In [1]:

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

In [2]:

```
df = pd.read_csv('scaler_apollo_hospitals.csv')
```

In [3]:

```
df.head()
```

Out[3]:

	Unnamed: 0	age	sex	smoker	region	viral load	severity level	hospitalization charges
0	0	19	female	yes	southwest	9.30	0	42212
1	1	18	male	no	southeast	11.26	1	4314
2	2	28	male	no	southeast	11.00	3	11124
3	3	33	male	no	northwest	7.57	0	54961
4	4	32	male	no	northwest	9.63	0	9667

removing the unnamed column from the dataset

In [4]:

```
df.drop('Unnamed: 0',axis=1,inplace=True)
```

from the info command it is clear that their are total 7 columns(features) and 1338 rows(values).

In [5]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1338 entries, 0 to 1337
Data columns (total 7 columns):
 #   Column                   Non-Null Count  Dtype  
---  ------                   --------------  -----  
 0   age                      1338 non-null   int64  
 1   sex                      1338 non-null   object 
 2   smoker                   1338 non-null   object 
 3   region                   1338 non-null   object 
 4   viral load               1338 non-null   float64
 5   severity level           1338 non-null   int64  
 6   hospitalization charges  1338 non-null   int64  
dtypes: float64(1), int64(3), object(3)
memory usage: 73.3+ KB
```

from the below cell we see that their are no missing values in the data.

In [24]:

```
df.isna().sum()
```

Out[24]:

```
age                        0
sex                        0
smoker                     0
region                     0
viral load                 0
severity level             0
hospitalization charges    0
dtype: int64
```

from the describe command we see that mean age is 39 years median age is also 39 yaers minimum age is 18 years and the maximum age is 64 years

mean viral load is 10 and also the median viral load is also 10 min viral load is 5 and the maximim viral load is 17

mean severity is 1 median severity is 1 min severity is 0 and the maximum severity is 5

mean hostitalization charges are 33176 median charges are 23455 min charges are 2805 and the max charges are 159426(this value is effected by outlyers as the difference between mean and median is too large)

In [6]:

```
df.describe()
```

Out[6]:

	age	viral load	severity level	hospitalization charges
count	1338.000000	1338.000000	1338.000000	1338.000000
mean	39.207025	10.221233	1.094918	33176.058296
std	14.049960	2.032796	1.205493	30275.029296
min	18.000000	5.320000	0.000000	2805.000000
25%	27.000000	8.762500	0.000000	11851.000000
50%	39.000000	10.130000	1.000000	23455.000000
75%	51.000000	11.567500	2.000000	41599.500000
max	64.000000	17.710000	5.000000	159426.000000

In [7]:

```
df.describe(include='object')
```

Out[7]:

	sex	smoker	region
count	1338	1338	1338
unique	2	2	4
top	male	no	southeast
freq	676	1064	364

In [8]:

```
df['age'].value_counts()
```

Out[8]:

```
18    69
19    68
51    29
45    29
46    29
47    29
48    29
50    29
52    29
20    29
26    28
54    28
53    28
25    28
24    28
49    28
23    28
22    28
21    28
27    28
28    28
31    27
29    27
30    27
41    27
43    27
44    27
40    27
42    27
57    26
34    26
33    26
32    26
56    26
55    26
59    25
58    25
39    25
38    25
35    25
36    25
37    25
63    23
60    23
61    23
62    23
64    22
Name: age, dtype: int64
```

In [9]:

```
df['viral load'].value_counts()
```

Out[9]:

```
10.77    13
9.63     13
10.17    12
11.37    12
9.94     10
         ..
12.51     1
11.02     1
8.21      1
6.77      1
11.56     1
Name: viral load, Length: 462, dtype: int64
```

for the severity 0 their are 574 cases and for the severity 1 their are 324 cases and for th eseverity 2 their are 240 cases etc

In [10]:

```
df['severity level'].value_counts()
```

Out[10]:

```
0    574
1    324
2    240
3    157
4     25
5     18
Name: severity level, dtype: int64
```

the hospitilazition charges vary depends on the case

In [28]:

```
df['hospitalization charges'].value_counts()
```

Out[28]:

```
26504    2
20836    2
11799    2
33677    2
35986    2
        ..
4083     1
36187    1
26501    1
99679    1
6144     1
Name: hospitalization charges, Length: 1320, dtype: int64
```

for the column region their are 4 unique values southwest southeast nortwest and northeast

In [12]:

```
df['region'].unique()
```

Out[12]:

```
array(['southwest', 'southeast', 'northwest', 'northeast'], dtype=object)
```

from the below we are converting the categorical values to category like for sex we are replacing male with 1 and female with 0 etc

In [13]:

```
cal_num = dict({'smoker':{'yes':1,"no":0},'sex':{'male':1,'female':0},'region':{'southwest'
df = df.replace(cal_num)
```

Univariate Analysis

the following function will plot the boxplots of all the columns present in the dataframe

In [14]:

