TP FINAL - ALGORITHMES D'APPRENTISSAGE SUPERVISÉ

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1. LOAD DATA

In [1]:
```
import pandas as pd
import matplotlib.pyplot as plt
import statistics
import numpy as np
import scipy.stats
import seaborn as sns

dataOriginal = pd.read_csv("covid.csv")
pd.set_option('display.max_rows', None)
dataOriginal.head(5)
```

Out[1]:

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

5 rows × 23 columns

1.1. LOAD METADA

In [2]:
```
cat_si_no = pd.read_excel("Catalogs.xlsx", 'Catálogo SI_NO')
pd.set_option('display.max_rows', None)
cat_si_no.head(5)
```

Out[2]:

	CLAVE	DESCRIPCIÓN
0	1	SI
1	2	NO
2	97	NO APLICA
3	98	SE IGNORA
4	99	NO ESPECIFICADO

In [3]:
```
cat_pacient_type = pd.read_excel("Catalogs.xlsx", 'Catálogo TIPO_PACIENTE')
pd.set_option('display.max_rows', None)
cat_pacient_type.head(5)
```

Out[3]:

	CLAVE	DESCRIPCIÓN
0	1	AMBULATORIO
1	2	HOSPITALIZADO
2	99	NO ESPECIFICADO

In [4]:
```
cat_sex = pd.read_excel("Catalogs.xlsx", 'Catálogo SEXO')
pd.set_option('display.max_rows', None)
cat_sex.head(5)
```

Out[4]:

	CLAVE	DESCRIPCIÓN
0	1	MUJER
1	2	HOMBRE
2	99	NO ESPECIFICADO

In [5]:
```
cat_result = pd.read_excel("Catalogs.xlsx", 'Catálogo RESULTADO')
pd.set_option('display.max_rows', None)
cat_sex.head(5)
```

Out[5]:

	CLAVE	DESCRIPCIÓN
0	1	MUJER
1	2	HOMBRE
2	99	NO ESPECIFICADO

2. IDENTIFYING MODEL VARIABLES

We are gooing to predict if the pacient needs ICU

In [6]:
```
dataInfo = pd.read_excel("covidInfo.xlsx", "DataTypes")
pd.set_option('display.max_rows', None)
dataInfo
```

Out[6]:

	Variable Name	DB Type	Model Type	CATALOG
0	id	String	Non informative	N.A
1	sex	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SEXO
2	patient_type	String / Date	Categorical, Numerical, Non-ordinal, Nominal	Catálogo TIPO_PACIENTE
3	entry_date	String / Date	Date	N.A
4	date_symptoms	String / Date	Date	N.A
5	date_died	String / Date	Date	N.A
6	intubed	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO
7	pneumonia	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO
8	age	int	Categorical, Numerical, Non-ordinal, Nominal	N.A
9	pregnancy	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO
10	diabetes	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO
11	copd	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO
12	asthma	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO
13	inmsupr	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO
14	hypertension	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO
15	other_disease	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO
16	cardiovascular	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO
17	obesity	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO
18	renal_chronic	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO
19	tobacco	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO
20	contact_other_covid	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO
21	covid_res	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo RESULTADO
22	icu	int	Categorical, Numerical, Non-ordinal, Nominal	Catálogo SI_NO

In [2]:
```
# All labels
datalabels = ['id', 'sex', 'patient_type', 'entry_date', 'date_symptoms',
              'date_died','intubed','pneumonia','age','pregnancy','diabetes','copd','asthma','inmsupr','hypertensi
on',
              'other_disease','cardiovascular','obesity','renal_chronic','tobacco','contact_other_covid'
              ,'covid_res','icu']

# Ignored: id, entrydate, date_symptons, date_died, icu
predictors = ['sex', 'patient_type',
              'intubed','pneumonia','age','pregnancy','diabetes','copd','asthma','inmsupr','hypertension',
              'other_disease','cardiovascular','obesity','renal_chronic','tobacco',
              'contact_other_covid','covid_res']

target_column= 'icu'

model_columns = ['sex', 'patient_type',
              'intubed','pneumonia','age','pregnancy','diabetes','copd','asthma','inmsupr','hypertension',
              'other_disease','cardiovascular','obesity','renal_chronic','tobacco',
              'contact_other_covid','covid_res', target_column]

prefered_columns = ['sex','cardiovascular','obesity','tobacco','contact_other_covid','covid_res', target_column]
```

3. DATA EXPLORATION

3.1. Applying Catalogs

In [ ]:

In [ ]:

3.1. Inspecting for types and Null values detection

In [8]:
```
dataOriginal.info()
```

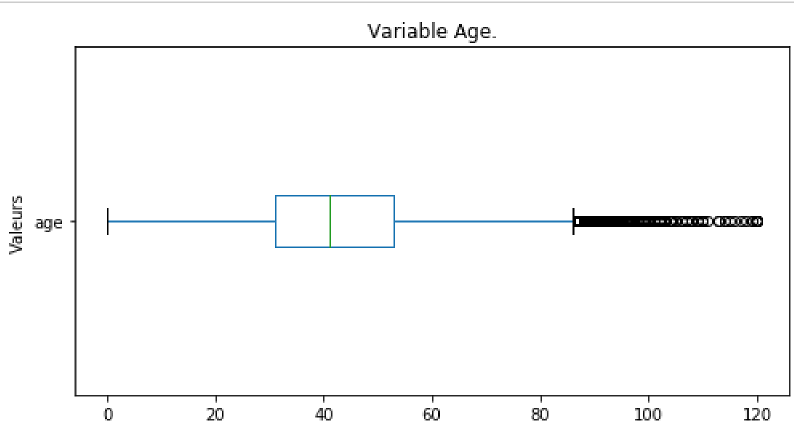
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 566602 entries, 0 to 566601
Data columns (total 23 columns):
 #   Column              Non-Null Count   Dtype 
---  ------              --------------   ----- 
 0   id                  566602 non-null  object
 1   sex                 566602 non-null  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: 99.4+ MB
```

In [9]:
```
dataOriginal.isnull().values.sum()
```

Out[9]: 0

3.1.1. Searching odd information in numerical descriptor - AGE

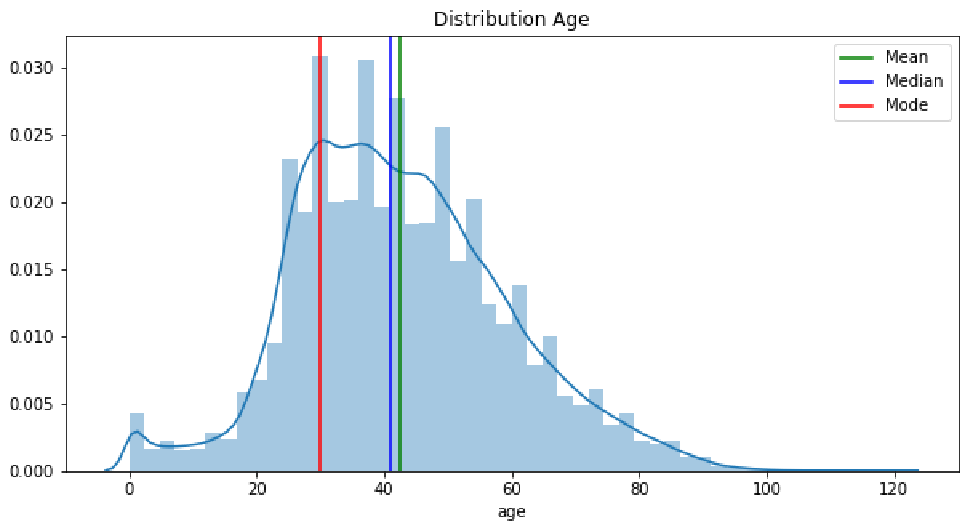
In [10]:
```
#Diagram de moustache

dataOriginal.boxplot(column='age', figsize=(8,4), vert=False)
plt.ylabel("Valeurs")
plt.title("Variable Age." )
plt.grid()
plt.show()
```



There are 2944 samples with age greater than 100 ans.. to DO ???

3.2. Inspecting variables quantitatives - Age

In [11]:
```
import seaborn as sns

mean=dataOriginal['age'].mean();
median=dataOriginal['age'].median();
mode=dataOriginal['age'].mode();
fig, ax = plt.subplots(figsize=(10,5));

sns.distplot(dataOriginal['age']);
plt.title('Distribution Age');
plt.axvline(mean,color='green',label='Mean');
plt.axvline(median,color='blue',label='Median');
plt.axvline(mode[0],color='red',label='Mode')

