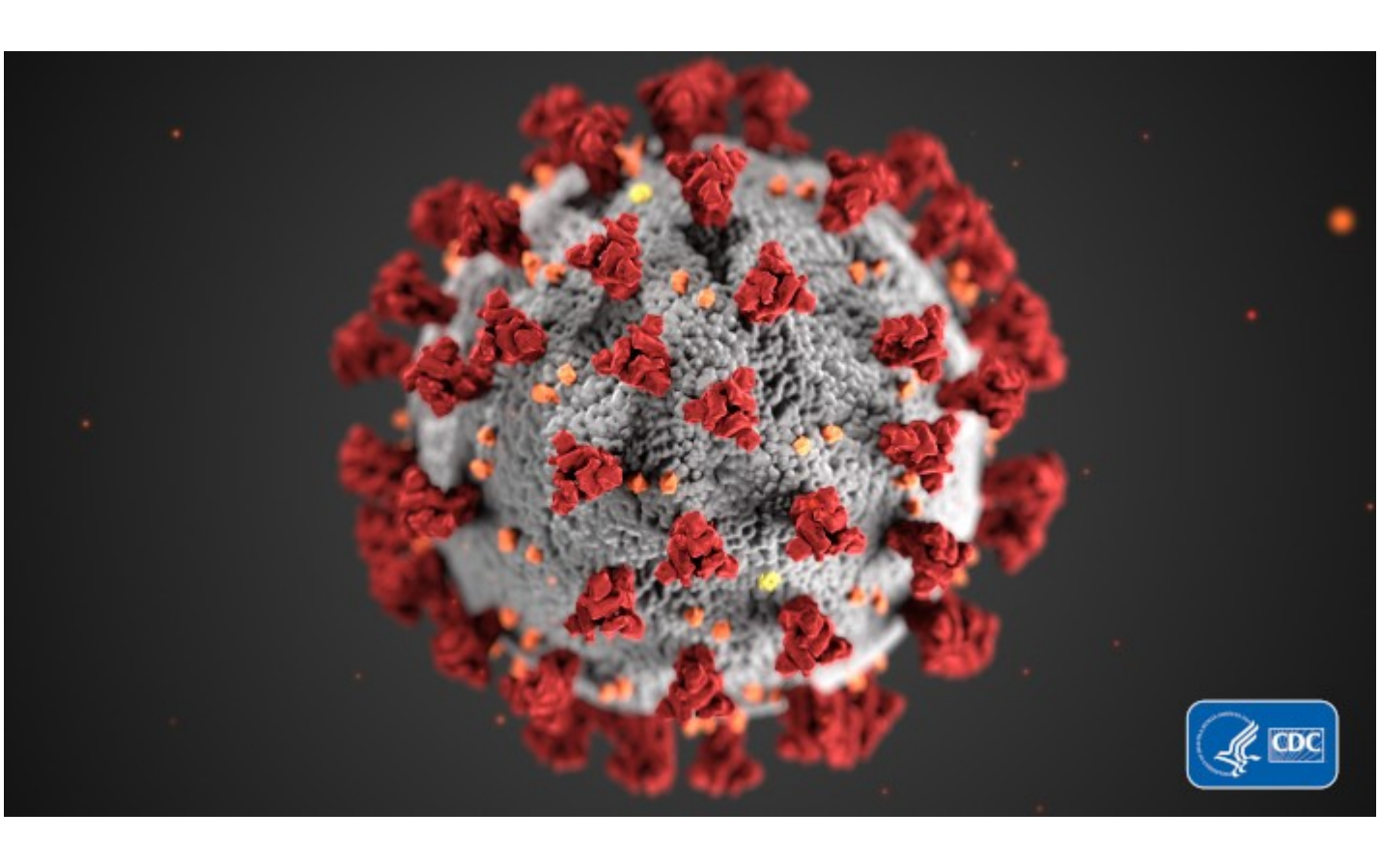
Notes:

COVID-19 was first discovered in December of 2019 in the Wuhan province of China and has since been classified as a pandemic. COVID-19 is the disease caused by coronavirus (SARS CoV-2), which primarly effects the upper respiratory tract of its victims. In the time of its initial discovery to today, around 38 million cases have been reported and over a million cases of these cases have resulted in death worldwide. In addition to the staggering mortality rate, this pandemic has also crippled the global economy, temporarly stopped most non-domestic travel, and is the prime cause of countless lost jobs.

Due to this disease being caused by a virus, the rate of mutation is high and this poses as a serious challenge in all attempts by virology researchers and scientists to create a vaccine. Mutations generally occur to allow the virus to better adapt to its climate and since this is a dataset released by the Mexican government, the analysis gathered from this dataset can only valid for Mexico and its neighboring regions.

Some questions we are looking to answer while analyzing

Thank you to Tanmoy Mukherjee for uploading this dataset on Kaggle.



Gathering our data and importing the nescessary packages

In [1]:
```
import pandas as pd, numpy as np, matplotlib.pyplot as plt, seaborn as sns
from sklearn.linear_model import LinearRegression
pd.set_option('display.max_columns', None)
df = pd.read_csv('covid.csv')
df.head(5)
```

Out[1]:

	id	sex	patient_type	entry_date	date_symptoms	date_died	intubed	pneumonia	age	pregnancy	diabetes	copd	asthma	inm
0	16169f	2	1	04-05-2020	02-05-2020	9999-99-99	97	2	27	97	2	2	2	
1	1009bf	2	1	19-03-2020	17-03-2020	9999-99-99	97	2	24	97	2	2	2	
2	167386	1	2	06-04-2020	01-04-2020	9999-99-99	2	2	54	2	2	2	2	
3	0b5948	2	2	17-04-2020	10-04-2020	9999-99-99	2	1	30	97	2	2	2	
4	0d01b5	1	2	13-04-2020	13-04-2020	22-04-2020	2	2	60	2	1	2	2	

Cleaning up our dataset and creating visuals - Since data isnt always created in a manner that can be properly used, we must format and clean up much of it. These steps include normalizing and standardizing our data, filling in null/missing values, and changing the datatypes to allow for proper analysis

-Data descriptors Sex 1 = Female 2 = Male Patient_type 1 = Outpatient 2 = Inpatient Colums with descriptors such as intubed, pneumonia, diabetes, copd...etc. 1 = Yes 2 = No (97,98,99, etc) = No Data/Unknown Now that we are familiar with the information the dataset is conveying to us, lets move on to the cleaning up steps!

In [2]:
```
df.info()
```

```
<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: 90.8+ MB
```

Lets begin by fixing the colums which have a Date Object within them; entry_date, date_symptoms, and date_died. The entry_date and date_symptoms columns are straight forward, but the date_died has a blank value of 99-99-9999 if the patient survived. We will replace the dates of the survivors to NaN for better visualization.

In [3]:
```
date_objects=['entry_date','date_symptoms']
for dates in date_objects:
    df[dates]=pd.to_datetime(df[dates],infer_datetime_format=True)
df['date_died'].replace('9999-99-99','Not Applicable',inplace=True)
```

Since we know that the values of 97,98, and 99 are codes for null values, lets replace them. We have to make sure to not effect the ages column since they could have actual ages with those values. Also, we have no need for the id column so we will drop it. The column name for covid_res is not ideally labeled so we will change it to test_result.

In [4]:
```
# select the needed columns in an organizable order
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']]

# replacing the null values, and assigning readable values to the other entries
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')

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

# renaming the covid_res and sex columns
df.rename(columns={'covid_res':'test_result', 'sex':'gender'},inplace=True)
```

Lets take a look at our edited dataframe

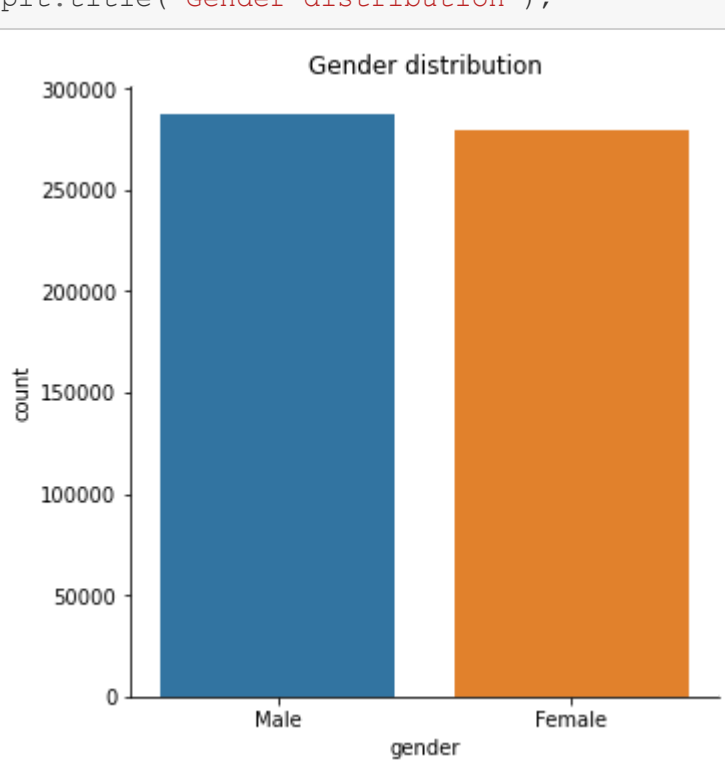
In [5]:
```
df.head(5)
```

Out[5]:

	gender	patient_type	entry_date	date_symptoms	date_died	age	intubed	pneumonia	pregnancy	diabetes	copd	asthma	inmsupr
0	Male	1	2020-04-05	2020-02-05	Not Applicable	27	NaN	No	NaN	No	No	No	No
1	Male	1	2020-03-19	2020-03-17	Not Applicable	24	NaN	No	NaN	No	No	No	No
2	Female	2	2020-06-04	2020-01-04	Not Applicable	54	No	No	No	No	No	No	No
3	Male	2	2020-04-17	2020-10-04	Not Applicable	30	No	Yes	NaN	No	No	No	No
4	Female	2	2020-04-13	2020-04-13	22-04-2020	60	No	No	No	Yes	No	No	No

Now that our dataset is cleaned up, lets take a look at some of the data to gauge the bias.

