In [1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
import seaborn as sns
```

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]:
```
df = pd.read_csv('/content/drive/MyDrive/Covid Data.csv')
df
```

Out[3]:

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

1048575 rows × 21 columns

Abot The Dataset

This dataset contains an enormous number of anonymized patient-related information including pre-conditions. The raw dataset consists of 21 unique features and 1,048,576 unique patients. In the Boolean features, 1 means "yes" and 0 means "no". values as 97 and 99 are missing data.

```
   usmer         : 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.
   sex           : female(1) or male(2)
   patient type  : hospitalized or not hospitalized.
   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.

   pneumonia     : whether the patient already have air sacs inflammation or not.
   pregnancy     : whether the patient is pregnant or not.
   diabetes      : whether the patient has diabetes or not.
   copd          : Indicates whether the patient has Chronic obstructive pulmonary disease or not.
   asthma        : whether the patient has asthma or not.
   inmsupr       : whether the patient is immunosuppressed or not.
   hypertension  : whether the patient has hypertension or not.
   cardiovascular: whether the patient has heart or blood vessels related disease.
   renal chronic : whether the patient has chronic renal disease or not.
   other disease : whether the patient has other disease or not.
   obesity       : whether the patient is obese or not.
   tobacco       : whether the patient is a tobacco user.
   medical unit  : type of institution of the National Health System that provided the care.
   intubed       : whether the patient was connected to the ventilator.
   icu           : Indicates whether the patient had been admitted to an Intensive Care Unit.
   death         : indicates whether the patient died or recovered.
```

In [4]:
```
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 [5]:
```
df.isna().sum().sum()
```

Out[5]: 0

In [6]:
```
for i in df.columns:
    print(i,"--\t",len(df[i].unique()))
```

```
USMER --         2
MEDICAL_UNIT --  13
SEX --   2
PATIENT_TYPE --  2
DATE_DIED --     401
INTUBED --       4
PNEUMONIA --     3
AGE --   121
PREGNANT --      4
DIABETES --      3
COPD --  3
ASTHMA --        3
INMSUPR --       3
HIPERTENSION --  3
OTHER_DISEASE --         3
CARDIOVASCULAR --        3
OBESITY --       3
RENAL_CHRONIC --         3
TOBACCO --       3
CLASIFFICATION_FINAL --  7
ICU --   4
```

We will check the value_counts() of the columns having more than two unique values

In [7]:
```
for i in ['INTUBED','PNEUMONIA','PREGNANT','DIABETES','COPD','ASTHMA','INMSUPR','HIPERTENSION','OTHER_DISEASE',
          'CARDIOVASCULAR','OBESITY','RENAL_CHRONIC','TOBACCO','ICU']:
    print(df[i].value_counts())
    print("*"*25)
```

```
97    848544
2     159050
1      33656
99      7325
Name: INTUBED, dtype: int64
*************************
2     892534
1     140038
99     16003
Name: PNEUMONIA, dtype: int64
*************************
97    523511
2     513179
1       8131
98      3754
Name: PREGNANT, dtype: int64
*************************
2     920248
1     124989
98      3338
Name: DIABETES, dtype: int64
*************************
2     1030510
1       15062
98       3003
Name: COPD, dtype: int64
*************************
2     1014024
1       31572
98       2979
Name: ASTHMA, dtype: int64
*************************
2     1031001
1       14170
98       3404
Name: INMSUPR, dtype: int64
*************************
2     882742
1     162729
98      3104
Name: HIPERTENSION, dtype: int64
*************************
2     1015490
1       28040
98       5045
Name: OTHER_DISEASE, dtype: int64
*************************
2     1024730
1       20769
98       3076
Name: CARDIOVASCULAR, dtype: int64
*************************
2     885727
1     159816
98      3032
Name: OBESITY, dtype: int64
*************************
2     1026665
1       18904
98       3006
Name: RENAL_CHRONIC, dtype: int64
*************************
2     960979
1      84376
98      3220
Name: TOBACCO, dtype: int64
*************************
97    848544
2     175685
1      16858
99      7488
Name: ICU, dtype: int64
*************************
```

DATA PREPROCESSING

All these values 97,98,99 are actually nan values. So we will create a fuction to replace these values with np.nan

In [8]:
```
def process_columns(x):
    if x in [97,98,99]:
        return np.nan
    else:
        return x
```

In [9]:
```
for i in ['INTUBED','PNEUMONIA','PREGNANT','DIABETES','COPD','ASTHMA','INMSUPR','HIPERTENSION','OTHER_DISEASE',
          'CARDIOVASCULAR','OBESITY','RENAL_CHRONIC','TOBACCO','ICU']:
    df[i] = df[i].apply(process_columns)
```

Also for all these columns we replace 2 with 0 which means 'No' and 1 will be same which means yes.