```
def box_plots(df):
    plt.figure(figsize=(10,25))
    for i in range(len(df.columns)):
        plt.subplot(7,1,i+1)
        sns.boxplot(data=df,x=df.columns[i])
        plt.ylabel(df.columns[i])
    plt.show()
```

except viral load and the hospitilization charges no other feature have outlyers

most of the seviarity level lyes between 0 and 2

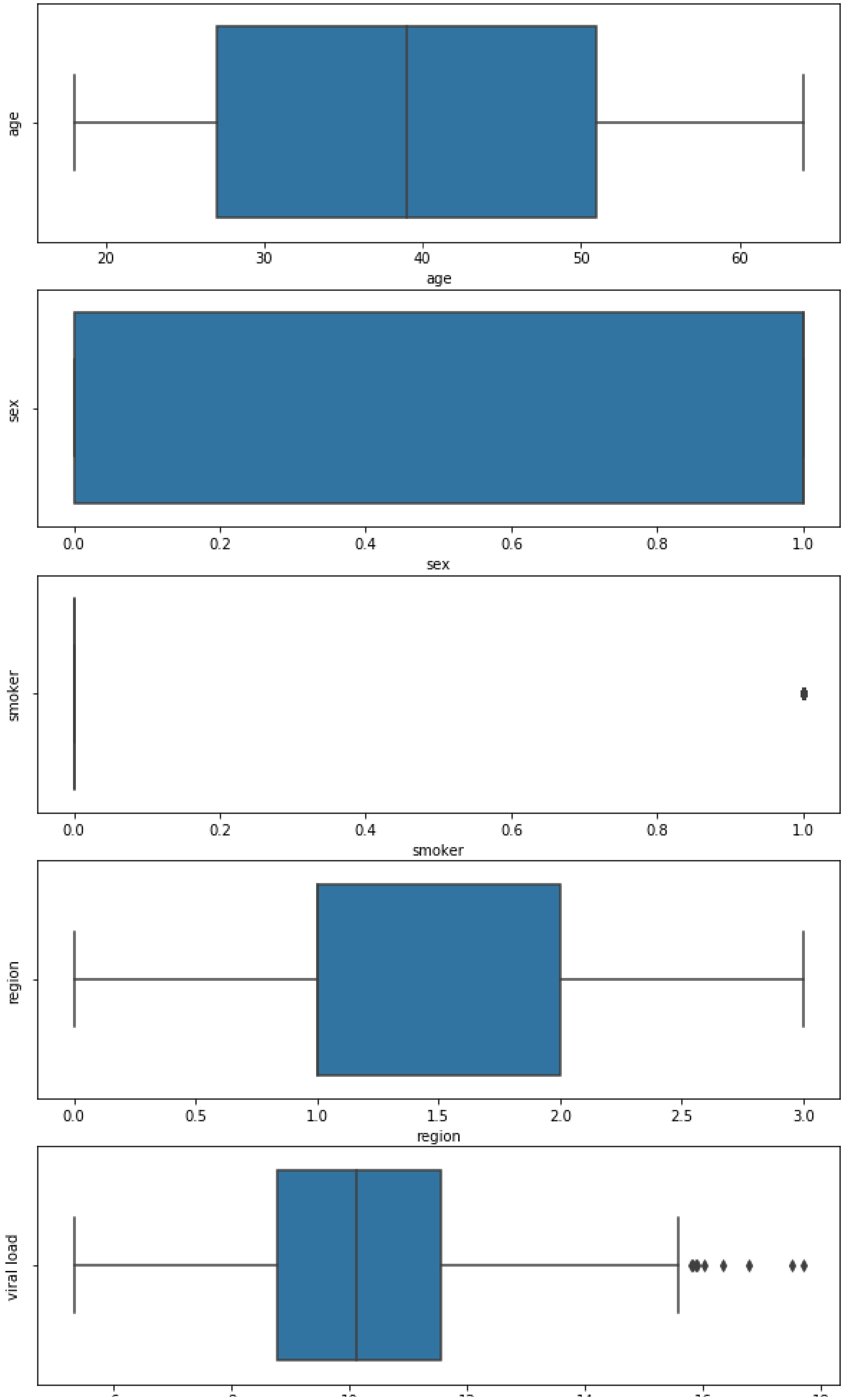
the are group 25 to 52 are the most effected people

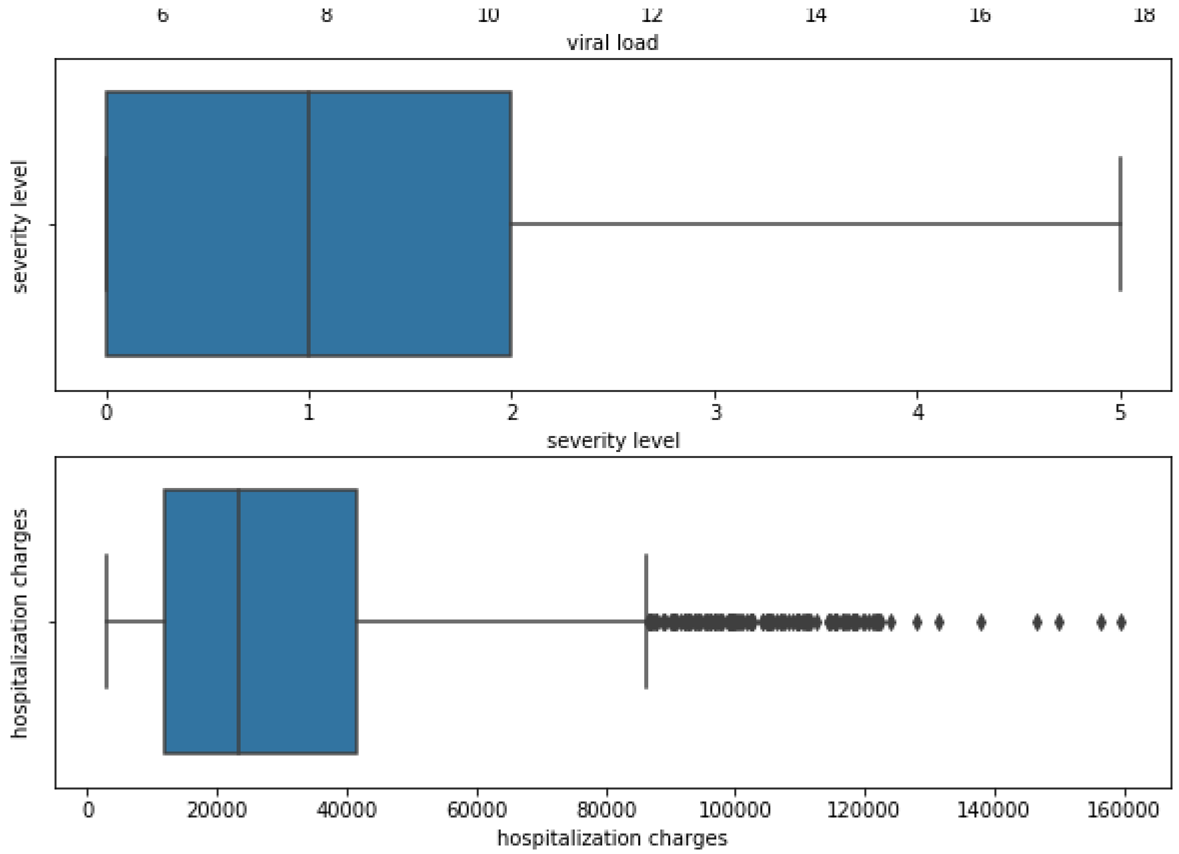
the regions 1 and 2 are most effected

mostly the viral load is between 8 and 10 viral load is having outlyers

In [15]:

