(by='Percentage_covid_positive',ascending=False).reset_index(drop=T

sns.catplot(x = 'Age_band', y ='Percentage_covid_positive', data = df_Age_Band, kind= 'bar
plt.title('Covid Positive vs Age group', size = 18)
```

```
/usr/local/lib/python3.7/dist-packages/ipykernel_launcher.py:4: FutureWarning: Index
  after removing the cwd from sys.path.
/usr/local/lib/python3.7/dist-packages/seaborn/categorical.py:3747: UserWarning: The
  warnings.warn(msg, UserWarning)
Text(0.5, 1.0, 'Covid Positive vs Age group')
```



Observations

There is high chance of infection to the people of age group 60-80

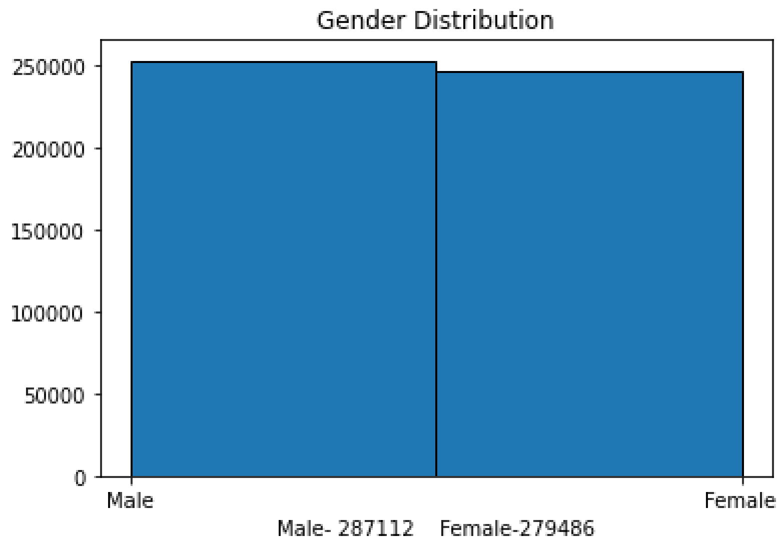
Senior citizens (age > 50) are most likely to be caught by Covid 19 virus.

Does Covid-19 positivity depends on Gender?, Lets analyse

7. Sex

```
df['sex'].replace(1,'Female',inplace=True)
df['sex'].replace(2,'Male',inplace=True)

plt.hist(df['sex'],bins=2,edgecolor='black')
plt.title('Gender Distribution')
plt.xlabel('Male- 287112    Female-279486')
```

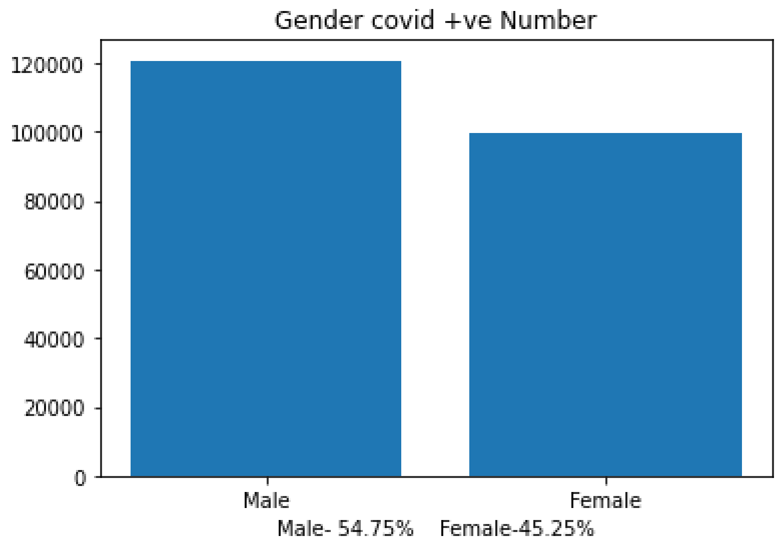
```
Text(0.5, 0, 'Male- 287112    Female-279486')
```