In [6]:
```
sns.catplot('gender',data=df,kind='count')
plt.title('Gender distribution');
```

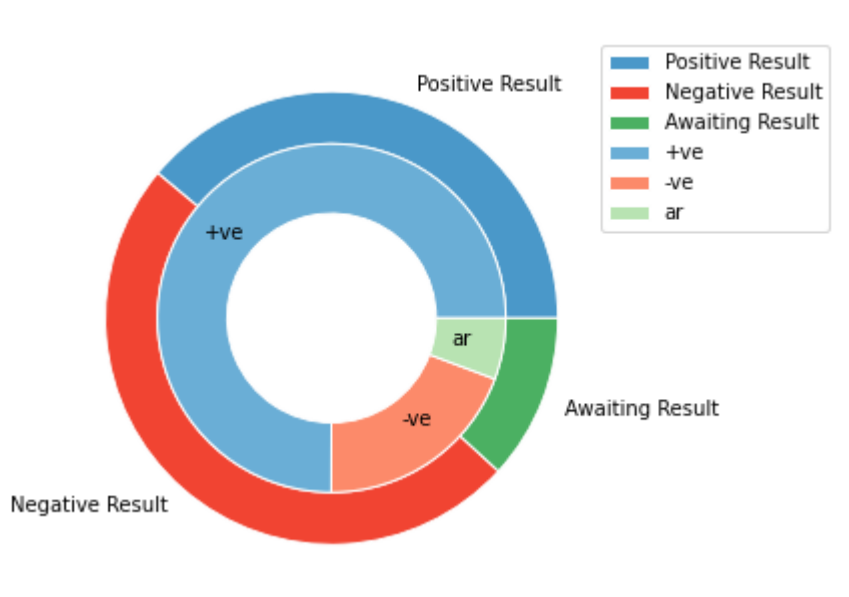


The ratio of male to female is pretty equal, which shows that there is no general bias in reporting.

To begin our analysis we will first create a time series to look at when patients originally contracted symptoms and the date of their hospital entry.

In [ ]:

In [ ]:
```
ved = len(df.query('test_result == "Positive" and date_died != "Not Applicable"'))
ve = len(df.query('test_result == "Positive"'))
ned = len(df.query('test_result == "Negative" and date_died != "Not Applicable"'))
ne = len(df.query('test_result == "Negative"'))
nod = len(df.query('test_result == "Results awaited" and date_died != "Not Applicable"'))
no = len(df.query('test_result == "Results awaited"'))

fig, ax = plt.subplots(subplot_kw=dict(polar=True))
# Make data: I have 3 groups and 7 subgroups
group_names=['Positive Result', 'Negative Result', 'Awaiting Result']
group_size=[ve,ne,no]
subgroup_names=['+ve', '-ve', 'ar']
subgroup_size=[ved, ned, nod]

# Create colors
a, b, c=[plt.cm.Blues, plt.cm.Reds, plt.cm.Greens]

# First Ring (outside)
fig, ax = plt.subplots()
ax.axis('equal')
mypie, _ = ax.pie(group_size, radius=1.3, labels=group_names, colors=
[a(0.6), b(0.6), c(0.6)] )
plt.setp( mypie, width=0.3, edgecolor='white')

# Second Ring (Inside)
mypie2, _ = ax.pie(subgroup_size, radius=1.3-0.3,
labels=subgroup_names, labeldistance=0.7, colors=[a(0.5), b(0.4),
c(0.3)])
plt.setp(mypie2, width=0.4, edgecolor='white')
plt.margins(0,0)

plt.legend(loc=(0.9, .7))
# show it
plt.show()
```

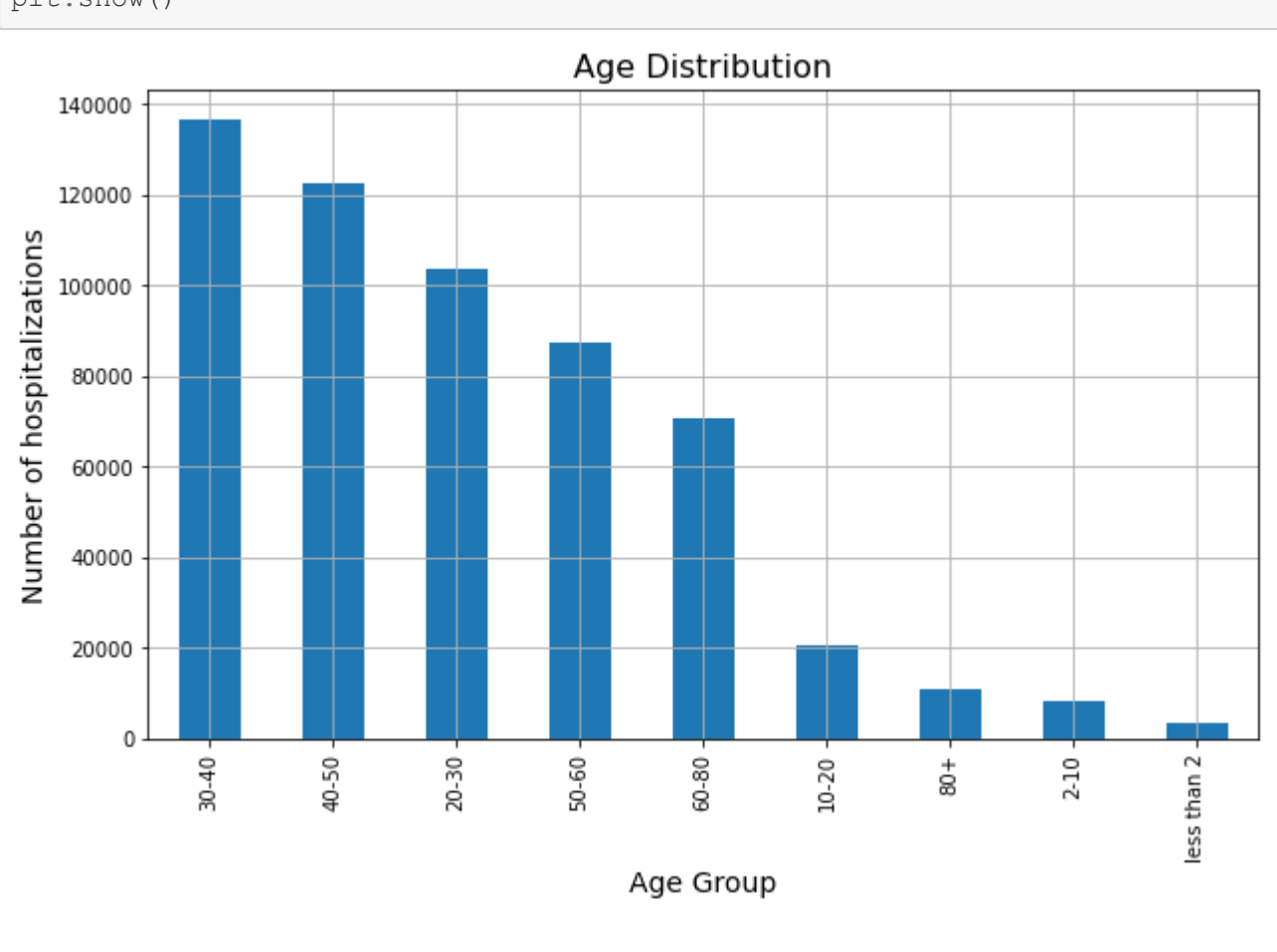


This 2-layer pie chart shows us the test result status on the outter ring, and assocciated mortality on the inner ring. This isnt rocket science but the coorelation between a positive test result and mortality is very clear to see.