```
box_plots(df)
```



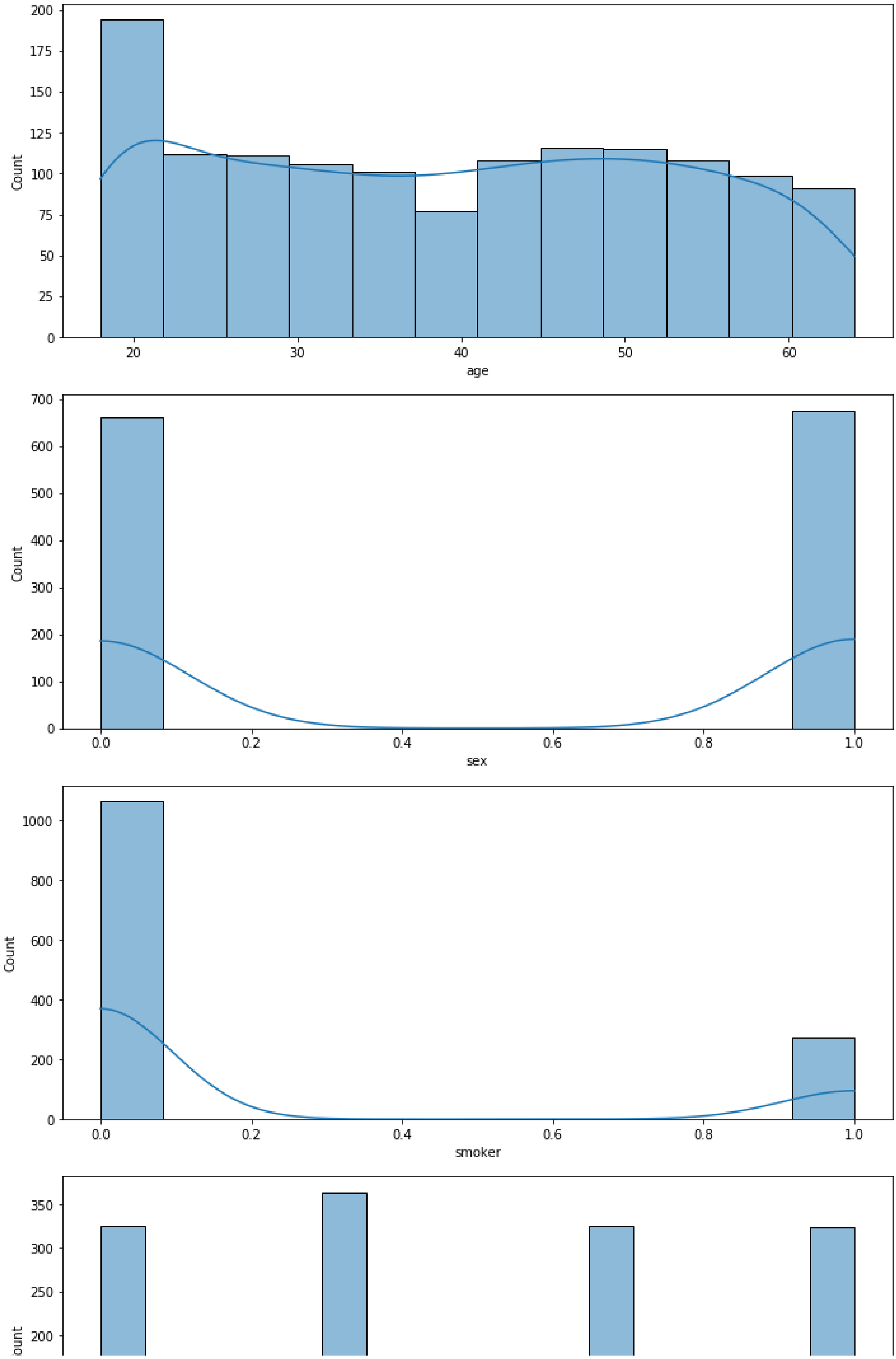


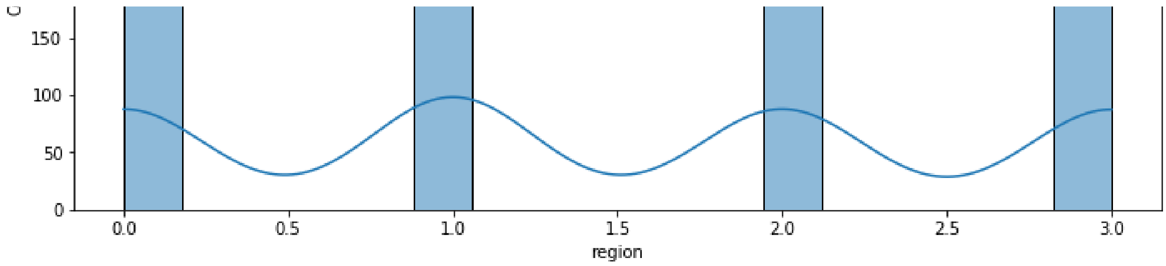
the following for loop will plot the univariate box histplot for all the features

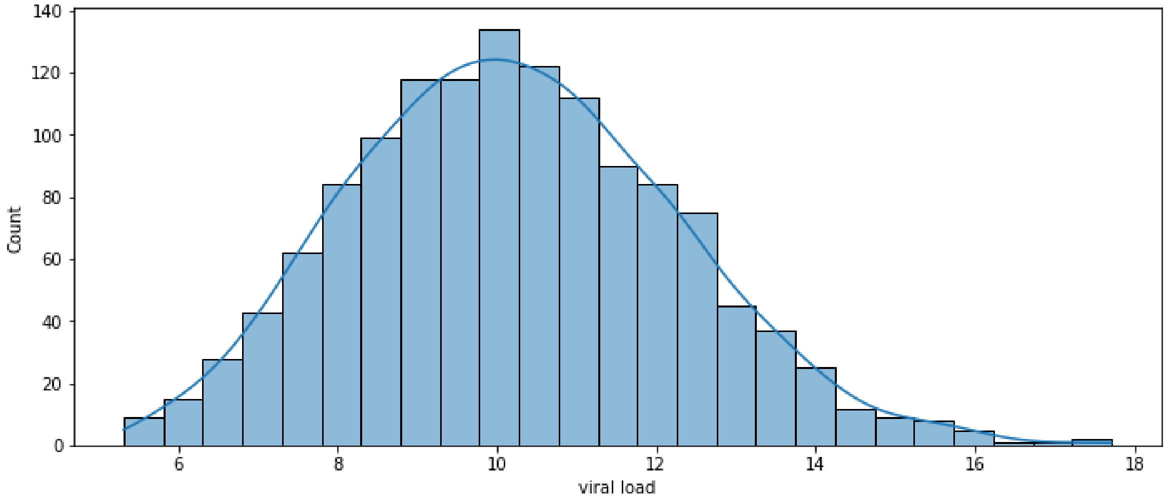
we infer the same conclusions as boxplot.

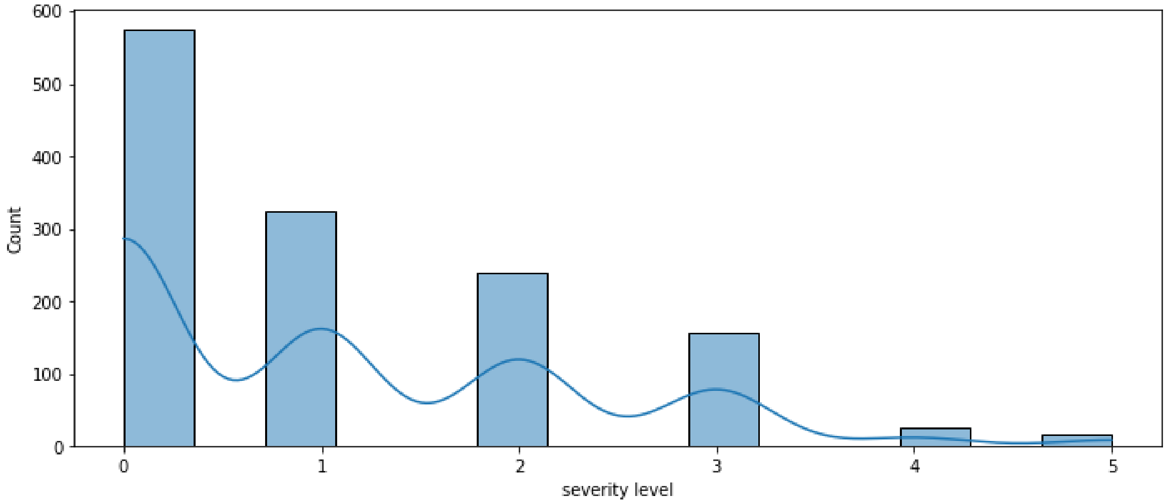
In [16]:

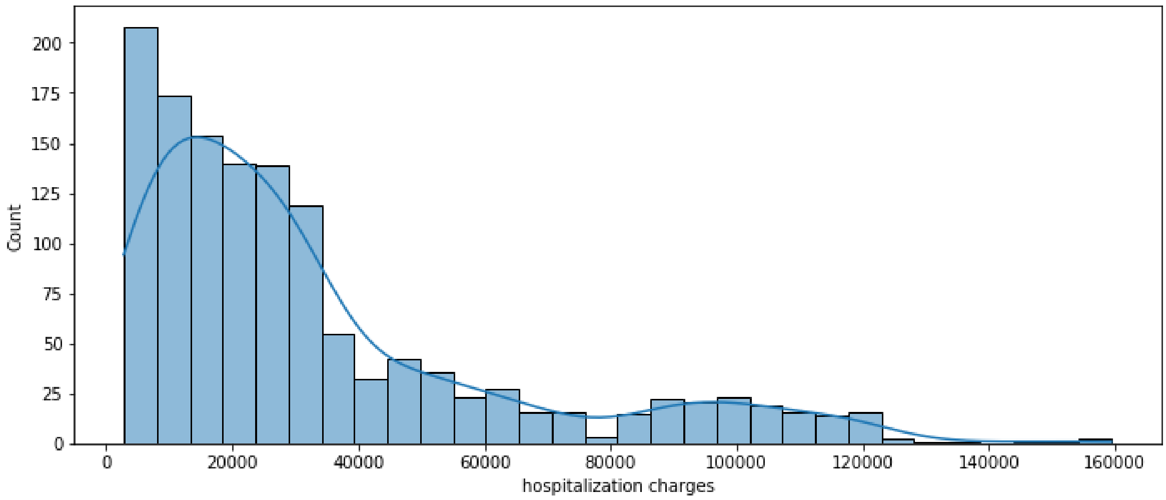
```
fig, axes = plt.subplots(7,1,figsize=(10,30))
for col, ax in zip(df.columns,axes.ravel()):
    sns.histplot(data=df,x=col,ax=ax,kde=True)
    plt.xlabel(col)
fig.tight_layout()
plt.show()
```




C
150
100
50
0
0.0
0.5
1.0
1.5
2.0
2.5
3.0
region


140
120
100
80
60
40
20
0
Count
6
8
10
12
14
16
18
viral load


600
500
400
300
200
100
0
Count
0
1
2
3
4
5
severity level


200
175
150
125
100
75
50
25
0
Count
0
20000
40000
60000
80000
100000
120000
140000
160000
hospitalization charges

In [17]:

```
df.head()
```

Out[17]:

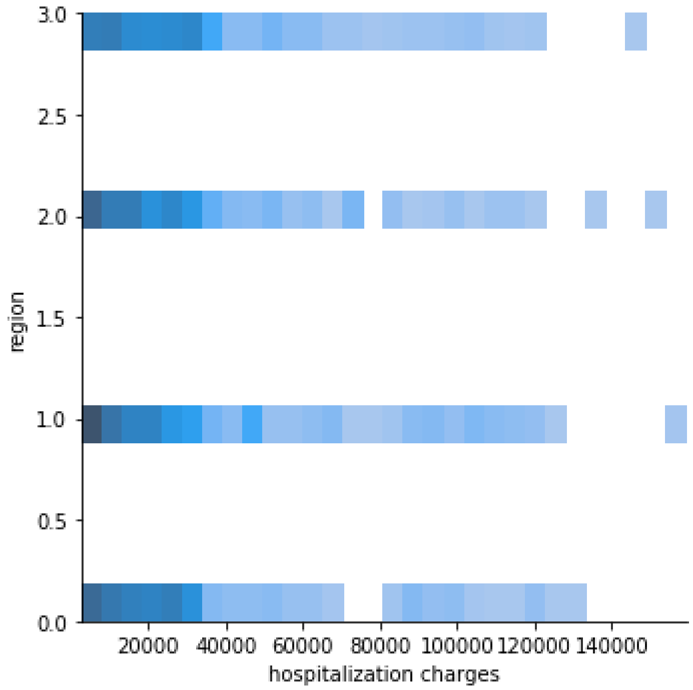
	age	sex	smoker	region	viral load	severity level	hospitalization charges
0	19	0	1	0	9.30	0	42212
1	18	1	0	1	11.26	1	4314
2	28	1	0	1	11.00	3	11124
3	33	1	0	2	7.57	0	54961
4	32	1	0	2	9.63	0	9667

Bivariate Analysis

the hospitilization charges does not depend on region

In [18]:

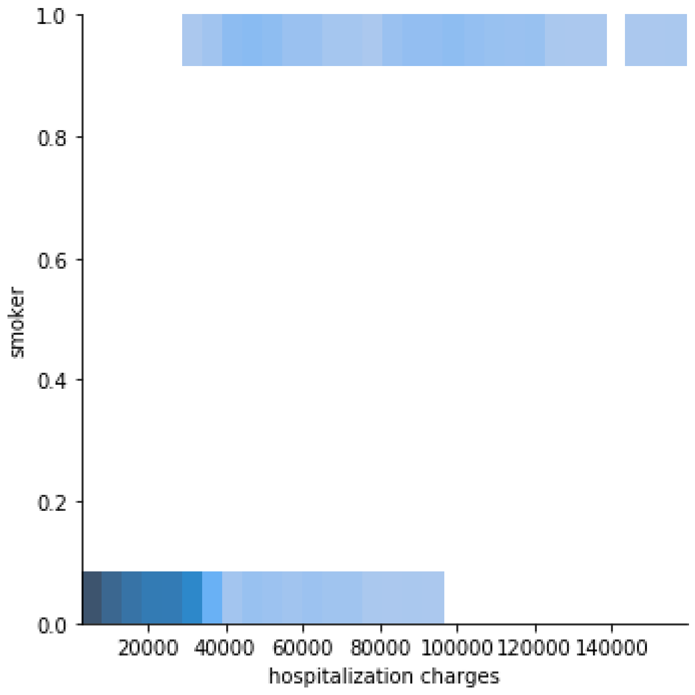
```
sns.displot(x=df['hospitalization charges'],y=df['region'])
plt.show()
```



the hospitalization charges of smokers tends to be higher side when compared to non smokers

In [19]:

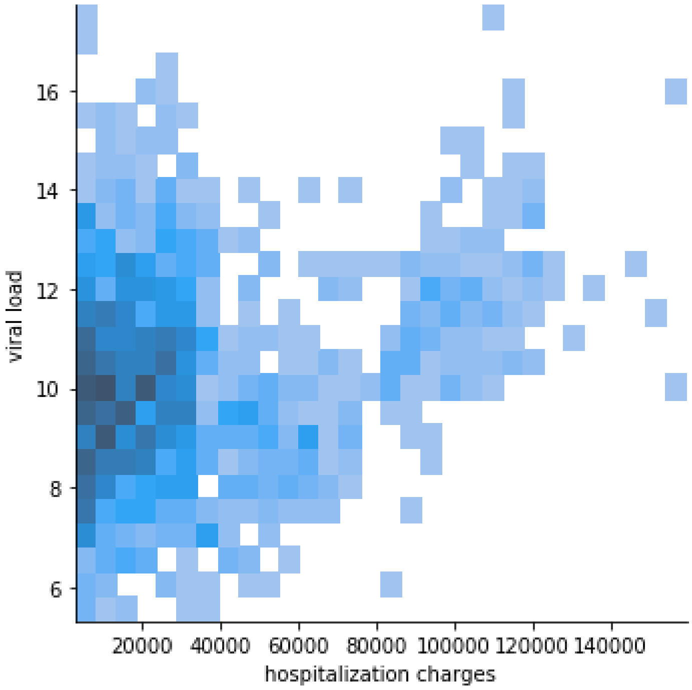
```
sns.displot(x=df['hospitalization charges'],y=df['smoker'])
plt.show()
```