In [10]:
```
for i in ['INTUBED','PNEUMONIA','PREGNANT','DIABETES','COPD','ASTHMA','INMSUPR','HIPERTENSION','OTHER_DISEASE',
          'CARDIOVASCULAR','OBESITY','RENAL_CHRONIC','TOBACCO','ICU']:
    df[i] = [0 if x==2 else x for x in df[i]]
```

In [11]:
```
# Percentage of null values present
df.isna().sum()/len(df)*100
```

Out[11]:
```
USMER                  0.000000
MEDICAL_UNIT           0.000000
SEX                    0.000000
PATIENT_TYPE           0.000000
DATE_DIED              0.000000
INTUBED               81.622106
PNEUMONIA              1.526166
AGE                    0.000000
PREGNANT              50.283957
DIABETES               0.318337
COPD                   0.286389
ASTHMA                 0.284100
INMSUPR                0.324631
HIPERTENSION           0.296021
OTHER_DISEASE          0.481129
CARDIOVASCULAR         0.293350
OBESITY                0.289154
RENAL_CHRONIC          0.286675
TOBACCO                0.307083
CLASIFFICATION_FINAL   0.000000
ICU                   81.637651
dtype: float64
```

Most of the columns have less than 5000 missing values except 'INTUBED','PREGNANT','ICU'.Drop these 3 columns and drop the missing values of other columns.

We are dropping nan values instead of filling because ours is a huge dataset.

In [12]:
```
df.drop(['INTUBED','PREGNANT','ICU'],axis=1,inplace=True)
```

In [13]:
```
df.dropna(inplace=True)
df
```

Out[13]:

	USMER	MEDICAL_UNIT	SEX	PATIENT_TYPE	DATE_DIED	PNEUMONIA	AGE	DIABETES	COPD	ASTHMA	INMSUPR	HIPERTENSION	OTHER_DISEASE	CARDIOVASCULAR	OB
0	2	1	1	1	03/05/2020	1.0	65	0.0	0.0	0.0	0.0	1.0	0.0	0.0	
1	2	1	2	1	03/06/2020	1.0	72	0.0	0.0	0.0	0.0	1.0	0.0	0.0	
2	2	1	2	2	09/06/2020	0.0	55	1.0	0.0	0.0	0.0	0.0	0.0	0.0	
3	2	1	1	1	12/06/2020	0.0	53	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
4	2	1	2	1	21/06/2020	0.0	68	1.0	0.0	0.0	0.0	1.0	0.0	0.0	
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
1048570	2	13	2	1	9999-99-99	0.0	40	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
1048571	1	13	2	2	9999-99-99	0.0	51	0.0	0.0	0.0	0.0	1.0	0.0	0.0	
1048572	2	13	2	1	9999-99-99	0.0	55	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
1048573	2	13	2	1	9999-99-99	0.0	28	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
1048574	2	13	2	1	9999-99-99	0.0	52	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

1025152 rows × 18 columns

In [14]:
```
df.isna().sum().sum()
```

Out[14]:
```
0
```

In 'DATE_DIED' column, we have 9999-99-99 values which represents the patients who have not died. Feature these into new DEATH column having 1 and 0, where 1 represents dead and 0 represents Alive.

DEATH column will be our target column.

In [15]:
```
df['DEATH'] = [0 if x=='9999-99-99' else 1 for x in df.DATE_DIED]
df.head()
```

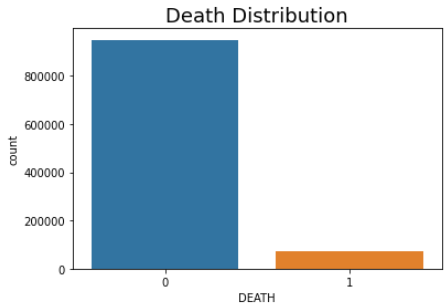
Out[15]:

	USMER	MEDICAL_UNIT	SEX	PATIENT_TYPE	DATE_DIED	PNEUMONIA	AGE	DIABETES	COPD	ASTHMA	INMSUPR	HIPERTENSION	OTHER_DISEASE	CARDIOVASCULAR	OBESITY
0	2	1	1	1	03/05/2020	1.0	65	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0
1	2	1	2	1	03/06/2020	1.0	72	0.0	0.0	0.0	0.0	1.0	0.0	0.0	1.0
2	2	1	2	2	09/06/2020	0.0	55	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
3	2	1	1	1	12/06/2020	0.0	53	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
4	2	1	2	1	21/06/2020	0.0	68	1.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0

VISUALIZATIONS

In [16]:
```
plt.title("Death Distribution", fontsize=18)
sns.countplot(x=df['DEATH'])
```

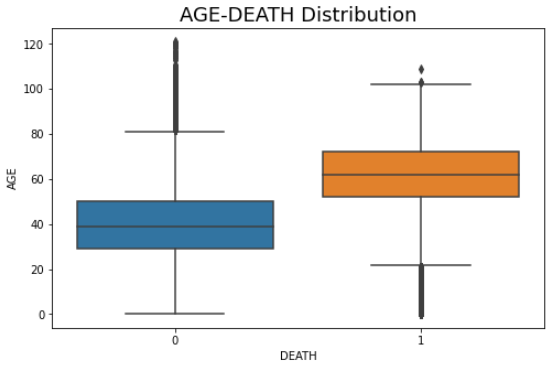
Out[16]: <matplotlib.axes._subplots.AxesSubplot at 0x7f071d296940>



>> Count of people who died are very low

In [17]:
```
plt.figure(figsize=(8,5))
sns.boxplot(x=df['DEATH'],y=df['AGE'],data=df)
plt.title("AGE-DEATH Distribution", fontsize=18)
```

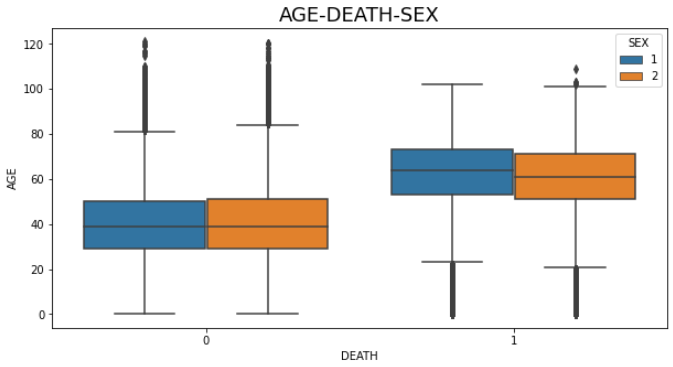
Out[17]: Text(0.5, 1.0, 'AGE-DEATH Distribution')



>> The average age distribution for dead people are around 60.
>> The average age distribution of alive people are around 40
>> This summarises young people survived than the older people

In [18]:
```
plt.figure(figsize=(10,5))
sns.boxplot(x=df['DEATH'],y=df['AGE'],data=df,hue='SEX')
plt.title("AGE-DEATH-SEX", fontsize=18)
```

Out[18]: Text(0.5, 1.0, 'AGE-DEATH-SEX')



>> Irrespective of the gender, the AGE-DEATH distribution follows the normal trend.

In [19]:
```
sns.displot(df['AGE'])
```

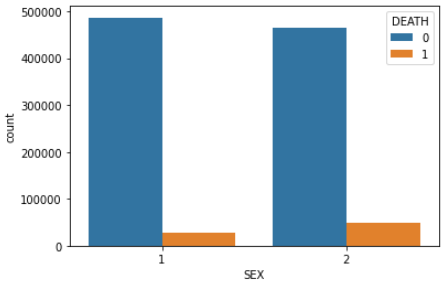
Out[19]: <seaborn.axisgrid.FacetGrid at 0x7f071bbdd460>

>> Age between 20 and 40 constitutes more in the dataset.
>> But they are the ones most survived also.