Lets look at hospitalizations by age group

In [8]:
```
age_band = [0, 2, 10, 20, 30, 40, 50, 60, 80, 150]
bin_labels = ['less than 2', '2-10', '10-20', '20-30','30-40','40-50','50-60', '60-80', '80+']
df['age_band'] = pd.cut(df.age, age_band, labels=bin_labels)
```

In [10]:
```
hp = df.age_band.value_counts()
hp.plot(x=hp.index, y=hp, kind='bar', figsize=(10, 6), grid=True)
plt.title("Age Distribution", fontsize=16)
plt.ylabel('Number of hospitalizations', fontsize=14)
plt.xlabel('Age Group', fontsize=14)
plt.show()
```

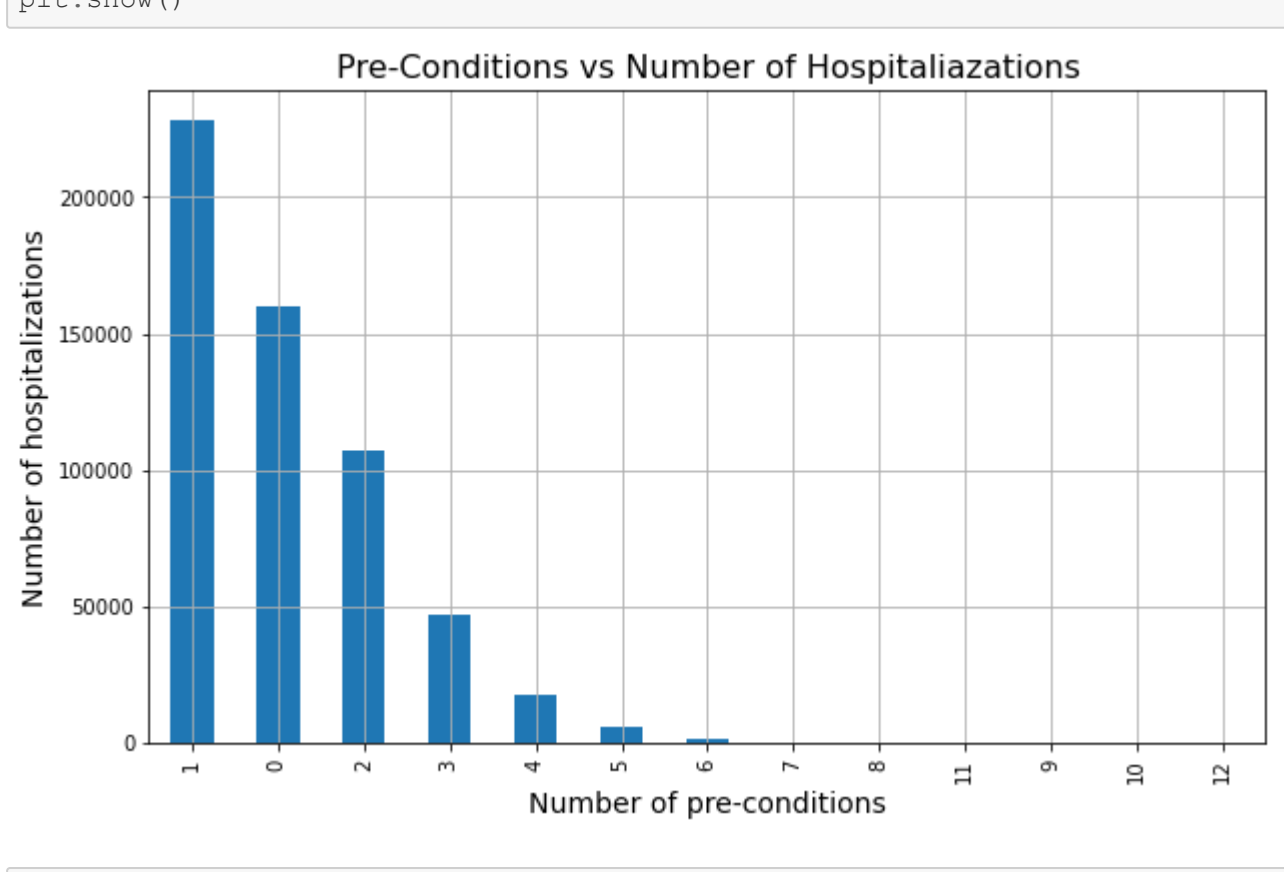


Here we can see a high hospitalization rate for ages 20-50, which can be generally assocciated with the working population. Since schools in mexico were under lockdown, the rate of infection amongst their population was controlled.

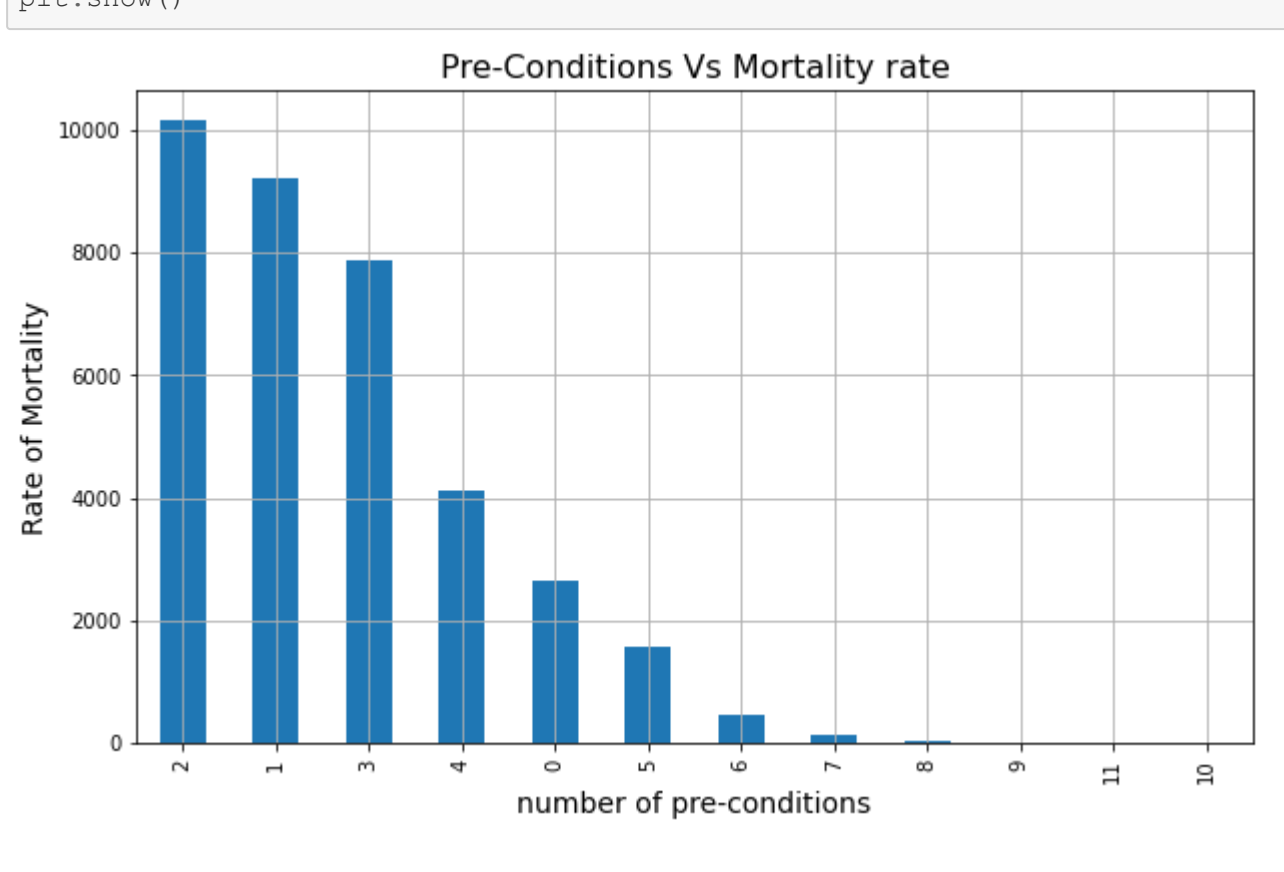
Lets take a look at the number of pre-conditions and look for any coorelations with mortality and overall hospitalizations.