```
df_pos=df[df['covid_res']==1]
```

```
#df_pos
pos_male = df_pos[df_pos['sex']=='Male']
pos_female = df_pos[df_pos['sex']=='Female']
#pos_female


pos=[len(pos_male),len(pos_female)]
gen=['Male','Female']
plt.bar(gen,pos)#,edgecolor='black')
plt.title('Gender covid +ve Number')
male_pos_percent = (len(pos_male)/len(df_pos))*100
female_pos_percent = (len(pos_female)/len(df_pos))*100
print(male_pos_percent)
print(female_pos_percent)
plt.xlabel('Male- 54.75%    Female-45.25%')
```

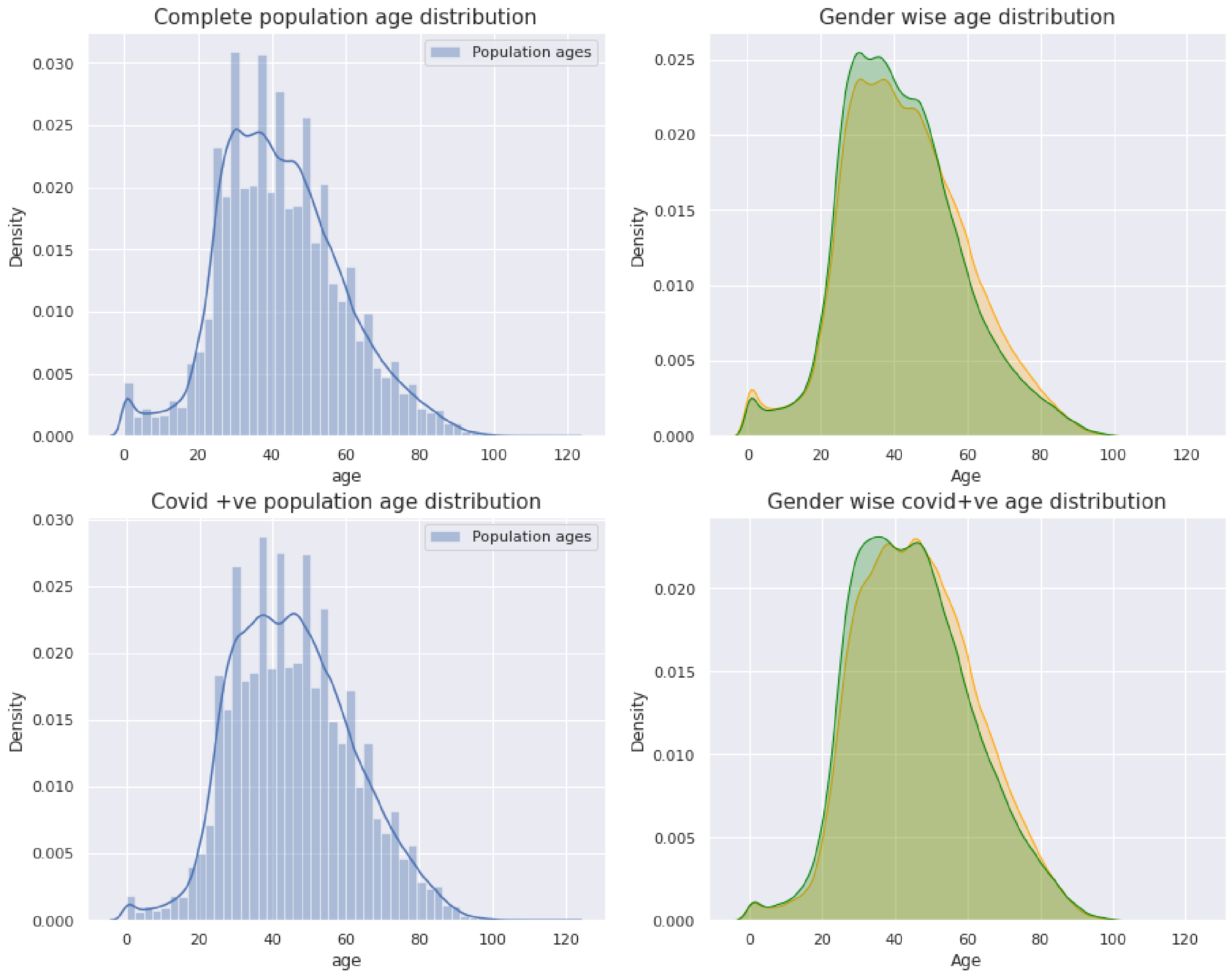
```
54.74514744603616
45.25485255396384
Text(0.5, 0, 'Male- 54.75%    Female-45.25%')
```