we can not estimate a clear relation between viral load and hospitalization charges

In [20]:

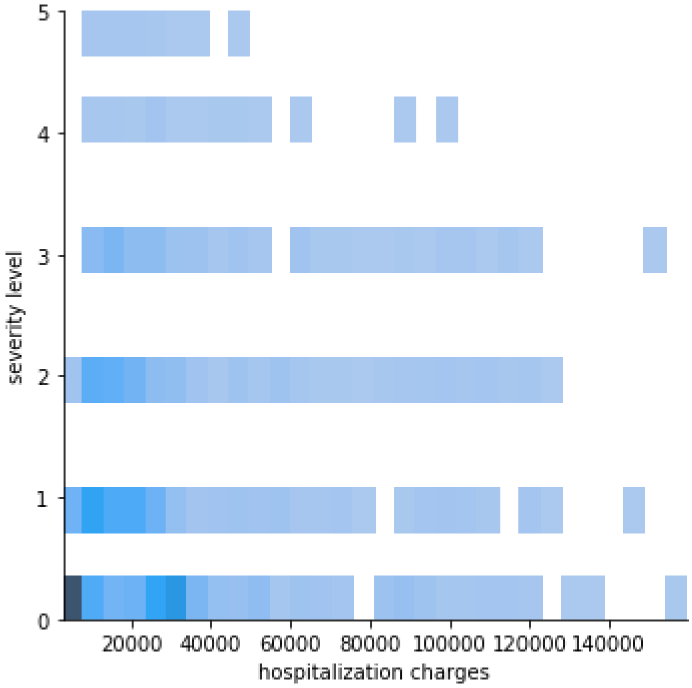
```
sns.displot(x=df['hospitalization charges'],y=df['viral load'])
plt.show()
```



their is an inverse relation between severity level and hospitalization charges

In [21]:

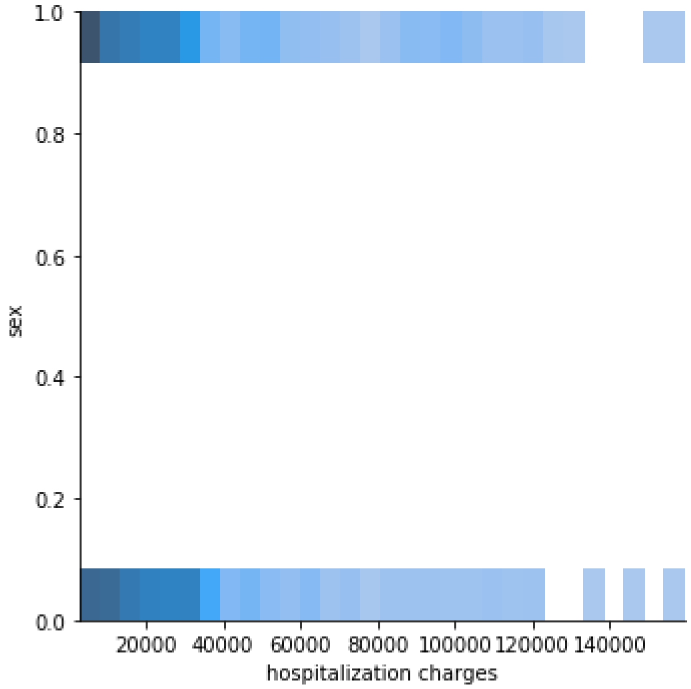
```
sns.displot(x=df['hospitalization charges'],y=df['severity level'])
plt.show()
```



the hospitilization charges does not depend on the sex

In [22]:

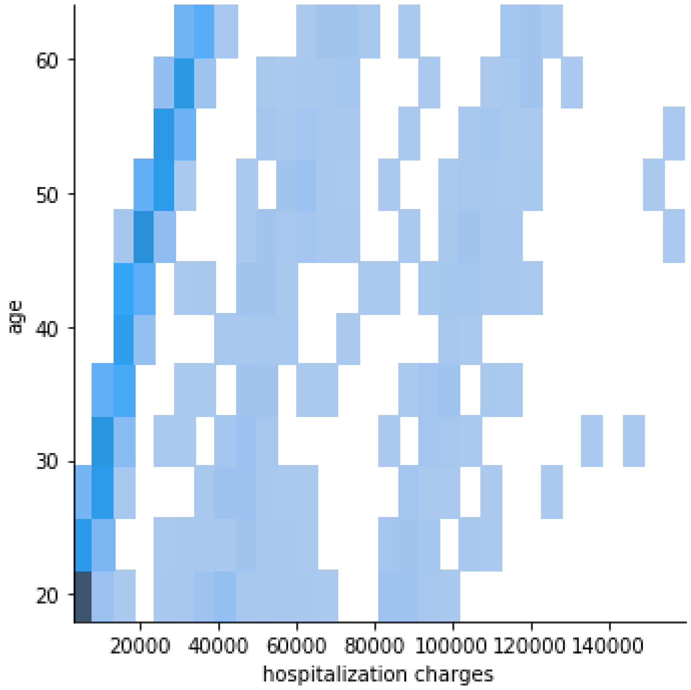
```
sns.displot(x=df['hospitalization charges'],y=df['sex'])
plt.show()
```



the hospitilazition charges does not depend on the age

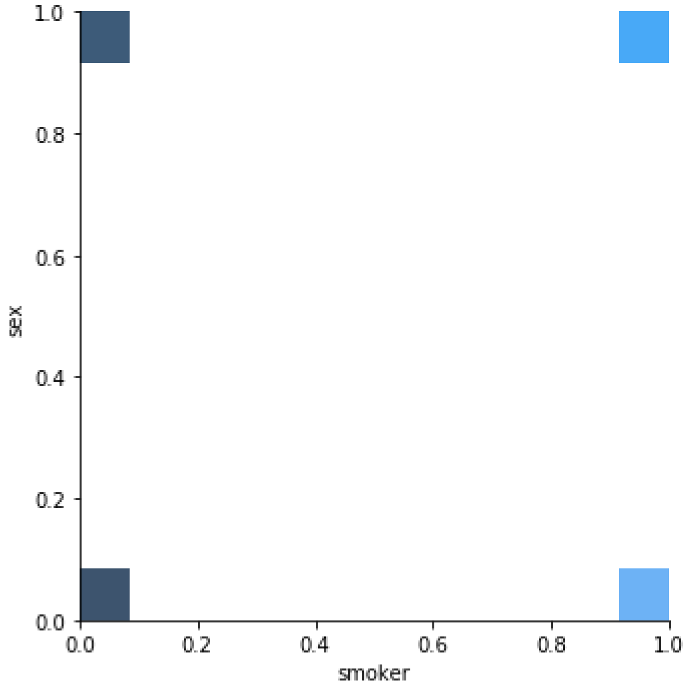
In [23]:

```
sns.displot(x=df['hospitalization charges'],y=df['age'])
plt.show()
```



```
In [37]:
```

```
sns.displot(x=df['smoker'],y=df['sex'])
plt.show()
```



Hypothesis Testing:

Prove (or disprove) that the hospitalization of people who do smoking is greater than those who don't?

Assumptions of z test

1) The population mean and standerd deviation are finite. 2) Population standerd deviation are known.

H0(Null Hypothesis)

In [16]:

```
df.head()
```

Out[16]:

	age	sex	smoker	region	viral load	severity level	hospitalization charges
0	19	0	1	0	9.30	0	42212
1	18	1	0	1	11.26	1	4314
2	28	1	0	1	11.00	3	11124
3	33	1	0	2	7.57	0	54961
4	32	1	0	2	9.63	0	9667

In [17]:

```
df_smoker = df[df['smoker']==1]
```

In [18]:

```
df_non_smoker = df[df['smoker']==0]
```

In [19]:

```
df_smoker.head()
```

Out[19]:

	age	sex	smoker	region	viral load	severity level	hospitalization charges
0	19	0	1	0	9.30	0	42212
11	62	0	1	1	8.76	0	69522
14	27	1	1	1	14.04	0	99029
19	30	1	1	0	11.77	0	92094
23	34	0	1	3	10.64	1	94255

In [20]:

```
df_non_smoker.head()
```

Out[20]:

	age	sex	smoker	region	viral load	severity level	hospitalization charges
1	18	1	0	1	11.26	1	4314
2	28	1	0	1	11.00	3	11124
3	33	1	0	2	7.57	0	54961
4	32	1	0	2	9.63	0	9667
5	31	0	0	1	8.58	0	9392

Prove (or disprove) that the hospitalization of people who do smoking is greater than those who don't?

Assumptions of Z-test

1) The population mean and standerd deviation are finite. 2) Population standerd deviation are known.

Ho(Null hypothesis):-

hospitialization of people does not depends on smoking(feature).

(U1) mean hosptilization rate of people who smoke <= (U2) mean hospitilization rate of people who does not smoke.

Ha(Alternate Hypothesis):-

(U1) mean hosptilization rate of people who smoke > (U2) mean hospitilization rate of people who does not smoke.

alpha(significance level or type I error):-

considering 0.025 significance level

In [21]:

```
np.mean(df_smoker['hospitalization charges']),np.mean(df_non_smoker['hospitalization charge
```

Out[21]:

```
(80125.57299270073, 21085.6757518797)
```

In [22]:

```
np.std(df_smoker['hospitalization charges']),np.std(df_non_smoker['hospitalization charges'
```

Out[22]:

```
(28801.18992162662, 14977.412277719432)
```

here the mean and the std are finet so wee can use z test

In [23]:

```
zscore = (np.mean(df_smoker['hospitalization charges'])-np.mean(df_non_smoker['hospitalizat
```

In [24]:

```
zscore
```

Out[24]:

```
32.80888958143
```

In [25]:

```
1-stats.norm.cdf(zscore)
```

Out[25]:

```
0.0
```

In [26]:

```
from statsmodels.stats.weightstats import ztest
```

In [27]:

```
ztest(df_smoker['hospitalization charges'],df_non_smoker['hospitalization charges'],alterna
```

Out[27]:

```
(46.66489219013773, 0.0)
```

pvalue is 0 < 0.025

as pvalue < 0.025(soignificance level) we reject null hypothesis and accept the alternate hypothesis

Prove (or disprove) with statistical evidence that the viral load of females is different from that of males

Assumptions of Z-test

1) The population mean and standerd deviation are finite. 2) Population standerd deviation are known.

Ho(Null hypothesis):-

hospitialization of people does not depends on sex(feature).

(U1) mean hosptilization rate of male = (U2) mean hospitilization rate female.

Ha(Alternate Hypothesis):-

(U1) mean hosptilization rate of male != (U2) mean hospitilization rate female.

alpha(significance level or type I error):-

considering 0.05 significance level

In [28]:

```
df_male = df[df['sex']==1]
```

In [29]:

```
df_female = df[df['sex']==0]
```

In [30]:

```
df_male.head()
```

Out[30]:

	age	sex	smoker	region	viral load	severity level	hospitalization charges
1	18	1	0	1	11.26	1	4314
2	28	1	0	1	11.00	3	11124
3	33	1	0	2	7.57	0	54961
4	32	1	0	2	9.63	0	9667
8	37	1	0	3	9.94	2	16016

In [31]:

```
np.mean(df_male['viral load']),np.mean(df_female['viral load'])
```

Out[31]:

```
(10.314423076923074, 10.126072507552859)
```

In [32]:

```
np.std(df_male['viral load']), np.std(df_female['viral load'])
```

Out[32]:

```
(2.045374661864287, 2.01387895412623)
```

mean and the std are known and finete so we can use z test

In [33]:

```
zscore = (np.mean(df_male['viral load'])-np.mean(df_female['viral load']))/np.sqrt((np.var(
```

In [34]:

```
zscore
```

Out[34]:

```
1.6972554799209714
```

In [35]:

```
(1-stats.norm.cdf(zscore))*2
```

Out[35]:

```
0.08964837020886884
```

pvale is 0.089 > 0.05

conclusion

as the pvalue is greater than 0.05(significance level) we failed to reject the null hypothesis

z test using inbuilt library

In [36]:

```
from statsmodels.stats.weightstats import ztest
```

In [37]:

```
ztest(df_male['viral load'],df_female['viral load'])
```

Out[37]:

```
(1.695711164450323, 0.08994059315726398)
```

Is the proportion of smoking significantly different across different regions?

Chi-square test

Test of independence(in this test we will be verifying are the 2 variables independent or not)

Assumptions of chi-square test

As Chi-square test is non-parameter test(i.e., it did not any assumptions).

Ho(Null hypothesis)

smoking is independent of region

Ha(Alternate hypothesis)

smoking id dependent on region

In [38]:

```
df.head()
```

Out[38]:

```
   age  sex  smoker  region  viral load  severity level  hospitalization charges
0   19    0       1       0        9.30               0                    42212
1   18    1       0       1       11.26               1                     4314
2   28    1       0       1       11.00               3                    11124
3   33    1       0       2        7.57               0                    54961
4   32    1       0       2        9.63               0                     9667
```

In [39]:

```
df_crosstab = pd.crosstab(df['smoker'],df['region'],margins=True)
```

In [40]:

```
df_crosstab
```

Out[40]:

```
 region    0    1    2    3   All
 smoker
      0  267  273  267  257  1064
      1   58   91   58   67   274
    All  325  364  325  324  1338
```

In [41]:

```
df_crosstab[2][1]
```

Out[41]:

```
58
```

In [42]:

```
chisquare = 0
for i in df['smoker'].unique():
    for j in df['region'].unique():
        observed = df_crosstab[j][i]
        expected = df_crosstab[j]['All']*df_crosstab['All'][i]/df_crosstab['All']['All']
        chisquare += pow((observed-expected),2)/expected
```

In [43]:

```
chisquare
```

Out[43]:

```
7.343477761407069
```

In [44]:

```
pvalue = 1 -  stats.chi2.cdf(chisquare,(len(df['smoker'].unique())-1)*(len(df['region'].uni
```

In [45]:

```
chisquare,pvalue
```

Out[45]:

```
(7.343477761407069, 0.06171954839170546)
```

pvalue is 0.061 > 0.05

conclusion

as the pvalue is greater than 0.05 significance level we fail to reject the null hypothesis.

Is the mean viral load of women with 0 Severity level , 1 Severity level, and 2 Severity level the same? Explain your answer with statistical evidence

Annova

Assumptions

Each group observations are qaussian(almost). Each group variance is almost the same.

Ho(Null hupothesis)

mean viral load of women does not change with severity level

Ha(Alternate hypothesis)

mean viral load of women change with severity level

alpha(significance level or type I error):-

considering 5% significance level

In [46]:

```
df.head()
```

Out[46]:

	age	sex	smoker	region	viral load	severity level	hospitalization charges
0	19	0	1	0	9.30	0	42212
1	18	1	0	1	11.26	1	4314
2	28	1	0	1	11.00	3	11124
3	33	1	0	2	7.57	0	54961
4	32	1	0	2	9.63	0	9667

In [47]:

```
df[(df['sex']==0) & (df['severity level']==1)]
```

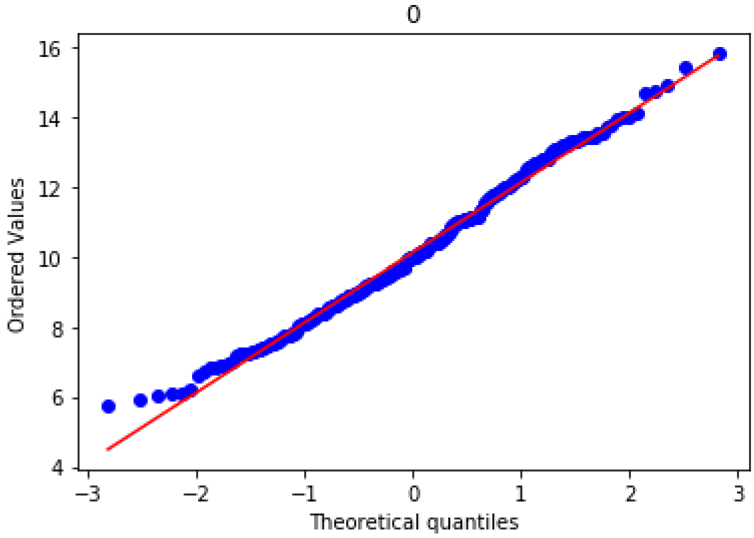
Out[47]:

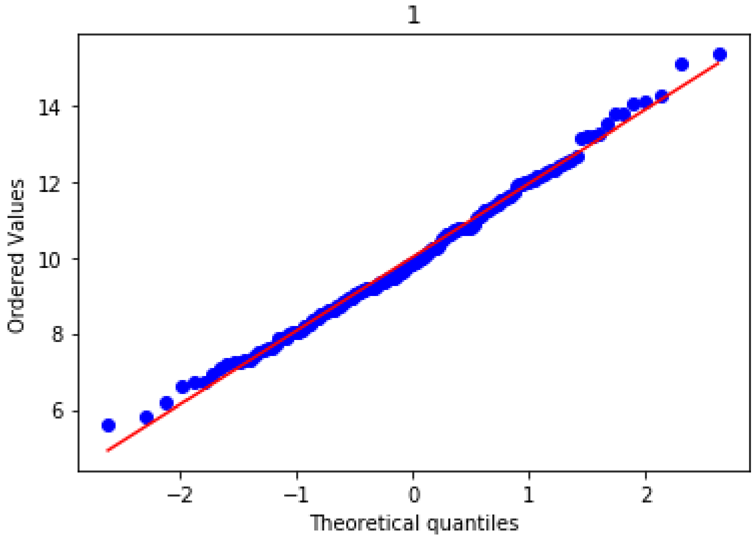
	age	sex	smoker	region	viral load	severity level	hospitalization charges
6	46	0	0	1	11.15	1	20601
16	52	0	0	3	10.26	1	26993
21	30	0	0	0	10.80	1	10374
23	34	0	1	3	10.64	1	94255
58	53	0	1	1	7.63	1	58112
...	...	...	...	...	...	...	...
1262	41	0	0	1	9.35	1	16925
1263	43	0	0	0	9.97	1	18344
1287	36	0	0	0	8.63	1	13681
1299	19	0	0	2	8.58	1	6777
1302	25	0	0	0	6.93	1	8022

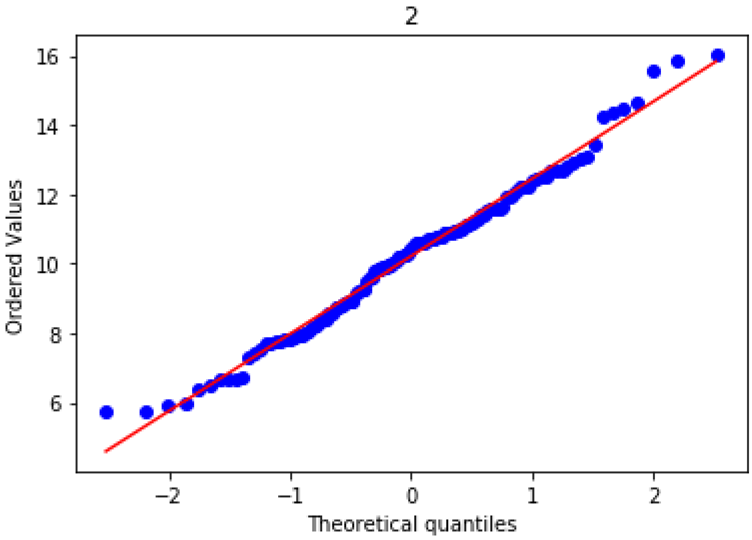
158 rows × 7 columns

In [48]:

```
for i in range(3):
    stats.probplot(df[(df['sex']==0) & (df['severity level']==i)]['viral load'],dist='norm'
    plt.title(i)
    plt.show()
```







the 3 seviarity levels follow normal distribution

In [35]:

```
np.std(df[(df['sex']==0) & (df['severity level']==0)]['viral load']),np.std(df[(df['sex']==
```

Out[35]:

```
(1.9856270286492823, 1.9229509682292343, 2.200382675951407)
```

the std of all the 3 seviarity level are almost same so we can use anova

In [49]:

```
stats.f_oneway(df[(df['sex']==0) & (df['severity level']==0)]['viral load'],df[(df['sex']==
```

Out[49]:

```
F_onewayResult(statistic=0.3355061434584082, pvalue=0.7151189650367746)
```

pvalue is 0.71 > 0.05

conclusion

as the pvalues is greater than 0.05 we failed to reject null null hypothesis and accept alternate hypothesis

Business insights

smokes tends to pay higher hospital charges

their are more male smokers than female smokers

hospitilization charges of seviarity level 0,1 2 are in higher side.

from chisquare test some is dependent on region.

the male hospitilization charges are almost the same as female hospitilization charges

Recommendations

as from chisquare test we can see that smoking is dependent on region and the avarage hospitilazation charges of the smokers is greater than the non smokers so we can say that the hospitilazition charges of the region with more smokers tends to be in higher side

as the hospitilization charges of seviarity level 0, 1 and 2 are in higher side and the seviarity level does not depends on the women so their is high chances that women pay more.

as males smoke more when compared to female and the person who smoke will have higher probability to pay more hospityilization charges so male tends to pay more hospitilization charges than female

In [ ]:

```
```