In [159]:
```
pre_conditions = []
for _ in range(len(df)):
    pre_conditions.append(df.iloc[_, 7:20].str.contains('Yes').sum())

df['pre_conditions'] = pre_conditions
```

In [178]:
```
pc = df['pre_conditions'].value_counts()
pc.plot(x=pc.index, y=pc, kind='bar', figsize=(10, 6), grid=True)
plt.title("Pre-Conditions vs Number of Hospitaliazations", fontsize=16)
plt.ylabel('Number of hospitalizations', fontsize=14)
plt.xlabel('Number of pre-conditions', fontsize=14)
plt.show()
```

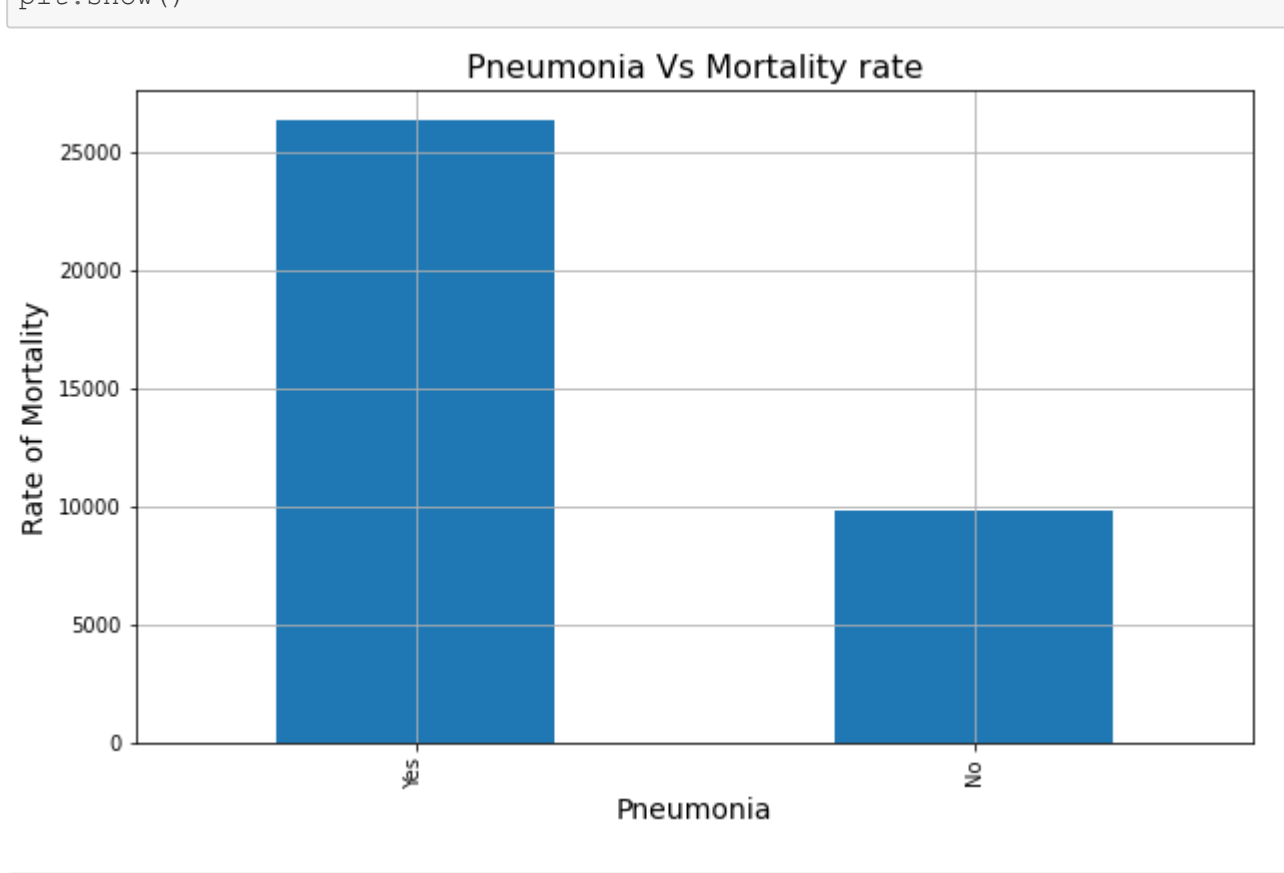


In [185]:
```
pcd = df.query('date_died != "Not Applicable"').pre_conditions.value_counts()
pcd.plot(x=pcd.index, y=pcd, kind='bar', figsize=(10,6), grid=True)
plt.title("Pre-Conditions Vs Mortality rate", fontsize=16)
plt.ylabel('Rate of Mortality', fontsize=14)
plt.xlabel('number of pre-conditions', fontsize=14)
plt.show()
```

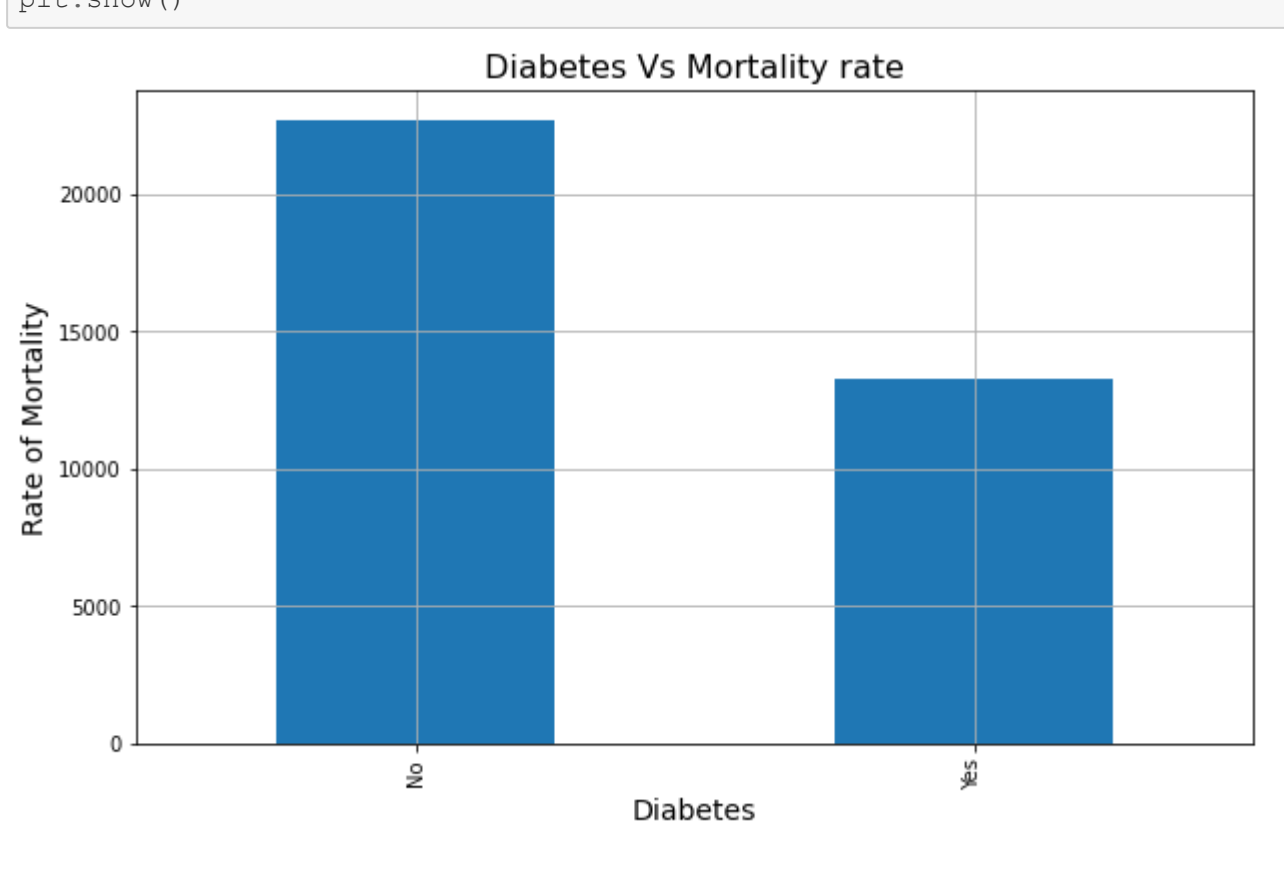


Here we can see that there is some positive coorelation between overall pre-conditions but it is not a high R rate. We can look at individual and some groups of pre-conditions to see if we can find a stronger coorelation.

In [217]:
```
pn = df.query('date_died != "Not Applicable"').pneumonia.value_counts()
pn.plot(x=pn.index, y=pn, kind='bar', figsize=(10,6), grid=True)
plt.title("Pneumonia Vs Mortality rate", fontsize=16)
plt.ylabel('Rate of Mortality', fontsize=14)
plt.xlabel('Pneumonia', fontsize=14)
plt.show()
```



In [218]:
```
pn = df.query('date_died != "Not Applicable"').diabetes.value_counts()
pn.plot(x=pn.index, y=pn, kind='bar', figsize=(10,6), grid=True)
plt.title("Diabetes Vs Mortality rate", fontsize=16)
plt.ylabel('Rate of Mortality', fontsize=14)
plt.xlabel('Diabetes', fontsize=14)
plt.show()
```