```
sns.set()
fig1=plt.figure(figsize=(15,12))
ax1=fig1.add_subplot(221)
a=sns.distplot(df['age'],ax=ax1,label='Population ages')
ax1.legend()
ax1.set_title('Complete population age distribution',size=15)
ax2=fig1.add_subplot(222)

df_m=df[df['sex']=='Male']
df_f=df[df['sex']=='Female']

b=sns.kdeplot(df_m['age'],shade=True,ax=ax2,label='Male age distribution',color='orange')
c=sns.kdeplot(df_f['age'],ax=ax2,label='Female age distribution',color='green',shade=True)
ax2.set_xlabel('Age')
ax2.set_title('Gender wise age distribution',size=15)
ax3=fig1.add_subplot(223)
a=sns.distplot(df_pos['age'],ax=ax3,label='Population ages')
ax3.legend()
ax3.set_title('Covid +ve population age distribution',size=15)
ax4=fig1.add_subplot(224)
```

```
df_m_pos=df_pos[df_pos['sex']=='Male']
df_f_pos=df_pos[df_pos['sex']=='Female']

b=sns.kdeplot(df_m_pos['age'],shade=True,ax=ax4,label='Male covid+ve age distribution',col
c=sns.kdeplot(df_f_pos['age'],ax=ax4,label='Female covid+ve age distribution',color='green
ax4.set_xlabel('Age')
ax4.set_title('Gender wise covid+ve age distribution',size=15)
```

```
/usr/local/lib/python3.7/dist-packages/seaborn/distributions.py:2557: FutureWarning:
  warnings.warn(msg, FutureWarning)
/usr/local/lib/python3.7/dist-packages/seaborn/distributions.py:2557: FutureWarning:
  warnings.warn(msg, FutureWarning)
Text(0.5, 1.0, 'Gender wise covid+ve age distribution')
```



From the above left graph, we can see that we have a bimodal graph with high distribution from 20-60 years. There is also a peak in the lower section of the graph meaning we have high number of infants in our distribution.

On the right, we see that the distribution for both women and men is nearly identical. This is great because it will let us understand the body responses of the sexes with an identical age distribution.

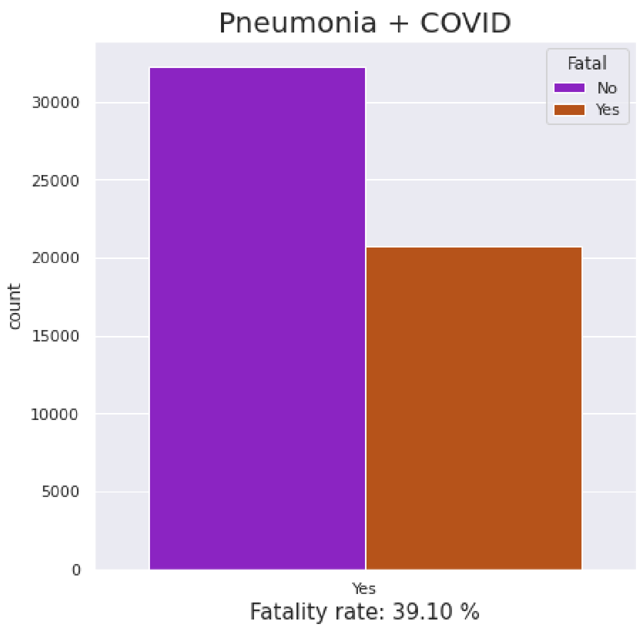
9. Fatality

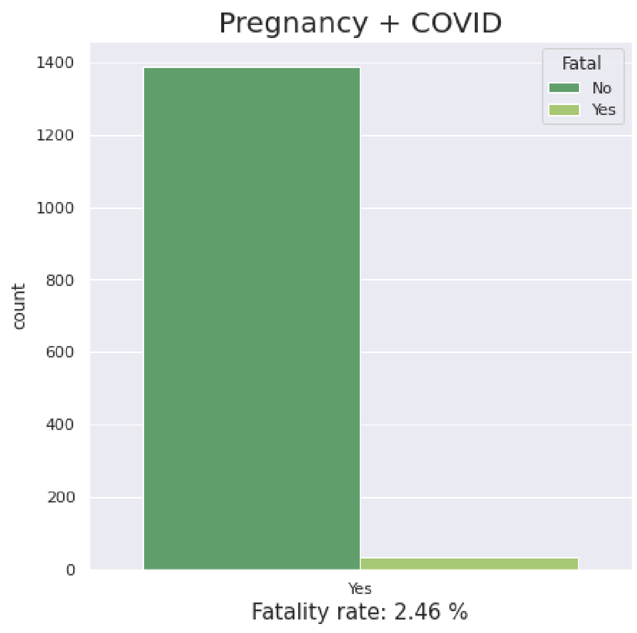
```
df_pos=df[df['covid_res']==1]
df_pos.reset_index(drop=True,inplace=True)
df_pos['Fatal']=np.nan