plt.legend();
```



In [12]:
```
mean
```

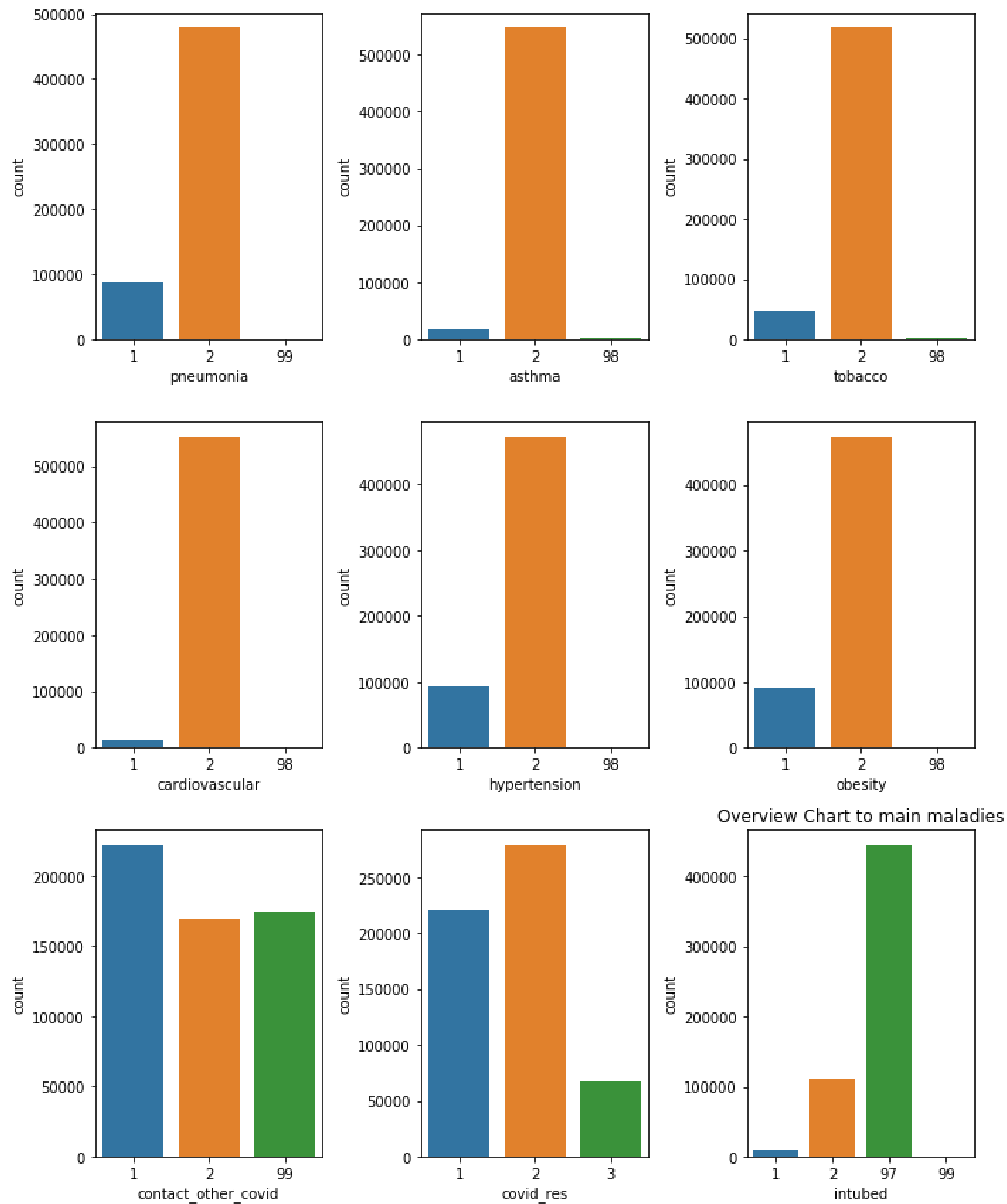
Out[12]:
```
42.62248280097847
```

In [13]:
```
mode
```

Out[13]:
```
0    30
dtype: int64
```

2.3. Inspecting categorical variables

In [14]:
```python
import matplotlib.pyplot as plt


fig, ax =plt.subplots(3,3)

fig.set_size_inches(10, 12, forward=True)
plt.title("Overview Chart to main maladies")
sns.countplot(x='pneumonia', data=dataOriginal, ax=ax[0,0])
sns.countplot(x='asthma', data=dataOriginal, ax=ax[0,1])
sns.countplot(x='tobacco', data=dataOriginal, ax=ax[0,2])
sns.countplot(x='cardiovascular', data=dataOriginal, ax=ax[1,0])
sns.countplot(x='hypertension', data=dataOriginal, ax=ax[1,1])
sns.countplot(x='obesity', data=dataOriginal, ax=ax[1,2])
sns.countplot(x='contact_other_covid', data=dataOriginal, ax=ax[2,0])
sns.countplot(x='covid_res', data=dataOriginal, ax=ax[2,1])
sns.countplot(x='intubed', data=dataOriginal, ax=ax[2,2])
#fig.legend() use handles
fig.tight_layout()
```



Calculate numerical values

In [15]:
```python
pd.DataFrame(dataOriginal['pneumonia'].value_counts())
```

Out[15]:

	pneumonia
2	478416
1	88175
99	11

In [16]:
```python
pd.DataFrame(dataOriginal['asthma'].value_counts())
```

Out[16]:

	asthma
2	546824
1	18026
98	1752

In [17]:
```python
pd.DataFrame(dataOriginal['tobacco'].value_counts())
```

Out[17]:

	tobacco
2	516678
1	48017
98	1907

In [18]:
```python
pd.DataFrame(dataOriginal['pregnancy'].value_counts())
```

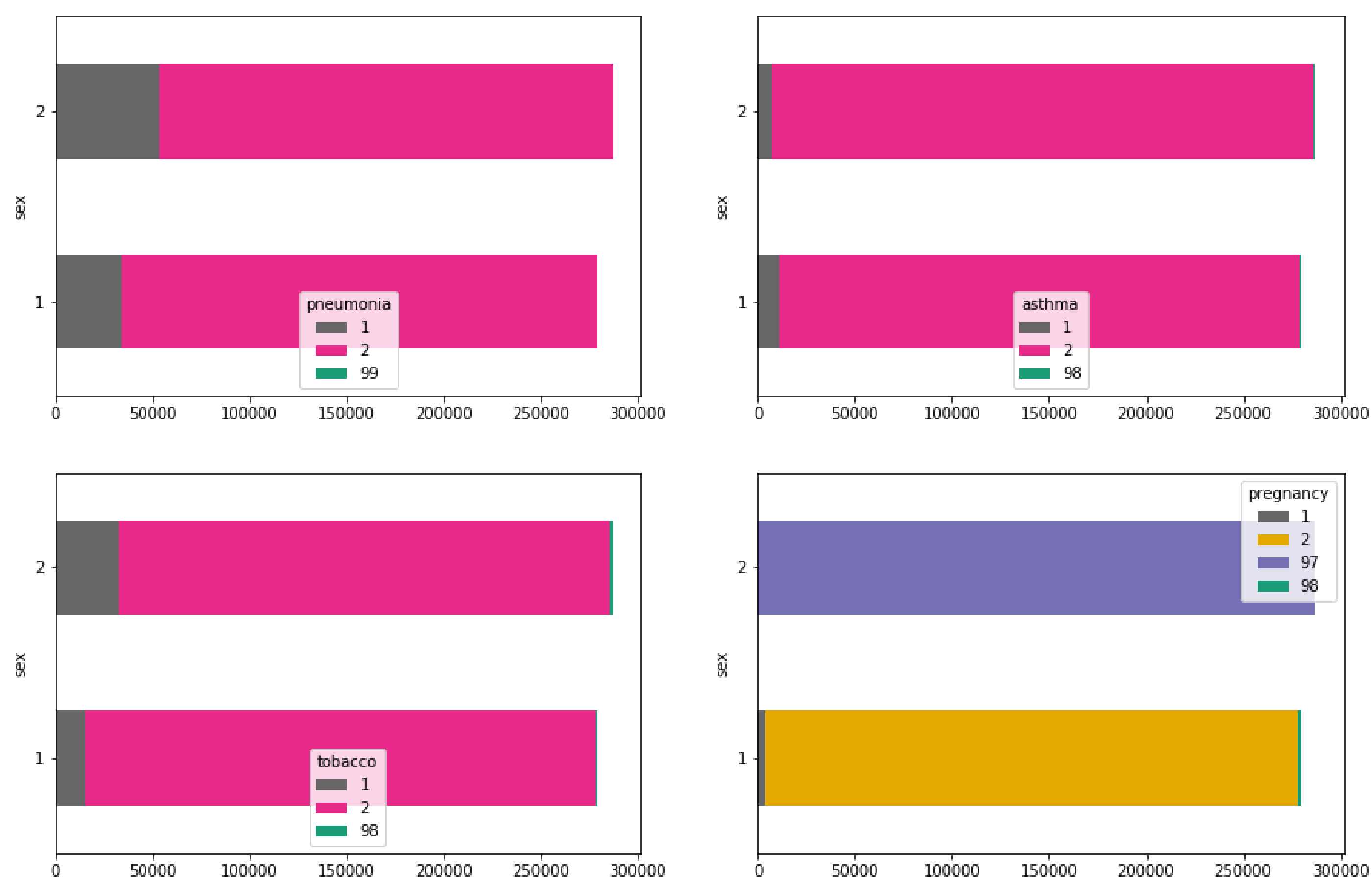
Out[18]:

	pregnancy
97	287112
2	273840
1	4063
98	1587

2.3.1. Inspecting categorical variables using bivariable relatioships with sex of patients.

In [19]:
```python
fig, axs = plt.subplots(2,2)