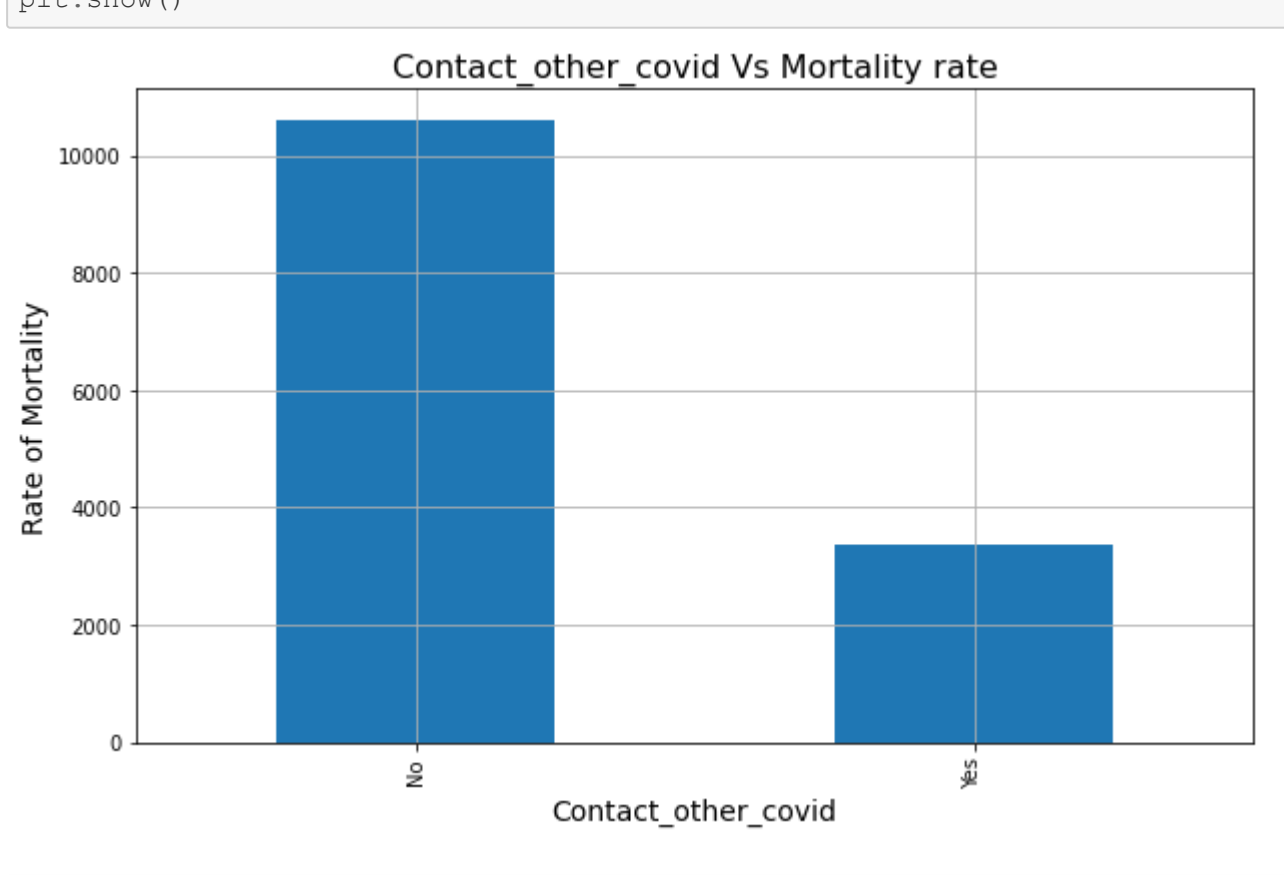


In [219]:
```
pn = df.query('date_died != "Not Applicable"').obesity.value_counts()
pn.plot(x=pn.index, y=pn, kind='bar', figsize=(10,6), grid=True)
plt.title("Obesity Vs Mortality rate", fontsize=16)
plt.ylabel('Rate of Mortality', fontsize=14)
plt.xlabel('Obesity', fontsize=14)
plt.show()
```

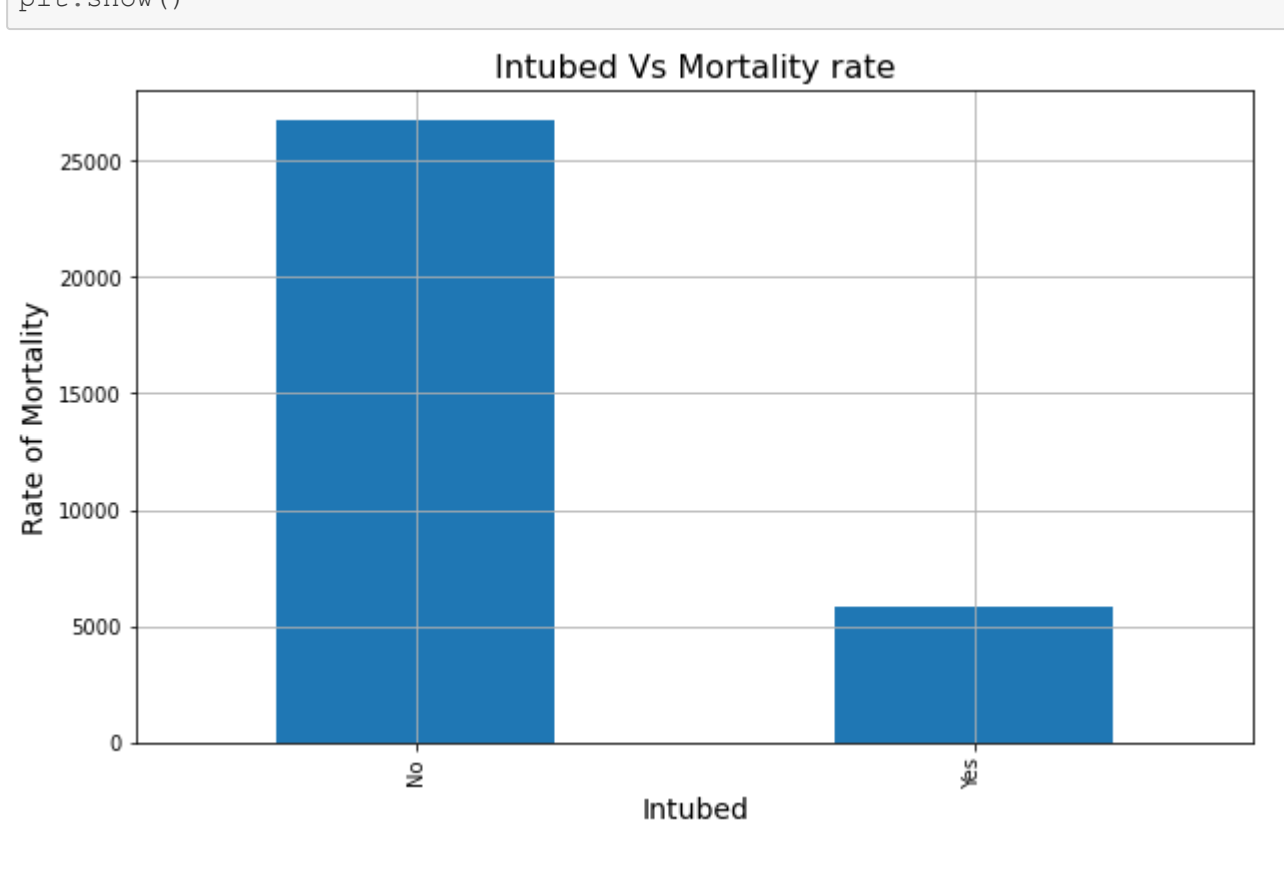
In [220]:
```
df.columns
```

Out[220]:
```
Index(['gender', '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',
       'test_result', 'icu', 'age_band', 'pre_conditions'],
      dtype='object')
```

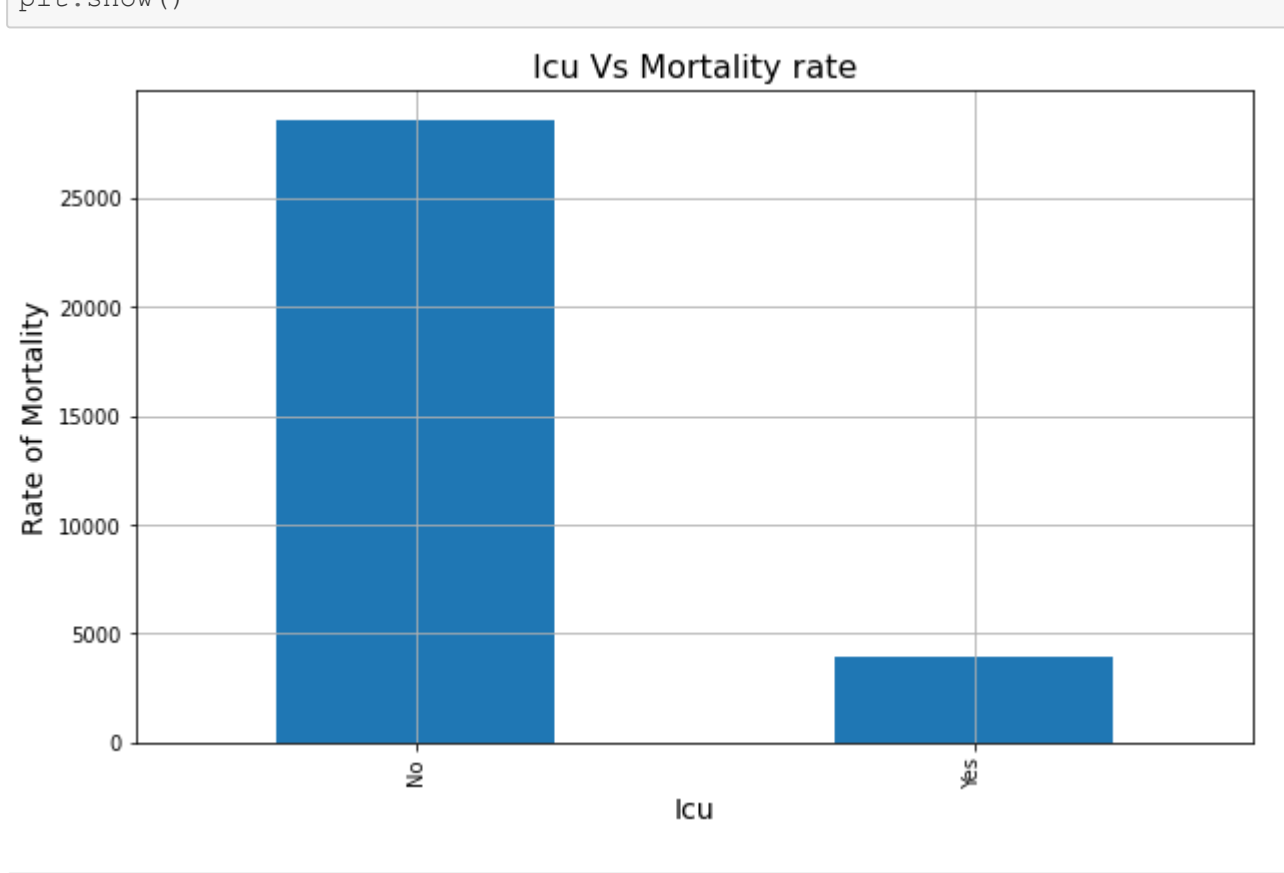
In [221]:
```
pn = df.query('date_died != "Not Applicable"').contact_other_covid.value_counts()
pn.plot(x=pn.index, y=pn, kind='bar', figsize=(10,6), grid=True)
plt.title("Contact_other_covid Vs Mortality rate", fontsize=16)
plt.ylabel('Rate of Mortality', fontsize=14)
plt.xlabel('Contact_other_covid', fontsize=14)
plt.show()
```