i=0
for i in range(len(df_pos)):
    if df_pos['date_died'][i]!='NA':
        df_pos['Fatal'][i]='Yes'

df_pos['Fatal']=df_pos['Fatal'].fillna('No')
df_pos['Fatal']
```

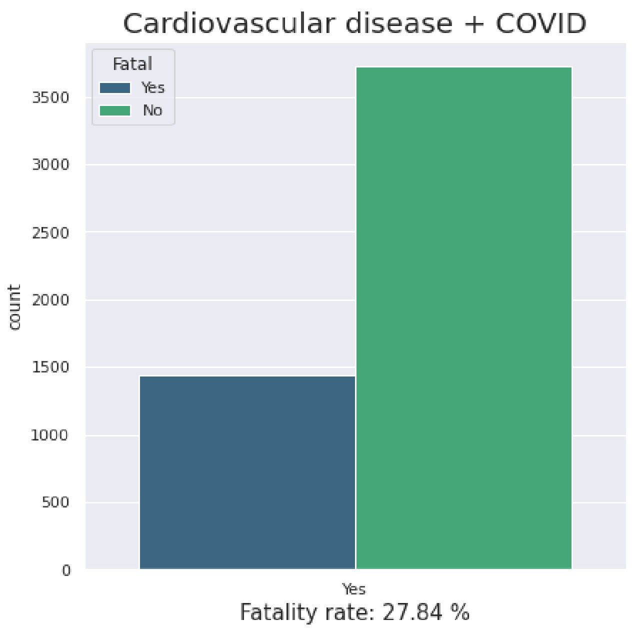
```
/usr/local/lib/python3.7/dist-packages/ipykernel_launcher.py:3: SettingWithCopyWarnin
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/us
  This is separate from the ipykernel package so we can avoid doing imports until
/usr/local/lib/python3.7/dist-packages/ipykernel_launcher.py:8: SettingWithCopyWarnin
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/us