pneumonia_bySex= dataOriginal.pivot_table(index='sex', columns='pneumonia', values='icu', aggfunc='count')
pneumonia_bySex.plot(kind='barh', stacked=True, figsize=[15,10], colormap='Dark2_r',ax=axs[0,0])

asthma_bySex= dataOriginal.pivot_table(index='sex', columns='asthma', values='icu', aggfunc='count')
asthma_bySex.plot(kind='barh', stacked=True, figsize=[15,10], colormap='Dark2_r',ax=axs[0,1])

tobacco_bySex= dataOriginal.pivot_table(index='sex', columns='tobacco', values='icu', aggfunc='count')
tobacco_bySex.plot(kind='barh', stacked=True, figsize=[15,10], colormap='Dark2_r',ax=axs[1,0])
,
pregnancy_bySex= dataOriginal.pivot_table(index='sex', columns='pregnancy', values='icu', aggfunc='count')
pregnancy_bySex.plot(kind='barh', stacked=True, figsize=[15,10], colormap='Dark2_r',ax=axs[1,1])
```

Out[19]: <matplotlib.axes._subplots.AxesSubplot at 0x2095f5e14c8>



Calculate numerical values

In [20]:
```python
pneumonia_bySex
```

Out[20]:

pneumonia	1	2	99
sex			
1	34752	244733	5
2	53423	233683	6

In [21]:
```
tobacco_bySex
```
Out[21]:

tobacco	1	2	98
sex			
1	15545	263171	774
2	32472	253507	1133

In [22]:
```
asthma_bySex
```
Out[22]:

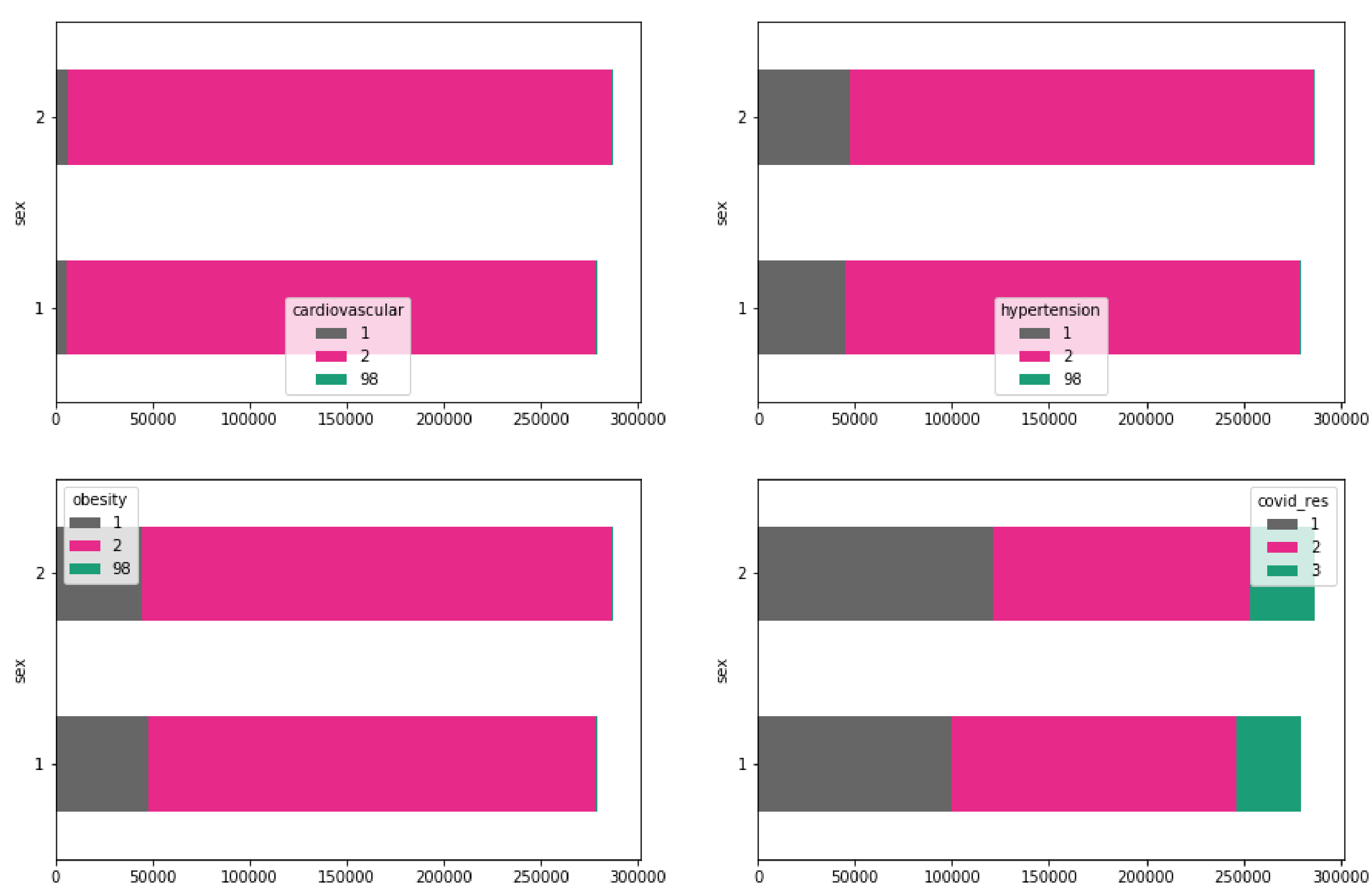
asthma	1	2	98
sex			
1	11203	267558	729
2	6823	279266	1023

In [23]:
```
pregnancy_bySex
```
Out[23]:

pregnancy	1	2	97	98
sex				
1	4063.0	273840.0	NaN	1587.0
2	NaN	NaN	287112.0	NaN

2.3.2. Inspecting categorical variables using bivariable relatioships with ICU (Intensive Care Medical Unit) reference

In [24]:
```
fig, axs = plt.subplots(2,2)

pneumonia_bySex= dataOriginal.pivot_table(index='sex', columns='cardiovascular', values='icu', aggfunc='count')
pneumonia_bySex.plot(kind='barh', stacked=True, figsize=[15,10], colormap='Dark2_r',ax=axs[0,0])

asthma_bySex= dataOriginal.pivot_table(index='sex', columns='hypertension', values='icu', aggfunc='count')
asthma_bySex.plot(kind='barh', stacked=True, figsize=[15,10], colormap='Dark2_r',ax=axs[0,1])

tobacco_bySex= dataOriginal.pivot_table(index='sex', columns='obesity', values='icu', aggfunc='count')
tobacco_bySex.plot(kind='barh', stacked=True, figsize=[15,10], colormap='Dark2_r',ax=axs[1,0])