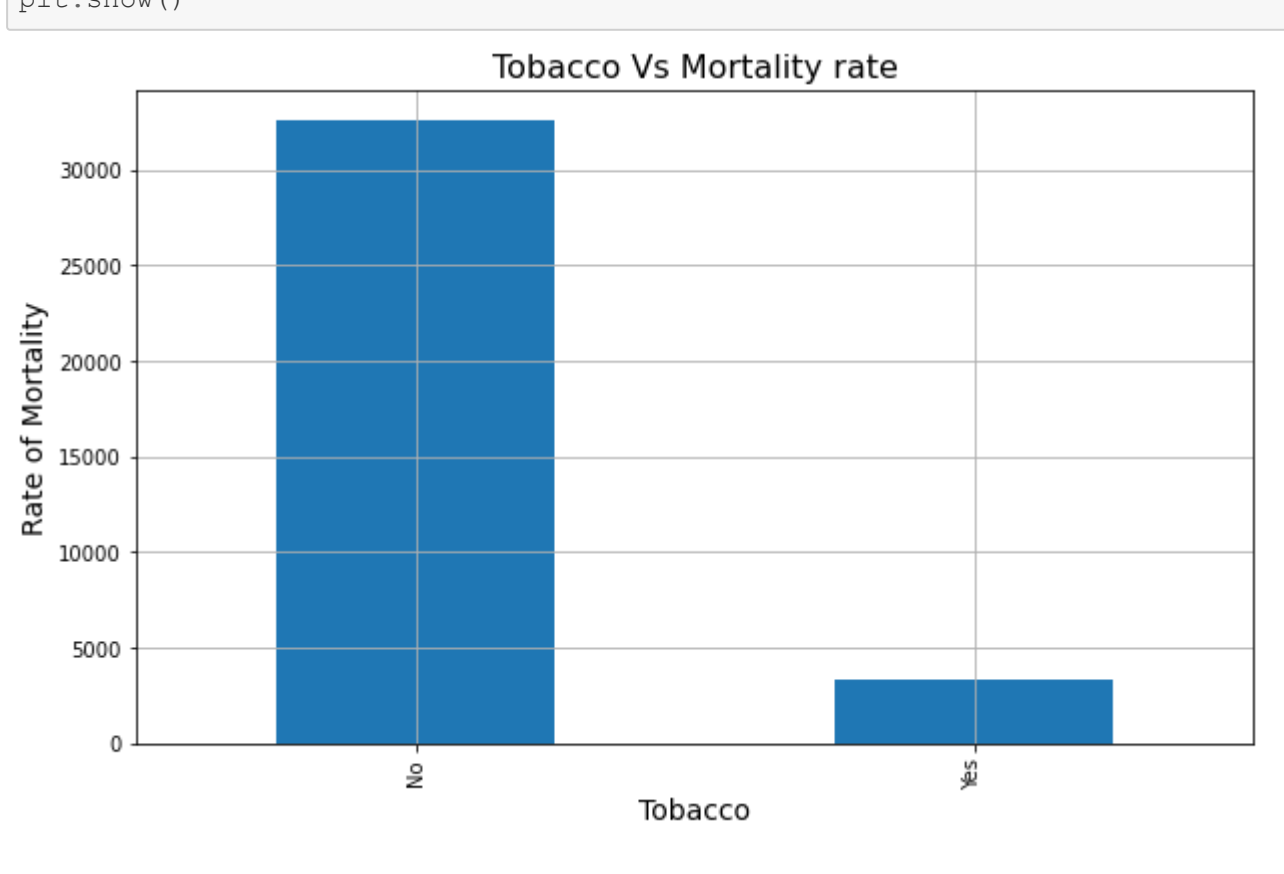
In [222]:
```
pn = df.query('date_died != "Not Applicable"').intubed.value_counts()
pn.plot(x=pn.index, y=pn, kind='bar', figsize=(10,6), grid=True)
plt.title("Intubed Vs Mortality rate", fontsize=16)
plt.ylabel('Rate of Mortality', fontsize=14)
plt.xlabel('Intubed', fontsize=14)
plt.show()
```



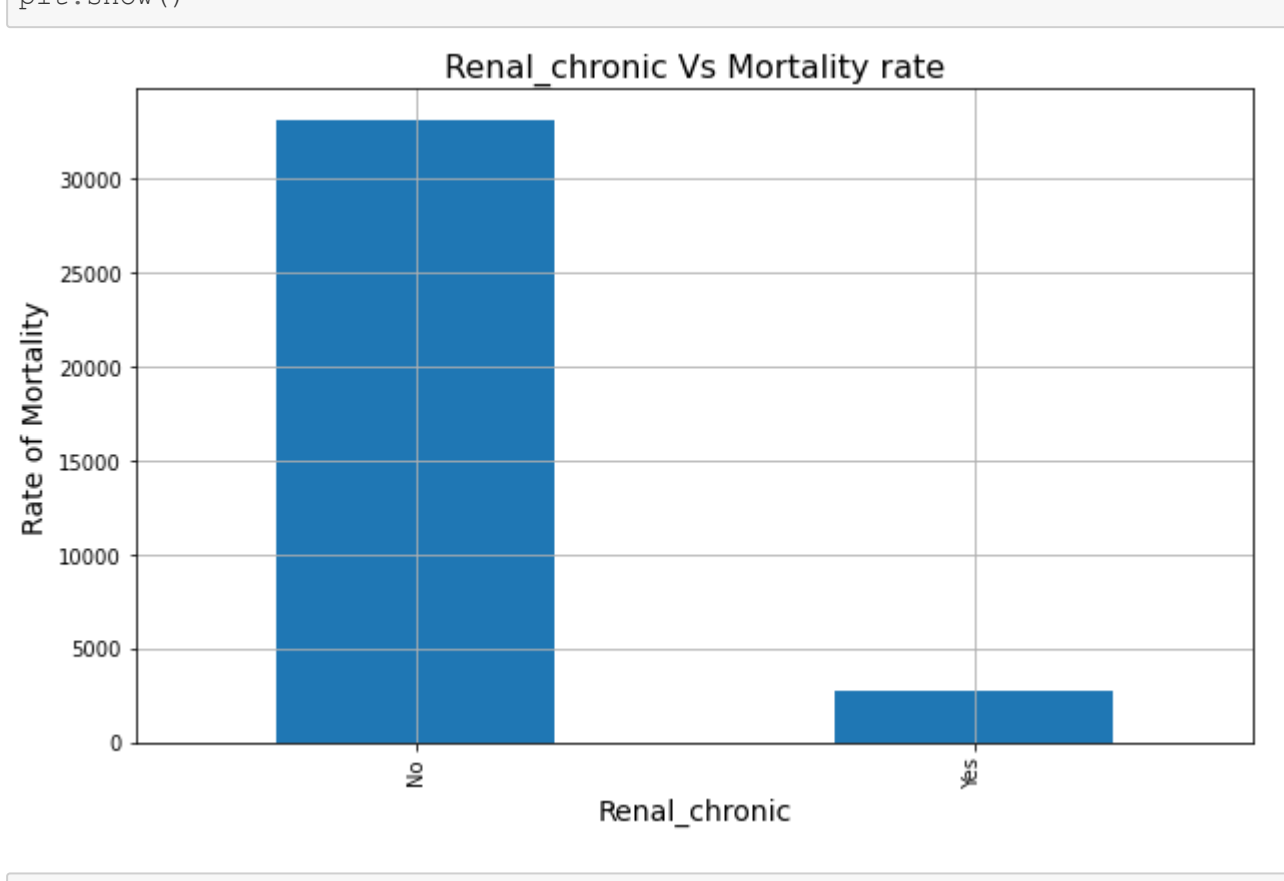
In [223]:
```
pn = df.query('date_died != "Not Applicable"').icu.value_counts()
pn.plot(x=pn.index, y=pn, kind='bar', figsize=(10,6), grid=True)
plt.title("Icu Vs Mortality rate", fontsize=16)
plt.ylabel('Rate of Mortality', fontsize=14)
plt.xlabel('Icu', fontsize=14)
plt.show()
```