/usr/local/lib/python3.7/dist-packages/pandas/core/indexing.py:670: SettingWithCopyWa
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/us
  iloc._setitem_with_indexer(indexer, value)
/usr/local/lib/python3.7/dist-packages/pandas/core/series.py:1009: SettingWithCopyWar
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/us
  self.loc[key] = value
/usr/local/lib/python3.7/dist-packages/IPython/core/interactiveshell.py:2882: Setting
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/us
  exec(code_obj, self.user_global_ns, self.user_ns)
/usr/local/lib/python3.7/dist-packages/ipykernel_launcher.py:10: SettingWithCopyWarni
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/us
  # Remove the CWD from sys.path while we load stuff.
0          No
1          No
2          No
```

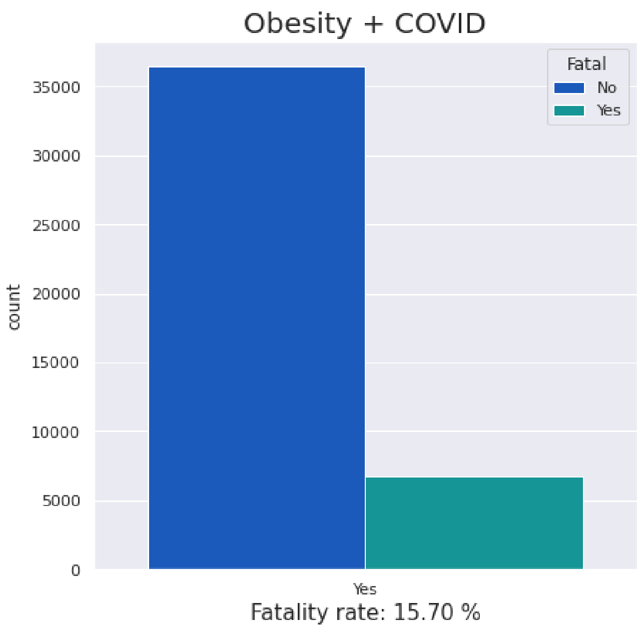
```
3           No
4          Yes
          ...
220652    Yes
220653     No
220654     No
220655     No
220656     No
Name: Fatal, Length: 220657, dtype: object
```

```
fig2=plt.figure(figsize=(15,15))
ax1=fig2.add_subplot(2,2,1)
ax2=fig2.add_subplot(2,2,2)
ax3=fig2.add_subplot(2,2,3)
ax4=fig2.add_subplot(2,2,4)
df_pneu=df_pos[df_pos['pneumonia']=='Yes']
df_preg=df_pos[df_pos['pregnancy']=='Yes']
df_card=df_pos[df_pos['cardiovascular']=='Yes']
df_obes=df_pos[df_pos['obesity']=='Yes']


sns.countplot('pneumonia',data=df_pneu,hue='Fatal',ax=ax1,palette='gnuplot')
sns.countplot('pregnancy',data=df_preg,hue='Fatal',ax=ax2,palette='summer')
sns.countplot('cardiovascular',data=df_card,hue='Fatal',ax=ax3,palette='viridis')
sns.countplot('obesity',data=df_obes,hue='Fatal',ax=ax4,palette='winter')

ax1.set_title('Pneumonia + COVID',size=20)
ax2.set_title('Pregnancy + COVID',size=20)
ax3.set_title('Cardiovascular disease + COVID',size=20)
ax4.set_title('Obesity + COVID',size=20)






ax1.set_xlabel('Fatality rate: {0:.2f} %'.format(100*df_pneu['Fatal'].value_counts()[1]/df


ax2.set_xlabel('Fatality rate: {0:.2f} %'.format(100*df_preg['Fatal'].value_counts()[1]/df


ax3.set_xlabel('Fatality rate: {0:.2f} %'.format(100*df_card['Fatal'].value_counts()[1]/df


ax4.set_xlabel('Fatality rate: {0:.2f} %'.format(100*df_obes['Fatal'].value_counts()[1]/df
     /usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pas
       FutureWarning
     /usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pas
       FutureWarning
     /usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pas
       FutureWarning
     /usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pas
       FutureWarning
     Text(0.5, 0, 'Fatality rate: 15.70 %')
```









Note:

Dropping date_died column as no relation with predicting covid positive.

Columns- pregnancy, intubed, contct_other_covid have more than 50% null values so dropping

```
df=df.drop(columns=['date_died','pregnancy','contact_other_covid','intubed','icu'])
```

Feature Extraction from date_symptom and entry_date

```
df['delta']=abs(df['entry_date']-df['date_symptoms'])
df.loc[1,'delta']
df['delta'] = df['delta'].dt.days.astype('int16')  #Converting Timedelta type to integer d
df['delta']
```

```
    0          60
    1           2
    2         152
    3         170
    4           0
             ...
    499687      6
    499688      5
    499689      3
    499690      2
    499691      8
    Name: delta, Length: 499692, dtype: int16
```

Note:

Dropping columns entry_date and date_symptoms