In [20]:
```
sns.countplot(df.SEX,hue=df.DEATH)
```

```
/usr/local/lib/python3.8/dist-packages/seaborn/_decorators.py:36: FutureWarning: Pass the following variable as a keyword arg: x. From version 0.12,
the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretat
ion.
  warnings.warn(
```

Out[20]: <matplotlib.axes._subplots.AxesSubplot at 0x7f071c13e100>



>> Both male and females have almost same death and survive distribution
>> But males are slightly more likely to die due to covid-19

In [21]:
```
df.columns
```

Out[21]:
```
Index(['USMER', 'MEDICAL_UNIT', 'SEX', 'PATIENT_TYPE', 'DATE_DIED',
       'PNEUMONIA', 'AGE', 'DIABETES', 'COPD', 'ASTHMA', 'INMSUPR',
       'HIPERTENSION', 'OTHER_DISEASE', 'CARDIOVASCULAR', 'OBESITY',
       'RENAL_CHRONIC', 'TOBACCO', 'CLASIFFICATION_FINAL', 'DEATH'],
      dtype='object')
```

Preprocessing DATE_DIED for Visulazation

In [22]:
```
data = df.copy()
```

In [23]:
```
data['DATE_DIED']=[np.nan if x=='9999-99-99' else x for x in data.DATE_DIED]
```

In [24]:
```
data['DATE_DIED']=pd.to_datetime(data.DATE_DIED)
```

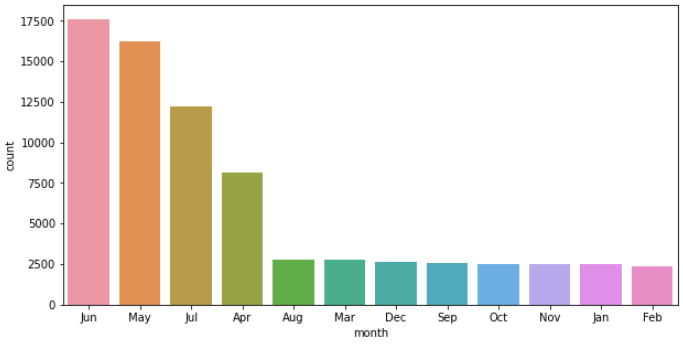
In [25]:
```
data['month'] = data['DATE_DIED'].dt.month
```

In [26]:
```
dict_month = {1.0:'Jan',2.0:'Feb',3.0:'Mar',4.0:'Apr',5.0:'May',6.0:'Jun',7.0:'Jul',8.0:'Aug',9.0:'Sep',10.0:'Oct',11.0:'Nov',12.0:'Dec'}
```

In [27]:
```
data['month'] = data['month'].map(dict_month)
```

In [28]:
```
plt.figure(figsize=(10,5))
sns.countplot(x=data['month'],order = data['month'].value_counts().index)
```

Out[28]: <matplotlib.axes._subplots.AxesSubplot at 0x7f071cd80580>



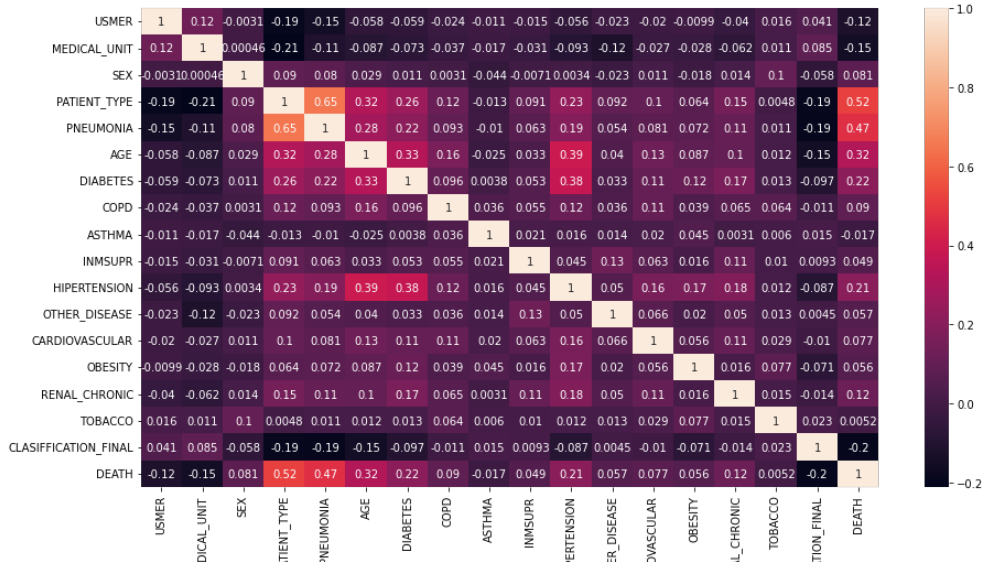
FEATURE SELECTION

We have to remove DATE_DIED column, because we already created a feature column called DEATH. Rest of the features can be selected using correlation or Mutual Info Regression