pregnancy_bySex= dataOriginal.pivot_table(index='sex', columns='covid_res', values='icu', aggfunc='count')
pregnancy_bySex.plot(kind='barh', stacked=True, figsize=[15,10], colormap='Dark2_r',ax=axs[1,1])
```
Out[24]: `<matplotlib.axes._subplots.AxesSubplot at 0x2095f7493c8>`



In [25]:
```
pneumonia_bySex
```

Out[25]:

cardiovascular	1	2	98
sex			
1	5837	272893	760
2	6938	279112	1062

In [26]:
```
asthma_bySex
```

Out[26]:

hypertension	1	2	98
sex			
1	44727	234018	745
2	47781	238252	1079

In [27]:
```
tobacco_bySex
```

Out[27]:

obesity	1	2	98
sex			
1	47518	231235	737
2	44754	241314	1044

In [28]:
```
pregnancy_bySex
```

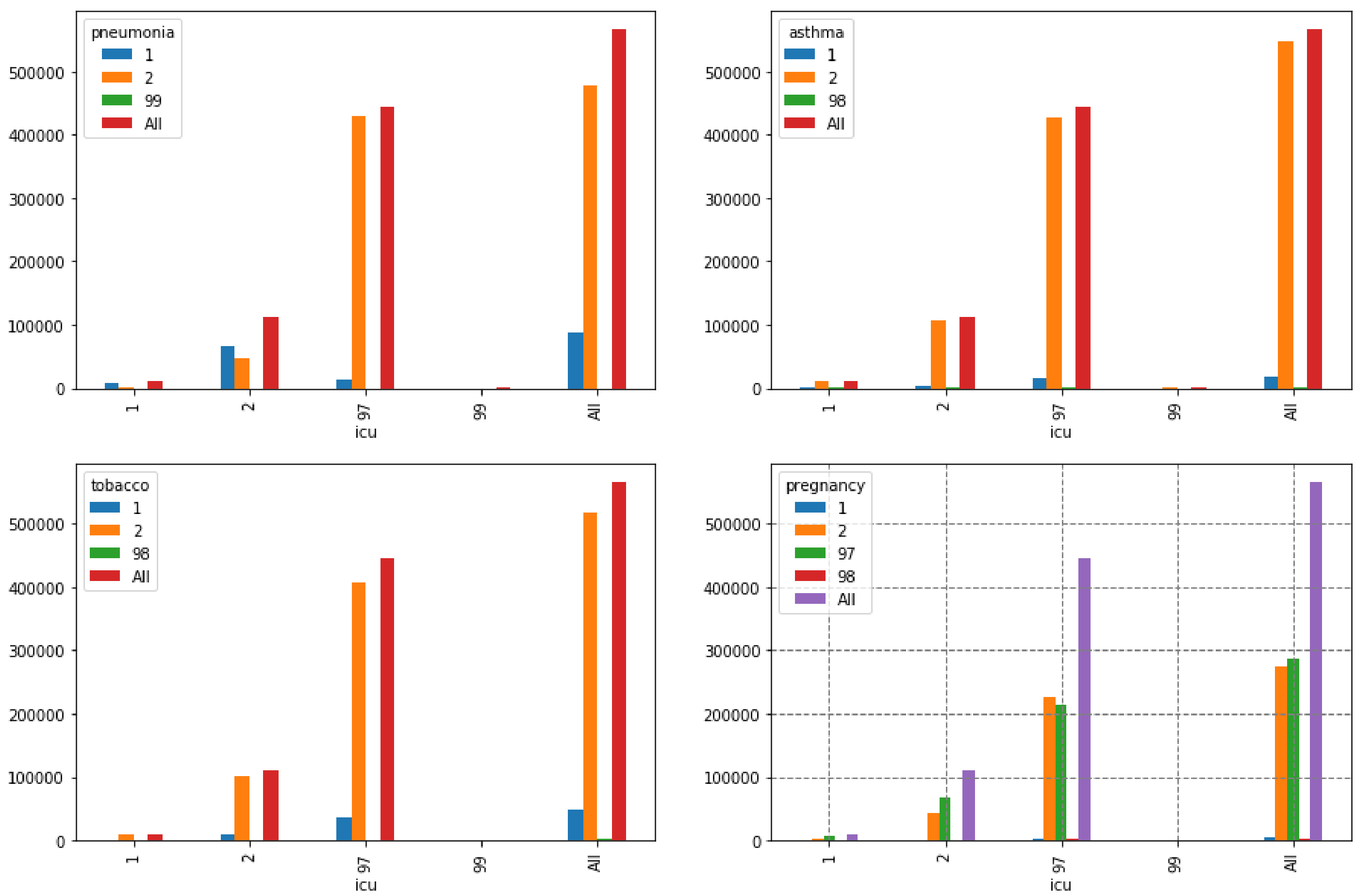
Out[28]:

covid_res	1	2	3
sex			
1	99858	146736	32896
2	120799	132299	34014

In [ ]:

Inspecting relationship between categorical variables - Diseases vs ICU assignation - Overview respiratory diseases

In [29]:
```python
fig, axs = plt.subplots(2,2)
pneumonia_byICU = pd.crosstab(index=dataOriginal['icu'],
            columns=dataOriginal['pneumonia'],
            margins=True)
pneumonia_byICU.plot(kind='bar',ax=axs[0,0], figsize=[15,10])
plt.grid(color='gray', linestyle='--', linewidth=1)
#plt.ylabel("Frequency")
#plt.title('Relationship between Asthma diagnostic and ICU assignation COVID')
asthma_byICU = pd.crosstab(index=dataOriginal['icu'],
            columns=dataOriginal['asthma'],
            margins=True)
asthma_byICU.plot(kind='bar',ax=axs[0,1])
plt.grid(color='gray', linestyle='--', linewidth=1)
#plt.ylabel("Frequency")
#plt.title('Relationship between Tobacco diagnostic and ICU assignation COVID')
tobacco_byICU = pd.crosstab(index=dataOriginal['icu'],
            columns=dataOriginal['tobacco'],
            margins=True)
tobacco_byICU.plot(kind='bar',ax=axs[1,0])
plt.grid(color='gray', linestyle='--', linewidth=1)
#plt.ylabel("Frequency")
#plt.title('Relationship between Pregnancy diagnostic and ICU assignation COVID')
pregnancy_byICU = pd.crosstab(index=dataOriginal['icu'],
            columns=dataOriginal['pregnancy'],
            margins=True)
pregnancy_byICU.plot(kind='bar',ax=axs[1,1])
plt.grid(color='gray', linestyle='--', linewidth=1)
#plt.ylabel("Frequency")
#plt.title('Relationship between Pneumonia diagnostic and ICU assignation COVID')
```



In [30]:
```python
pneumonia_byICU
```

Out[30]:

pneumonia	1	2	99	All
icu				
1	8393	1719	0	10112
2	65295	46381	0	111676
97	14428	430251	10	444689
99	59	65	1	125
All	88175	478416	11	566602

In [31]:
```python
asthma_byICU
```

Out[31]:

asthma	1	2	98	All
icu				
1	247	9751	114	10112
2	2894	108311	471	111676
97	14882	428640	1167	444689
99	3	122	0	125
All	18026	546824	1752	566602

In [32]:
```
tobacco_byICU
```

Out[32]:

tobacco	1	2	98	All
icu				
1	871	9128	113	10112
2	9865	101285	526	111676
97	37272	406149	1268	444689
99	9	116	0	125
All	48017	516678	1907	566602

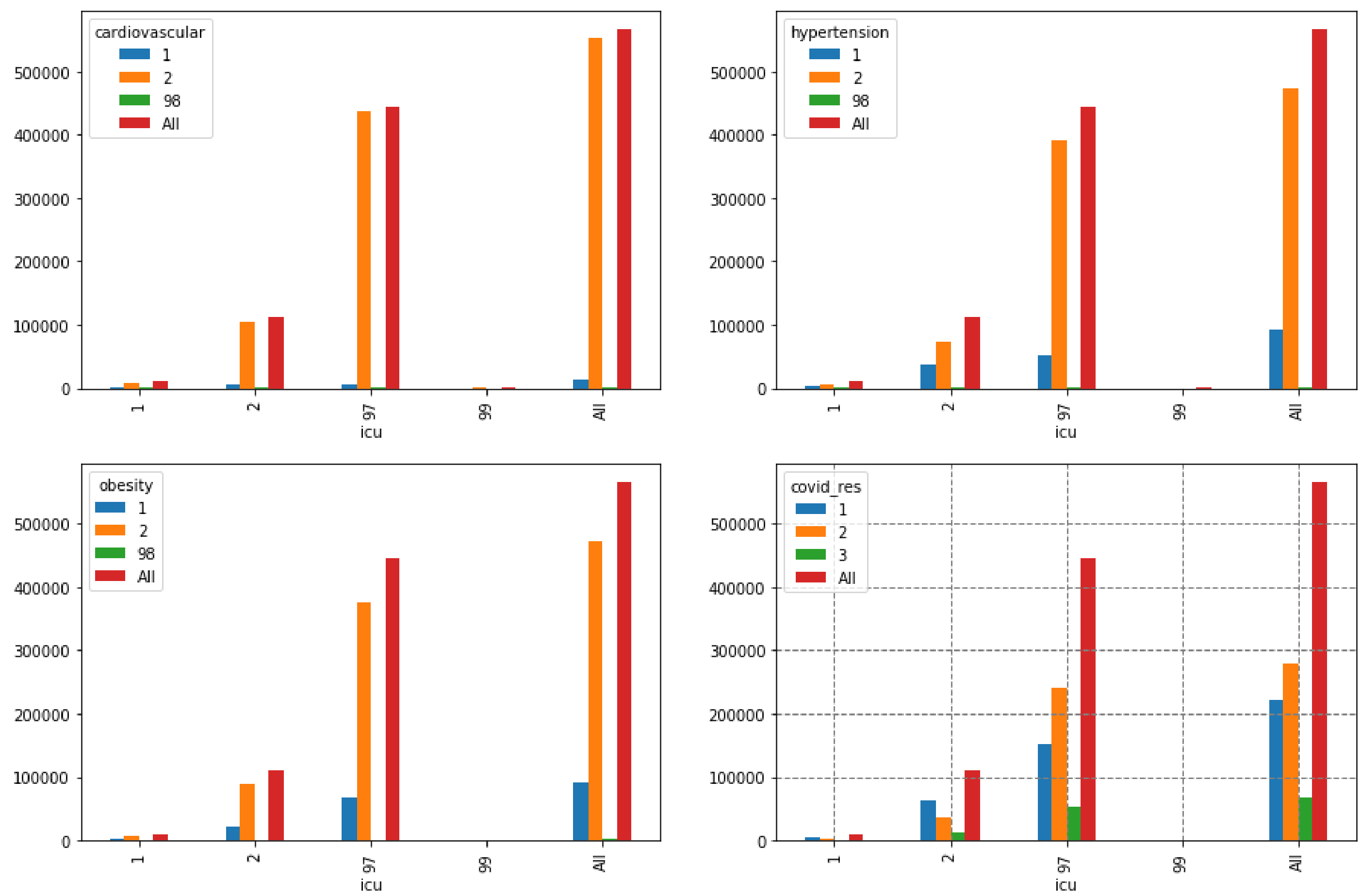
In [33]:
```
pregnancy_byICU
```

Out[33]:

pregnancy	1	2	97	98	All
icu					
1	74	3519	6500	19	10112
2	995	44035	66499	147	111676
97	2992	226235	214041	1421	444689
99	2	51	72	0	125
All	4063	273840	287112	1587	566602

Inspecting relationship between diseases and ICU assignation - Overview General diseases

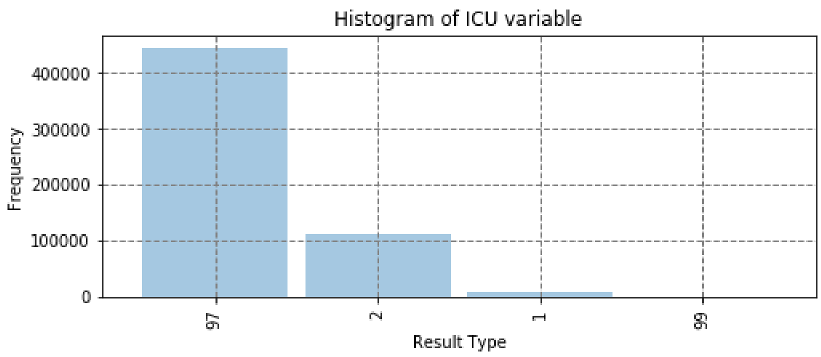
In [34]:
```
fig, axs = plt.subplots(2,2)
pneumonia_byICU = pd.crosstab(index=dataOriginal['icu'],
            columns=dataOriginal['cardiovascular'],
            margins=True)
pneumonia_byICU.plot(kind='bar',ax=axs[0,0], figsize=[15,10])
plt.grid(color='gray', linestyle='--', linewidth=1)
#plt.ylabel("Frequency")
#plt.title('Relationship between Asthma diagnostic and ICU assignation COVID')
asthma_byICU = pd.crosstab(index=dataOriginal['icu'],
            columns=dataOriginal['hypertension'],
            margins=True)
asthma_byICU.plot(kind='bar',ax=axs[0,1])
plt.grid(color='gray', linestyle='--', linewidth=1)
#plt.ylabel("Frequency")
#plt.title('Relationship between Tobacco diagnostic and ICU assignation COVID')
tobacco_byICU = pd.crosstab(index=dataOriginal['icu'],
            columns=dataOriginal['obesity'],
            margins=True)
tobacco_byICU.plot(kind='bar',ax=axs[1,0])
plt.grid(color='gray', linestyle='--', linewidth=1)
#plt.ylabel("Frequency")
#plt.title('Relationship between Pregnancy diagnostic and ICU assignation COVID')
pregnancy_byICU = pd.crosstab(index=dataOriginal['icu'],
            columns=dataOriginal['covid_res'],
            margins=True)
pregnancy_byICU.plot(kind='bar',ax=axs[1,1])
plt.grid(color='gray', linestyle='--', linewidth=1)
#plt.ylabel("Frequency")
#plt.title('Relationship between Pneumonia diagnostic and ICU assignation COVID')
```



In [ ]:

3.1. Classes identification

In [35]:
```
targetOriginal = dataOriginal['icu']
E1 = targetOriginal.value_counts()
E1.plot(kind = 'bar',
           stacked = 'True',          # Muestra las barras apiladas
           alpha = 0.4,               # nivel de transparencia
           width = 0.9,               # Grosor de las barras para dejar espacio entre ellas
           figsize=(8,3));