```
df=df.drop(columns=['entry_date','date_symptoms'])
```

```
df.columns
```

```
    Index(['sex', 'patient_type', 'age', 'pneumonia', 'diabetes', 'copd', 'asthma',
           'inmsupr', 'hypertension', 'other_disease', 'cardiovascular', 'obesity',
           'renal_chronic', 'tobacco', 'covid_res', 'delta'],
          dtype='object')
```

Note:

There are few Null values present in columns that are categorical variables so we will drop Null values

```
df=df.dropna()
```

```
len(df)
```

```
    496291
```

```
df
```

	sex	patient_type	age	pneumonia	diabetes	copd	asthma	inmsupr	hyper
0	Male	1	27	No	No	No	No	No	
1	Male	1	24	No	No	No	No	No	
2	Female	2	54	No	No	No	No	No	
3	Male	2	30	Yes	No	No	No	No	
4	Female	2	60	No	Yes	No	No	No	
...	...	...	...	...	...	...	...	...	
499687	Male	1	77	Yes	No	No	No	No	
499688	Male	2	63	Yes	No	No	No	No	
499689	Female	1	25	No	No	No	No	No	
499690	Female	1	45	No	No	No	No	No	
499691	Female	1	51	No	No	No	No	No	

496291 rows × 16 columns

```
from sklearn.preprocessing import OrdinalEncoder
oe = OrdinalEncoder()
```

```
X_=df[['sex', 'patient_type', 'pneumonia', 'diabetes', 'copd', 'asthma',
       'inmsupr', 'hypertension', 'other_disease', 'cardiovascular', 'obesity',
       'renal_chronic', 'tobacco']]
X_
```

	sex	patient_type	pneumonia	diabetes	copd	asthma	inmsupr	hypertensi
0	Male	1	No	No	No	No	No	N
1	Male	1	No	No	No	No	No	N
2	Female	2	No	No	No	No	No	N
3	Male	2	Yes	No	No	No	No	N
4	Female	2	No	Yes	No	No	No	Y
...	...	...	...	...	...	...	...	
499687	Male	1	Yes	No	No	No	No	N
499688	Male	2	Yes	No	No	No	No	Y
499689	Female	1	No	No	No	No	No	N
499690	Female	1	No	No	No	No	No	Y
499691	Female	1	No	No	No	No	No	N

496291 rows × 13 columns

```
oe.fit(X_)
X_=oe.transform(X_)
#X_
```

```
X_
```

```
array([[1., 0., 0., ..., 0., 0., 0.],
       [1., 0., 0., ..., 0., 0., 0.],
       [0., 1., 0., ..., 1., 0., 0.],
       ...,
       [0., 0., 0., ..., 0., 0., 0.],
       [0., 0., 0., ..., 0., 0., 0.],
       [0., 0., 0., ..., 0., 0., 0.]])
```

```
import numpy as np
arr=np.array(df[['delta','age']])
arr
```

```
array([[ 60,  27],
       [  2,  24],
       [152,  54],
       ...,
       [  3,  25],
       [  2,  45],
       [  8,  51]])
```

```
arr_=arr.reshape(496291,2)
X=np.append(arr_,X_,axis=1)
X
```

```
array([[ 60.,  27.,   1., ...,   0.,   0.,   0.],
       [  2.,  24.,   1., ...,   0.,   0.,   0.],
       [152.,  54.,   0., ...,   1.,   0.,   0.],
       ...,
       [  3.,  25.,   0., ...,   0.,   0.,   0.],
       [  2.,  45.,   0., ...,   0.,   0.,   0.],
       [  8.,  51.,   0., ...,   0.,   0.,   0.]])
```

```
y=np.array(df['covid_res'])
y=y.reshape(-1,1)
oe.fit(y)
y=oe.transform(y)
# y.reshape(496291,1)
print(type(y))
y
```

```
<class 'numpy.ndarray'>
array([[1.],
       [1.],
       [1.],
       ...,
       [0.],
       [0.],
       [0.]])
```