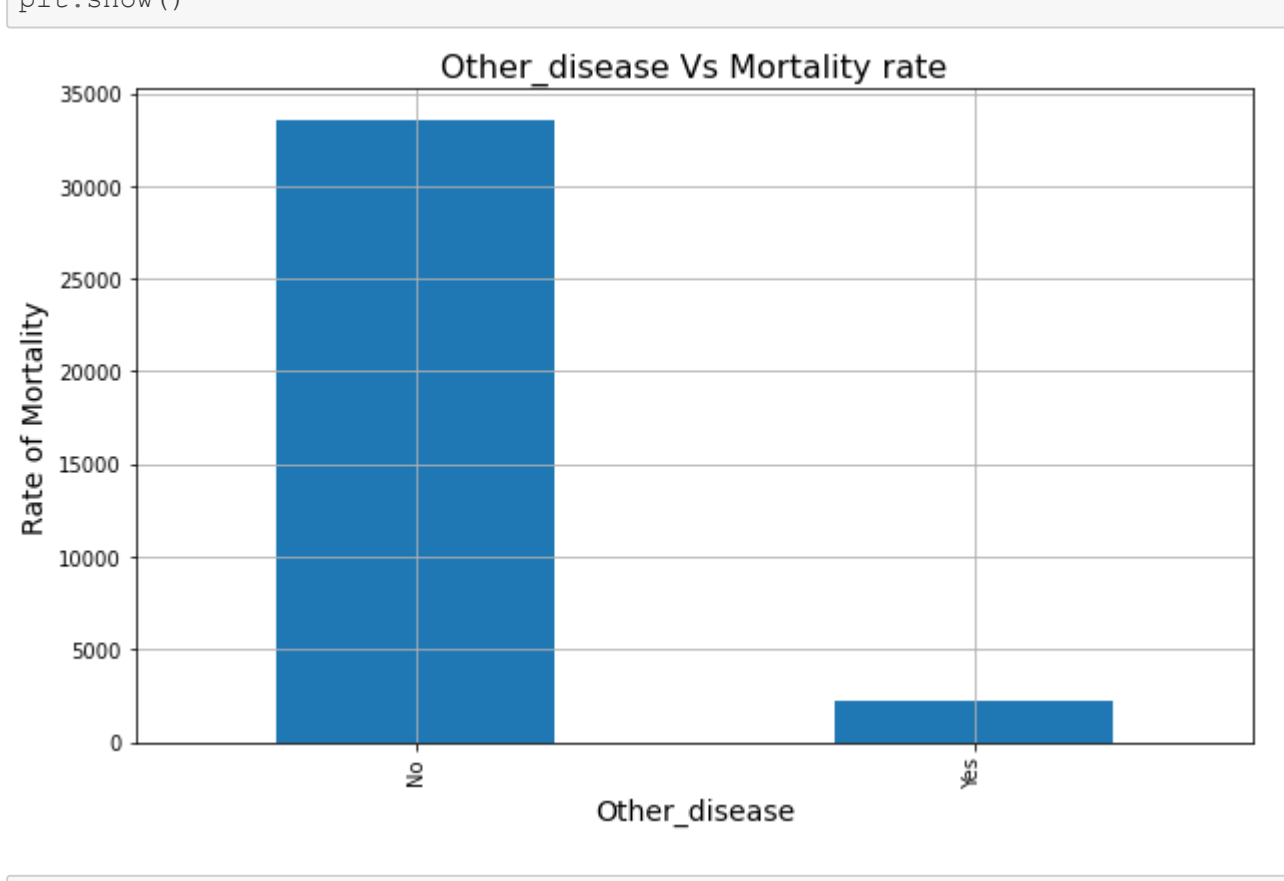
In [224]:
```
pn = df.query('date_died != "Not Applicable"').tobacco.value_counts()
pn.plot(x=pn.index, y=pn, kind='bar', figsize=(10,6), grid=True)
plt.title("Tobacco Vs Mortality rate", fontsize=16)
plt.ylabel('Rate of Mortality', fontsize=14)
plt.xlabel('Tobacco', fontsize=14)
plt.show()
```



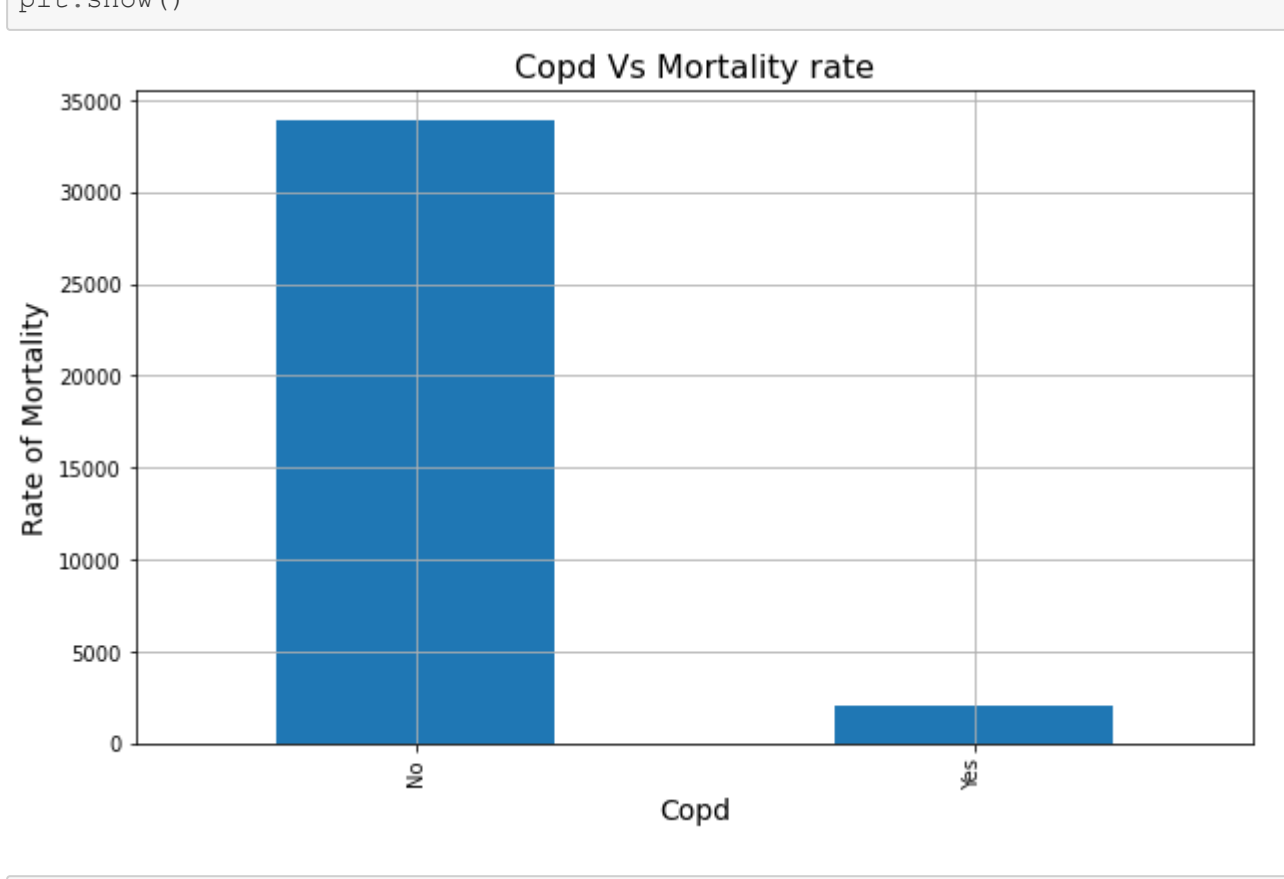
In [225]:
```
pn = df.query('date_died != "Not Applicable"').renal_chronic.value_counts()
pn.plot(x=pn.index, y=pn, kind='bar', figsize=(10,6), grid=True)
plt.title("Renal_chronic Vs Mortality rate", fontsize=16)
plt.ylabel('Rate of Mortality', fontsize=14)
plt.xlabel('Renal_chronic', fontsize=14)
plt.show()
```