plt.grid(color='gray', linestyle='--', linewidth=1)
plt.title('Histogram of ICU variable')
plt.xlabel("Result Type")
plt.ylabel("Frequency")
plt.show()
```



In [36]:
```
cat_si_no
```

Out[36]:

	CLAVE	DESCRIPCIÓN
0	1	SI
1	2	NO
2	97	NO APLICA
3	98	SE IGNORA
4	99	NO ESPECIFICADO

3.2. Check the distribution or instances of any class

In [37]:
```
pd.DataFrame(targetOriginal.value_counts())
```

Out[37]:

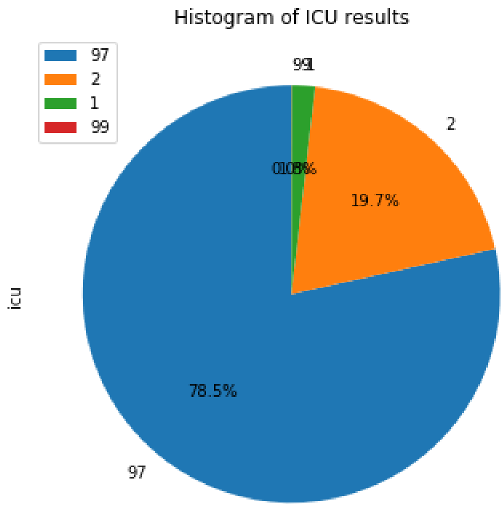
	icu
97	444689
2	111676
1	10112
99	125

In [38]:
```
pd.DataFrame(targetOriginal.value_counts(normalize=True) * 100)
```

Out[38]:

	icu
97	78.483486
2	19.709779
1	1.784674
99	0.022061

In [39]:
```python
E2 = targetOriginal.value_counts(normalize=True)
E2.plot.pie(subplots=True, figsize = (6,6), autopct = '%1.1f%%', startangle = 90)
plt.title('Histogram of ICU results')
plt.legend(E2.index, loc = 'upper left', fontsize = 10)
plt.show() #ok
```



4. Splitting DATA to create Training and Test sets.

In [3]:
```python
# Labels for descriptors

datalabels = ['id', 'sex', 'patient_type', 'entry_date', 'date_symptoms',
              'date_died','intubed','pneumonia','age','pregnancy','diabetes','copd','asthma','inmsupr','hypertensi
on',
              'other_disease','cardiovascular','obesity','renal_chronic','tobacco','contact_other_covid'
              ,'covid_res','icu']

# Ignored: id, entrydate, date_symptons, date_died, icu
predictors = ['sex', 'patient_type',
              'intubed','pneumonia','age','pregnancy','diabetes','copd','asthma','inmsupr','hypertension',
              'other_disease','cardiovascular','obesity','renal_chronic','tobacco',
              'contact_other_covid','covid_res']

target_column= 'icu'

model_columns = ['sex', 'patient_type',
              'intubed','pneumonia','age','pregnancy','diabetes','copd','asthma','inmsupr','hypertension',
              'other_disease','cardiovascular','obesity','renal_chronic','tobacco',
              'contact_other_covid','covid_res', target_column]
```

In [4]:
```python
# Split in traning and test sets

from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test =train_test_split(dataOriginal[predictors],
                                                    dataOriginal[target_column],
                                                    test_size=0.20, random_state=44)

print("Size training set: ", X_train.shape)
print("Size test set: ", X_test.shape)
```