In [29]:
```
df.drop('DATE_DIED',axis=1,inplace=True)
```

In [30]:
```
plt.figure(figsize=(15,8))
sns.heatmap(df.corr(),annot=True)
```

Out[30]: <matplotlib.axes._subplots.AxesSubplot at 0x7f071c05afa0>



While comparing with DEATH feature, correlation of SEX, COPD, ASTHMA, INMSUPR, OTHER_DISEASE, CARDIOVASCULAR, OBESITY, TOBACCO are very low (almost zero). So we will drop all these columns.

In [31]:
```
df.drop(["SEX","COPD","ASTHMA","INMSUPR","OTHER_DISEASE","CARDIOVASCULAR","OBESITY","TOBACCO"],axis=1,inplace=True)
df
```

Out[31]:

	USMER	MEDICAL_UNIT	PATIENT_TYPE	PNEUMONIA	AGE	DIABETES	HIPERTENSION	RENAL_CHRONIC	CLASIFFICATION_FINAL	DEATH
0	2	1	1	1.0	65	0.0	1.0	0.0	3	1
1	2	1	1	1.0	72	0.0	1.0	1.0	5	1
2	2	1	2	0.0	55	1.0	0.0	0.0	3	1
3	2	1	1	0.0	53	0.0	0.0	0.0	7	1
4	2	1	1	0.0	68	1.0	1.0	0.0	3	1
...	...	...	...	...	...	...	...	...	...	...
1048570	2	13	1	0.0	40	0.0	0.0	0.0	7	0
1048571	1	13	2	0.0	51	0.0	1.0	0.0	7	0
1048572	2	13	1	0.0	55	0.0	0.0	0.0	7	0
1048573	2	13	1	0.0	28	0.0	0.0	0.0	7	0
1048574	2	13	1	0.0	52	0.0	0.0	0.0	7	0

1025152 rows × 10 columns

Encoding categorical features which are not binary

In [32]:
```
MEDICAL_Unit = pd.get_dummies(df['MEDICAL_UNIT'],drop_first=True)
CLASSIFICATION_final = pd.get_dummies(df['CLASIFFICATION_FINAL'],drop_first=True)
```

In [33]:
```
df = pd.concat([df,MEDICAL_Unit,CLASSIFICATION_final],axis=1)
```

In [34]:
```
df.drop(['MEDICAL_UNIT','CLASIFFICATION_FINAL'],axis=1,inplace=True)
```

MACHINE LEARNING

In [35]:
```
X = df.drop('DEATH',axis=1).values
y = df['DEATH'].values
```

Train Test Split

In [36]:
```
from sklearn.model_selection import train_test_split
```

In [37]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3)
```

Scaling the data

In [38]:
```
from sklearn.preprocessing import StandardScaler
sc= StandardScaler()
X_train = sc.fit_transform(X_train)
X_test = sc.transform(X_test)
```

RANDOM FOREST CLASSIFICATION

In [39]:
```
from sklearn.ensemble import RandomForestClassifier

rf = RandomForestClassifier()
rf.fit(X_train,y_train)
rf_pred = rf.predict(X_test)
```

In [40]:
```
from sklearn.metrics import classification_report,confusion_matrix
```

In [41]:
```
print(classification_report(y_test,rf_pred))
```

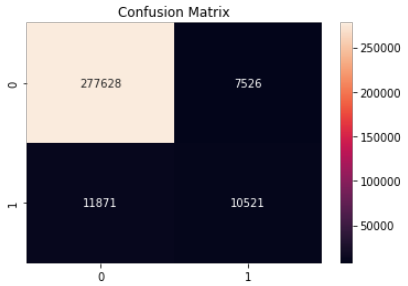
```
              precision    recall  f1-score   support