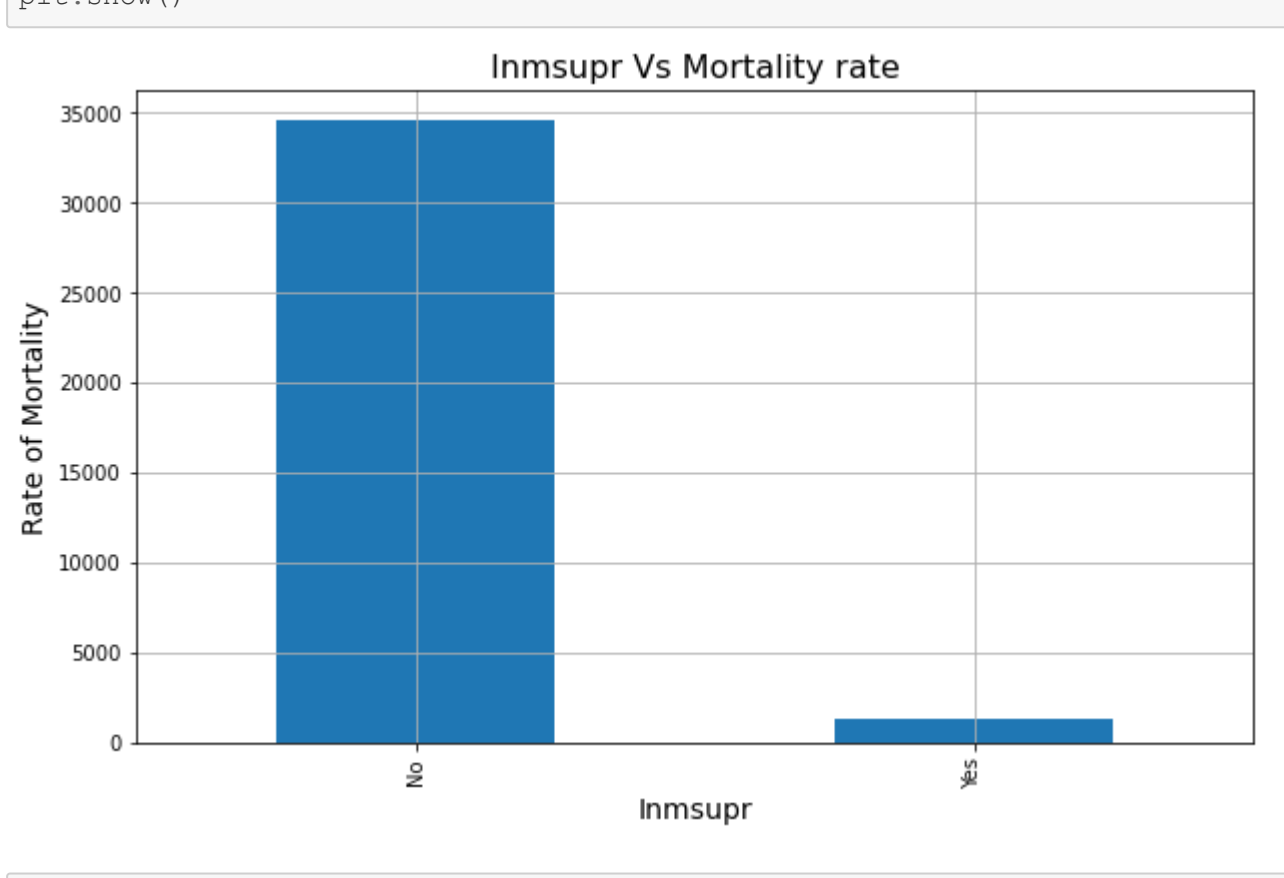
In [226]:
```
pn = df.query('date_died != "Not Applicable"').other_disease.value_counts()
pn.plot(x=pn.index, y=pn, kind='bar', figsize=(10,6), grid=True)
plt.title("Other_disease Vs Mortality rate", fontsize=16)
plt.ylabel('Rate of Mortality', fontsize=14)
plt.xlabel('Other_disease', fontsize=14)
plt.show()
```



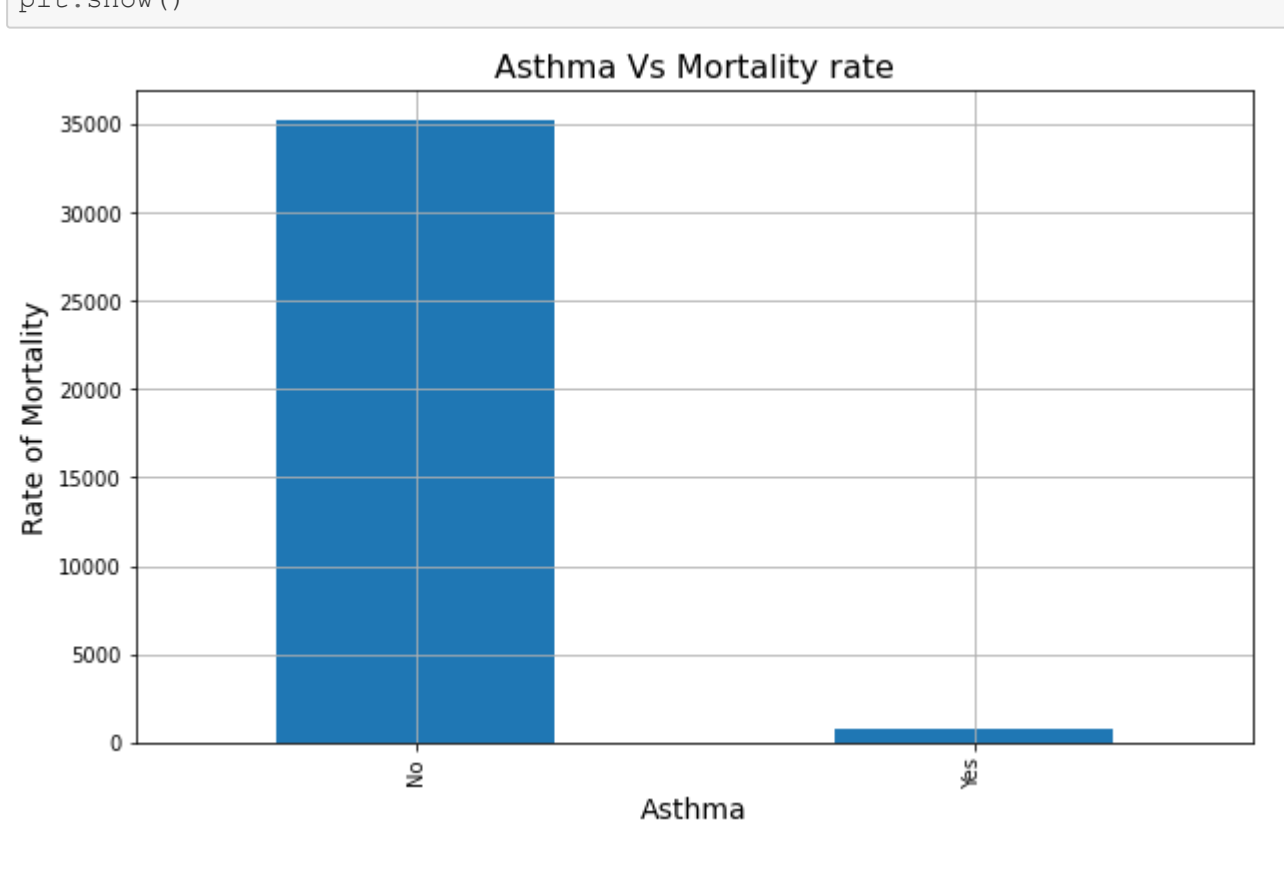
In [227]:
```
pn = df.query('date_died != "Not Applicable"').copd.value_counts()
pn.plot(x=pn.index, y=pn, kind='bar', figsize=(10,6), grid=True)
plt.title("Copd Vs Mortality rate", fontsize=16)
plt.ylabel('Rate of Mortality', fontsize=14)
plt.xlabel('Copd', fontsize=14)
plt.show()
```



In [228]:
```
pn = df.query('date_died != "Not Applicable"').inmsupr.value_counts()
pn.plot(x=pn.index, y=pn, kind='bar', figsize=(10,6), grid=True)
plt.title("Inmsupr Vs Mortality rate", fontsize=16)
plt.ylabel('Rate of Mortality', fontsize=14)
plt.xlabel('Inmsupr', fontsize=14)
plt.show()
```



In [229]:
```
pn = df.query('date_died != "Not Applicable"').asthma.value_counts()
pn.plot(x=pn.index, y=pn, kind='bar', figsize=(10,6), grid=True)
plt.title("Asthma Vs Mortality rate", fontsize=16)
plt.ylabel('Rate of Mortality', fontsize=14)
plt.xlabel('Asthma', fontsize=14)
plt.show()
```



By looking mortality trends for the pre-conditions, we can see that there is a very strong positive coorelation for pneumonia. Knowing that pneumonia is not listed as an official symptom of COVID we can safely say that contracting a pneumonia is near fatal for patients who have COVID or vice versa. For obesity and contact with other COVID patients, the risk factor is significantly higher than the patients who have not. For the other conditions, it seems to have little to no coorelation, which for some is understandable, but for others like Asthma, COPD, and Tobacco use, is surprising.