```
Size training set:  (453281, 18)
Size test set:  (113321, 18)
```

In [ ]:

4. IMPUTATION AND DETECTION OF NULL AND ODD VALUES.

Make transformations with mocked data in order to show competences???

I didnt find odd values.

In [42]:
```python
print(model_columns)
```

```
['sex', 'patient_type', 'intubed', 'pneumonia', 'age', 'pregnancy', 'diabetes', 'copd', 'asthma', 'inmsupr', 'hype
rtension', 'other_disease', 'cardiovascular', 'obesity', 'renal_chronic', 'tobacco', 'contact_other_covid', 'covid
_res', 'icu']
```

Check for null values in the dataset

/

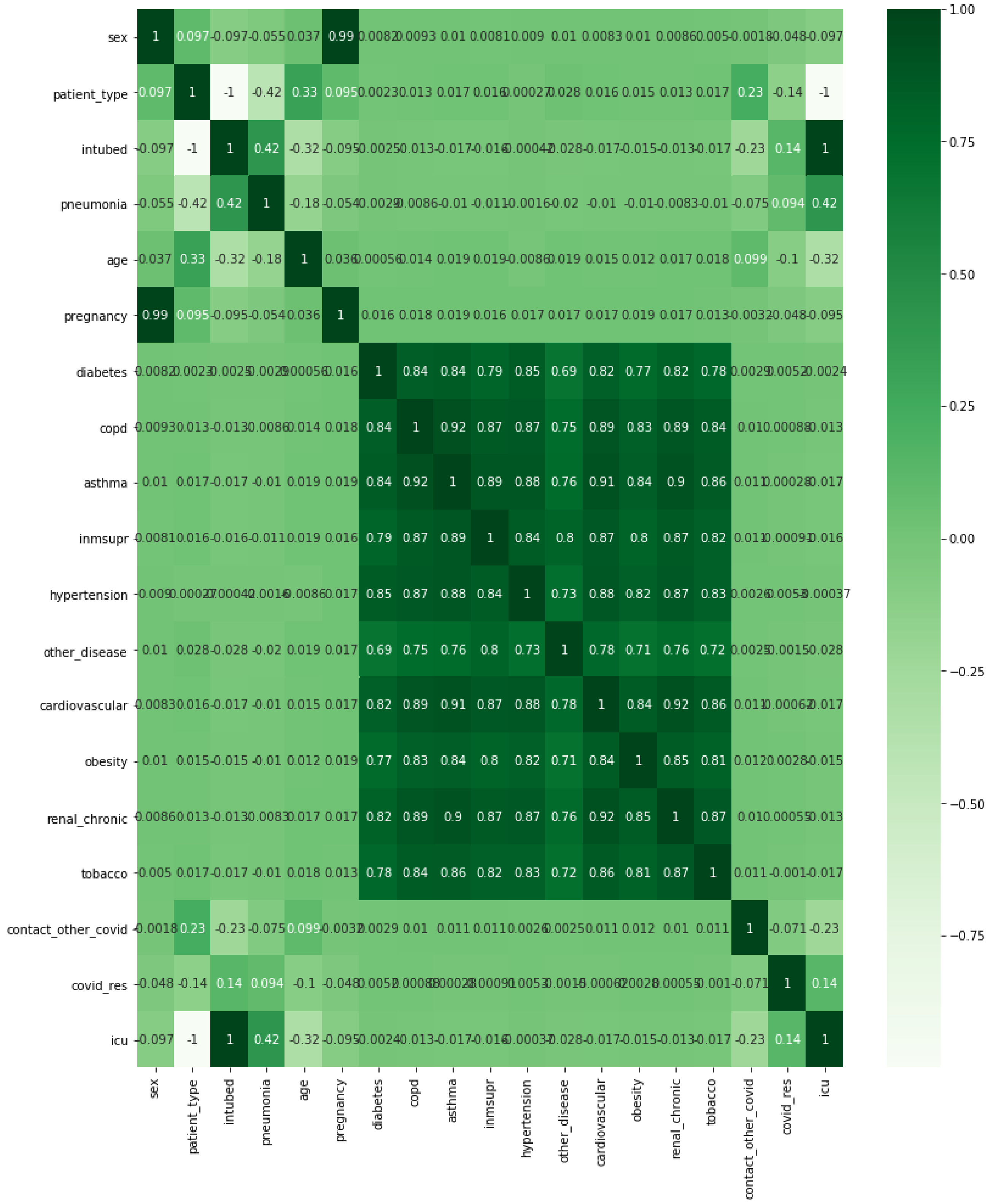
```
In [43]: X_train[predictors].isnull().values.sum()
Out[43]: 0
```

```
In [44]: y_train.isnull().values.sum()
Out[44]: 0
```

5. CORRELATION ANALYSIS

5.1 Correlation Matrix

```
In [37]: import seaborn as sn

         #The default correlation Algorithme user is Pearson, which its not appropiate for categorical
         #variables but its interesting to see  its able to detect  dependent variables detected with Chi-squared too.

         df = pd.DataFrame(dataOriginal[model_columns], columns=model_columns)
         plt.figure(figsize=(13,16))
         corrMatrix = df.corr()
         sn.heatmap(corrMatrix, annot=True, cmap="Greens")
         plt.show()
```



All the maladies are really corelated, for example: - Renal_chronic vs Tobacco - Asthma et tobaccon are highly corelated to all diseases. - Sex correlated with age?

In [38]:
```
df.corr()
```

Out[38]:

	sex	patient_type	intubed	pneumonia	age	pregnancy	diabetes	copd	asthma	inmsupr	hyperte
sex	1.000000	0.097025	-0.097029	-0.054758	0.036709	0.994293	0.008153	0.009339	0.010119	0.008096	0.00
patient_type	0.097025	1.000000	-0.999319	-0.420400	0.325059	0.095472	0.002315	0.013227	0.016670	0.016359	0.00
intubed	-0.097029	-0.999319	1.000000	0.421256	-0.324869	-0.095481	-0.002456	-0.013363	-0.016807	-0.016424	-0.00
pneumonia	-0.054758	-0.420400	0.421256	1.000000	-0.183492	-0.054031	-0.002875	-0.008592	-0.010370	-0.010979	-0.00
age	0.036709	0.325059	-0.324869	-0.183492	1.000000	0.036239	0.000556	0.014440	0.018668	0.018625	-0.00
pregnancy	0.994293	0.095472	-0.095481	-0.054031	0.036239	1.000000	0.016239	0.018035	0.018931	0.016412	0.01
diabetes	0.008153	0.002315	-0.002456	-0.002875	0.000556	0.016239	1.000000	0.838368	0.843817	0.794140	0.84
copd	0.009339	0.013227	-0.013363	-0.008592	0.014440	0.018035	0.838368	1.000000	0.922057	0.866870	0.87
asthma	0.010119	0.016670	-0.016807	-0.010370	0.018668	0.018931	0.843817	0.922057	1.000000	0.886307	0.88
inmsupr	0.008096	0.016359	-0.016424	-0.010979	0.018625	0.016412	0.794140	0.866870	0.886307	1.000000	0.84
hypertension	0.009019	0.000274	-0.000419	-0.001568	-0.008617	0.017474	0.845727	0.872321	0.883549	0.844534	1.00
other_disease	0.010155	0.028232	-0.028389	-0.019541	0.018627	0.017392	0.688245	0.748066	0.756712	0.800965	0.73
cardiovascular	0.008344	0.016446	-0.016587	-0.010392	0.015049	0.016854	0.821716	0.893562	0.906039	0.872862	0.87
obesity	0.010199	0.014967	-0.015101	-0.010070	0.012068	0.018692	0.765574	0.827598	0.839128	0.804051	0.82
renal_chronic	0.008577	0.013240	-0.013384	-0.008296	0.016643	0.016970	0.817052	0.889774	0.901793	0.866491	0.87
tobacco	0.004980	0.016603	-0.016738	-0.009996	0.017531	0.013060	0.777978	0.844021	0.855136	0.821285	0.82
contact_other_covid	-0.001791	0.228929	-0.228811	-0.074756	0.099339	-0.003185	0.002895	0.010322	0.010714	0.010554	0.00
covid_res	-0.047575	-0.135931	0.135738	0.093832	-0.102643	-0.047589	0.005156	0.000882	0.000276	-0.000914	0.00
icu	-0.097024	-0.999314	0.999989	0.421182	-0.324791	-0.095474	-0.002429	-0.013308	-0.016759	-0.016299	-0.00

5.2. Correlation between numerique and categorical information - Age vs diseases.

In [46]:
```
#ANOVA
```

In [ ]:

6. VARIABLE REDUCTION

[https://machinelearningmastery.com/feature-selection-with-real-and-categorical-data/ (https://machinelearningmastery.com/feature-selection-with-real-and-categorical-data/)](https://machinelearningmastery.com/feature-selection-with-real-and-categorical-data/)

Jai essaie Variance Tresholding, normalisation et standarisation, mais ca marche pas pour notre cas.

6.1. Based on exploration info

In [72]:
```
# Reduce variables based on correlation

# Patient_type and intubed are the same information of icu.  We have to eliminate from dataModel.

predictors.remove('intubed')
predictors.remove('patient_type')
```

6.2. Variances Tresholding

Normalisation, Variance Tresholding and Standarisation doesnt apply for most of our model descriptors, variance its important in descriptors where means, mode distribution has significant information value.

the degree of association between predictor and outcome can be measured with statistics such as X2 (chi-squared) tests.

i did it but doesnt work well with categorical

6.2. Chi-Squared Feature Selection

Pearson’s chi-squared statistical hypothesis test is an example of a test for independence between categorical variables

The degree of association between predictor and outcome can be measured with statistics such as X2 (chi-squared) tests.

1.Define Hypothesis Null Hypothesis (H0): Two variables are independent. Alternate Hypothesis (H1): Two variables are not independent.

https://towardsdatascience.com/the-search-for-categorical-correlation-a1cf7f1888c9 https://towardsdatascience.com/categorical-feature-selection-via-chi-square-fc558b09de43 https://towardsdatascience.com/feature-selection-with-pandas-e3690ad8504b https://towardsdatascience.com/the-search-for-categorical-correlation-a1cf7f1888c9

In [73]:
```
# Labels for descriptors

model_columns = ['sex', 'pneumonia','age','pregnancy','diabetes','copd','asthma','inmsupr','hypertension',
              'other_disease','cardiovascular','obesity','renal_chronic','tobacco',
              'contact_other_covid','covid_res', target_column]
```

In [75]:
```
import scipy.stats as ss #import chi2_contingency

def cramers_v(x, y):
    confusion_matrix = pd.crosstab(x,y)
    chi2 = ss.chi2_contingency(confusion_matrix)[0]
    n = confusion_matrix.sum().sum()
    phi2 = chi2/n
    r,k = confusion_matrix.shape
    phi2corr = max(0, phi2-((k-1)*(r-1))/(n-1))
    rcorr = r-((r-1)**2)/(n-1)
    kcorr = k-((k-1)**2)/(n-1)
    return round(np.sqrt(phi2corr/min((kcorr-1),(rcorr-1))),3)


cramers_v(X_train['pneumonia'], X_train['sex'])
```

Out[75]:
```
0.085
```

In [76]:
```
cramers_v(X_train['hypertension'], X_train['obesity'])
```

Out[76]:
```
0.593
```

In [77]:
```
model_columns
```

Out[77]:
```
['sex',
 'pneumonia',
 'age',
 'pregnancy',
 'diabetes',
 'copd',
 'asthma',
 'inmsupr',
 'hypertension',
 'other_disease',
 'cardiovascular',
 'obesity',
 'renal_chronic',
 'tobacco',
 'contact_other_covid',
 'covid_res',
 'icu']
```

In [78]:
```python
XY = X_train
XY['icu'] = y_train

df2 = pd.DataFrame(columns=model_columns, index=model_columns)
for i in range(len(model_columns)):
    for j in range(len(model_columns)):
      #  print("f: " + fname + "    c: "+ cname)
        fname = model_columns[i]
        cname = model_columns[j]
        df2.loc[fname, cname] = cramers_v(X_train[fname], X_train[cname])

display(df2)
```

	sex	pneumonia	age	pregnancy	diabetes	copd	asthma	inmsupr	hypertension	other_disease	cardiovascular	ob
sex	1	0.085	0.054	1	0.017	0.011	0.047	0.01	0.013	0.027	0.014	(
pneumonia	0.085	1	0.227	0.061	0.153	0.068	0.015	0.048	0.135	0.041	0.057	
age	0.054	0.227	1	0.067	0.255	0.157	0.03	0.054	0.294	0.058	0.123	(
pregnancy	1	0.061	0.067	1	0.056	0.056	0.065	0.053	0.058	0.051	0.055	(
diabetes	0.017	0.153	0.255	0.056	1	0.597	0.599	0.565	0.657	0.488	0.588	(
copd	0.011	0.068	0.157	0.056	0.597	1	0.652	0.614	0.621	0.529	0.634	(
asthma	0.047	0.015	0.03	0.065	0.599	0.652	1	0.628	0.626	0.535	0.642	(
inmsupr	0.01	0.048	0.054	0.053	0.565	0.614	0.628	1	0.599	0.576	0.618	
hypertension	0.013	0.135	0.294	0.058	0.657	0.621	0.626	0.599	1	0.52	0.633	(
other_disease	0.027	0.041	0.058	0.051	0.488	0.529	0.535	0.576	0.52	1	0.55	
cardiovascular	0.014	0.057	0.123	0.055	0.588	0.634	0.642	0.618	0.633	0.55	1	(
obesity	0.021	0.05	0.092	0.057	0.549	0.585	0.596	0.57	0.593	0.5	0.599	
renal_chronic	0.018	0.074	0.086	0.055	0.593	0.63	0.641	0.619	0.632	0.541	0.654	(
tobacco	0.105	0.013	0.051	0.091	0.554	0.601	0.61	0.584	0.59	0.513	0.614	(
contact_other_covid	0.049	0.131	0.123	0.042	0.078	0.041	0.016	0.034	0.081	0.091	0.029	(
covid_res	0.069	0.135	0.118	0.05	0.071	0.012	0.021	0.015	0.062	0.013	0.011	(
icu	0.098	0.464	0.24	0.058	0.187	0.088	0.02	0.07	0.168	0.068	0.075	(

In [79]:
```python
X_train.head(5)
```

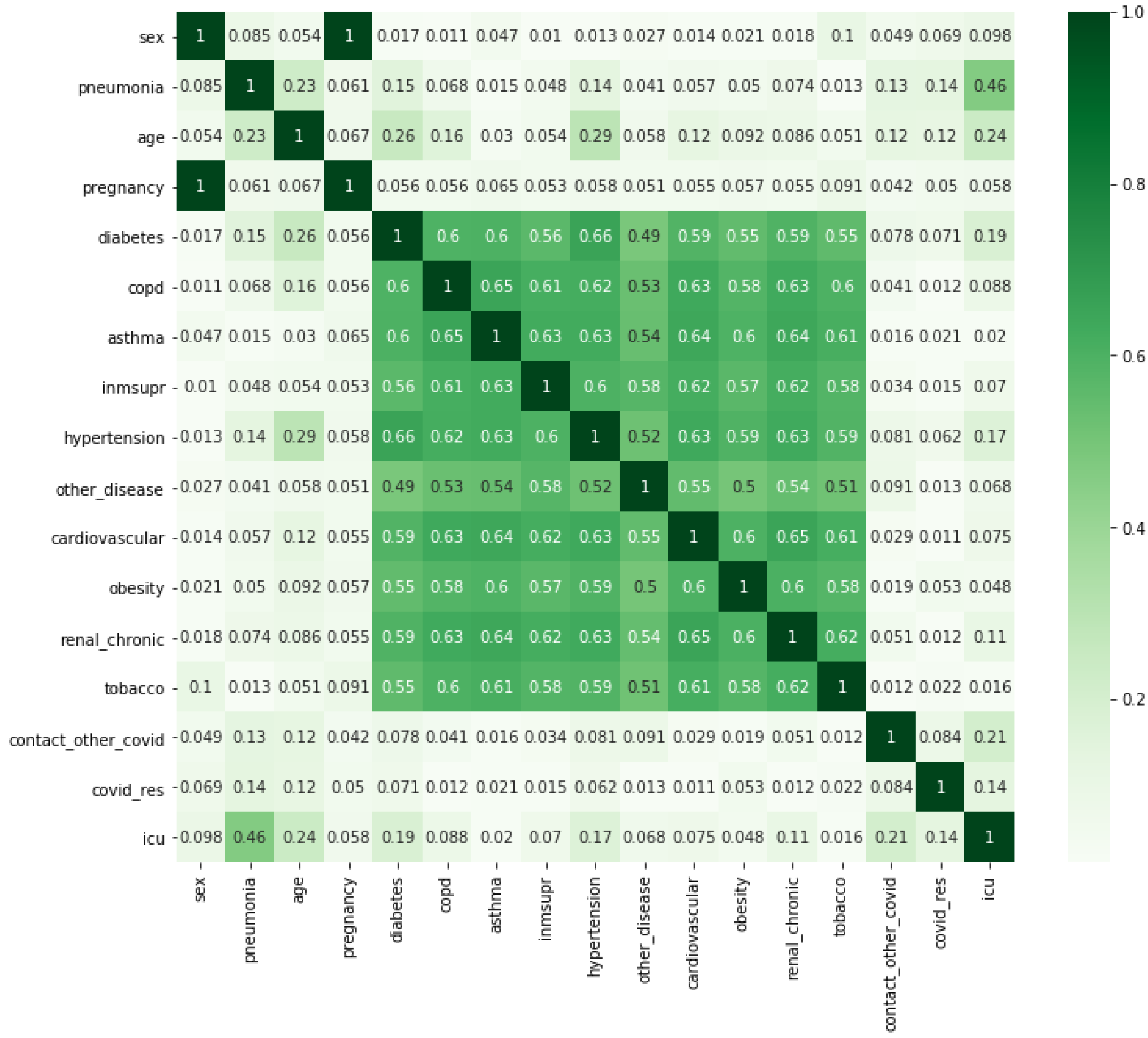
Out[79]:

	sex	patient_type	intubed	pneumonia	age	pregnancy	diabetes	copd	asthma	inmsupr	hypertension	other_disease	cardiovascul
380621	1	1	97	2	42	2	2	2	2	2	2	2	
215435	2	2	1	1	60	97	2	2	2	2	2	2	
81577	2	1	97	2	25	97	2	2	2	2	2	2	
508482	1	1	97	2	29	2	2	2	2	2	2	2	
430578	1	1	97	2	41	2	2	2	2	2	2	2	

In [80]:
```python
df2.shape
```

Out[80]:
```
(17, 17)
```

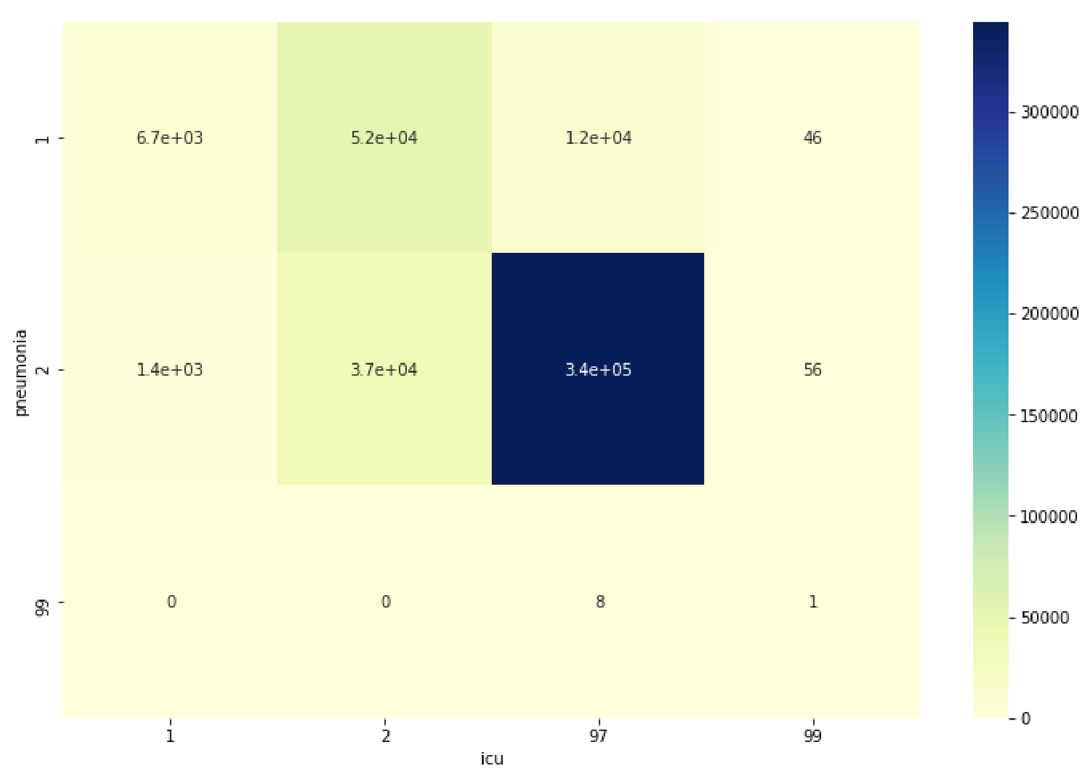
In [81]:
```python
#df = pd.DataFrame(index=predictors, columns=predictors)
import seaborn as sns

df2 = df2.astype('float')  # !! Neccessary for Heatmap

plt.figure(figsize=(12,10))
sns.heatmap(df2, annot=True, cmap="Greens")
plt.show()
```



In [67]:
```python
# TODO UTIL?
```

In [9]:
```python
contigency= pd.crosstab(X_train['pneumonia'], y_train)
contigency
plt.figure(figsize=(12,8))
sns.heatmap(contigency, annot=True, cmap="YlGnBu")
```

Out[9]: <matplotlib.axes._subplots.AxesSubplot at 0x16aeee32e08>



6.3. Componenent Analysis

7. MODELISATION & PREDICTION

In [5]:
```
# Define variables to eliminate and continue

predictors = ['sex','pneumonia','age','pregnancy','diabetes','copd','asthma','inmsupr','hypertension',
              'other_disease','cardiovascular','obesity','renal_chronic','tobacco',
              'contact_other_covid','covid_res']

target_column= 'icu'


model_columns = ['sex','pneumonia','age','pregnancy','diabetes','copd','asthma','inmsupr','hypertension',
              'other_disease','cardiovascular','obesity','renal_chronic','tobacco',
              'contact_other_covid','covid_res', target_column]
```

7.1 KNN

In [6]:
```
from sklearn import neighbors, datasets

weights = 'uniform'
k_neighbors = 15
model1 = neighbors.KNeighborsClassifier(weights=weights)
model1.fit(X_train, y_train.values.ravel())
```

Out[6]:
```
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                     metric_params=None, n_jobs=None, n_neighbors=5, p=2,
                     weights='uniform')
```

7.1.1 Model Evaluation

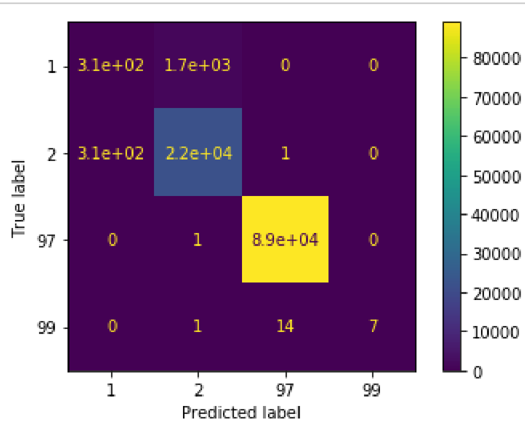
In [7]:
```
# METRIQUES

from sklearn import metrics
from sklearn.metrics import accuracy_score
from sklearn.metrics import classification_report, confusion_matrix

y_predicted_train = model1.predict(X_train)
y_predicted_test = model1.predict(X_test)

print("Accuracy:", metrics.accuracy_score(y_predicted_test, y_test))
```

```
Accuracy: 0.9822716001447216
```

In [8]:
```
print(confusion_matrix(y_test, y_predicted_test))
```

```
[[  312  1678     0     0]
 [  314 21924     1     0]
 [    0     1 89069     0]
 [    0     1    14     7]]
```

In [12]:
```
from sklearn.metrics import plot_confusion_matrix

plot_confusion_matrix(model1, X_test, y_test)
plt.show()
```



In [9]:
```
print("Precision: ", metrics.precision_score(y_test, y_predicted_test, labels=None, pos_label=1, average='weighte
d',
                                        sample_weight=None,zero_division='warn'))
```

```
Precision:  0.9770914170233116
```

In [10]:
```
print ("Recall:", metrics.recall_score(y_test, y_predicted_test,  average='macro') )
```

```
Recall: 0.6151975511765166
```

In [11]:
```
print ("F1 score:", metrics.f1_score(y_test, y_predicted_test, average='macro'))
```

```
F1 score: 0.6694207066190329
```

7.1.1. Model

```
In [ ]:
```

```
In [ ]:
```

```
In [ ]:
```

```
In [ ]:
```

7.1.2. Prediction

```
In [ ]:
```

7.2. Desicion Tree

```
In [ ]:
```

7.3. Nayve Bayes

8. CONCLUSIONS

```
In [ ]:
```