           0       0.96      0.97      0.97    285154
           1       0.58      0.47      0.52     22392

    accuracy                           0.94    307546
   macro avg       0.77      0.72      0.74    307546
weighted avg       0.93      0.94      0.93    307546
```

In [42]:
```
plt.title('Confusion Matrix')
sns.heatmap(confusion_matrix(y_test,rf_pred),annot=True,fmt=".0f")
```

Out[42]: <matplotlib.axes._subplots.AxesSubplot at 0x7f0717162f70>



Inference

>> We have got an high accuracy score of 94%.
>> Our model performed well on survived category predictions.
>> But the f1-score and recall is very low for those who are 'dead'.
>> This is due to an imbalanced data set. Our dataset is an highly imbalanced dataset.

DEALING WITH IMBALANCED DATASET

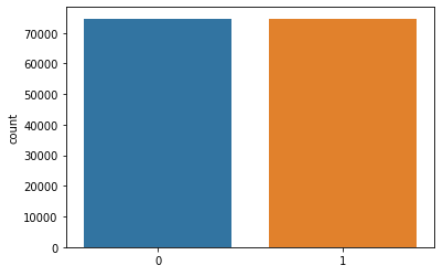
>> Here we will under sample our data set, since our dataset is a huge dataset.(more than 10 lakh rows)

In [43]:
```
from imblearn.under_sampling import RandomUnderSampler

rus = RandomUnderSampler(random_state=0)
X_resampled,y_resampled = rus.fit_resample(X,y)
```

In [44]:
```
sns.countplot(x=y_resampled)
```

Out[44]: <matplotlib.axes._subplots.AxesSubplot at 0x7f0716d53a00>



Train Test Split and Scaling after Under Sampling

In [53]:
```
X_train, X_test, y_train, y_test = train_test_split(X_resampled, y_resampled, test_size=0.3,random_state=42)
```

In [54]:
```
X_train = sc.fit_transform(X_train)
X_test = sc.transform(X_test)
```

Cross Validation

To select best algorithm for our model

In [47]:
```
from sklearn.model_selection import cross_val_score

from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.linear_model import LogisticRegression
lg = LogisticRegression()
kn = KNeighborsClassifier()
tree = DecisionTreeClassifier()
```

In [48]:
```
# KNeighbours
cross_val_score(kn,X_train,y_train)
```

Out[48]: array([0.90650096, 0.90487572, 0.90578394, 0.9042065 , 0.90769157])

In [50]:
```
# Decision Tree
cross_val_score(tree,X_train,y_train)
```

Out[50]: array([0.89216061, 0.88785851, 0.89220841, 0.88905354, 0.88938286])

In [51]:
```
# Random Forest
cross_val_score(rf,X_train,y_train)
```

Out[51]:
```
array([0.90186424, 0.89899618, 0.90023901, 0.89866157, 0.90190736])
```

In [52]:
```
# Logistic Regression
cross_val_score(lg,X_train,y_train)
```

Out[52]:
```
array([0.90750478, 0.90358509, 0.90807839, 0.90635755, 0.91070319])
```

Since most of the algorithms have almost same cross validation score we will go with Random Forest, since several of its paramters can be tuned to get a better model.

In [64]:
```
rf_model = RandomForestClassifier(n_estimators=100,criterion='gini',min_samples_split=2,min_samples_leaf=2,max_features='auto',n_jobs=-1,random_sta
rf_model.fit(X_train,y_train)
y_pred = rf_model.predict(X_test)
```

In [65]:
```
print(classification_report(y_test,y_pred))
```

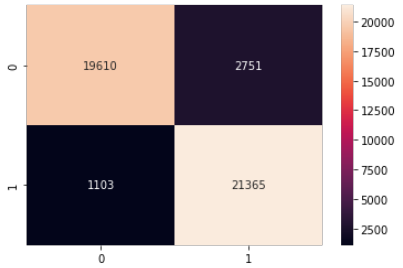
```
              precision    recall  f1-score   support

           0       0.94      0.88      0.91     22361
           1       0.89      0.95      0.92     22468

    accuracy                           0.91     44829
   macro avg       0.91      0.91      0.91     44829
weighted avg       0.91      0.91      0.91     44829
```

In [57]:
```
sns.heatmap(confusion_matrix(y_test,y_pred),annot=True,fmt='0.0f')
```

Out[57]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x7f0716d13c10>
```



Conclusion

```
>> The model has an high accuracy of 91%
>> Also it has higher F1-score and recall.
>> Hypertuning this model is highly time consuming since this is a large dataset.
>> But with the given paramters our model has performed well and predicted both Death and Alive cases effectively.
```

In [ ]: