In [1]:

```
#from google.colab import drive
#drive.mount('/content/drive')
```

In [2]:

```
# Importing necessary libraries

import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline
```

In [3]:

```
medi = pd.read_csv("C:/Users/HP/Documents/GitHub/medical_cost/Medical cost.csv")
medi.head(5)
```

Out[3]:

	age	sex	bmi	children	smoker	region	charges
0	19	female	27.900	0	yes	southwest	16884.92400
1	18	male	33.770	1	no	southeast	1725.55230
2	28	male	33.000	3	no	southeast	4449.46200
3	33	male	22.705	0	no	northwest	21984.47061
4	32	male	28.880	0	no	northwest	3866.85520

In [4]:

```
# bmi: Body mass index, providing an understanding of body, weights that are relatively high or low relative to height,
# objective index of body weight (kg / m ^ 2) using the ratio of height to weight, ideally 18.5 to 24.9
```

In [5]:

```
# Can you accurately predict insurance costs?
```

In [6]:

```
medi.shape
```

Out[6]:

```
(1338, 7)
```

In [7]:

```
medi.describe()
```

Out[7]:

	age	bmi	children	charges
count	1338.000000	1338.000000	1338.000000	1338.000000
mean	39.207025	30.663397	1.094918	13270.422265
std	14.049960	6.098187	1.205493	12110.011237
min	18.000000	15.960000	0.000000	1121.873900
25%	27.000000	26.296250	0.000000	4740.287150
50%	39.000000	30.400000	1.000000	9382.033000
75%	51.000000	34.693750	2.000000	16639.912515
max	64.000000	53.130000	5.000000	63770.428010

In [8]:

```
medi.isnull().sum()
```

Out[8]:

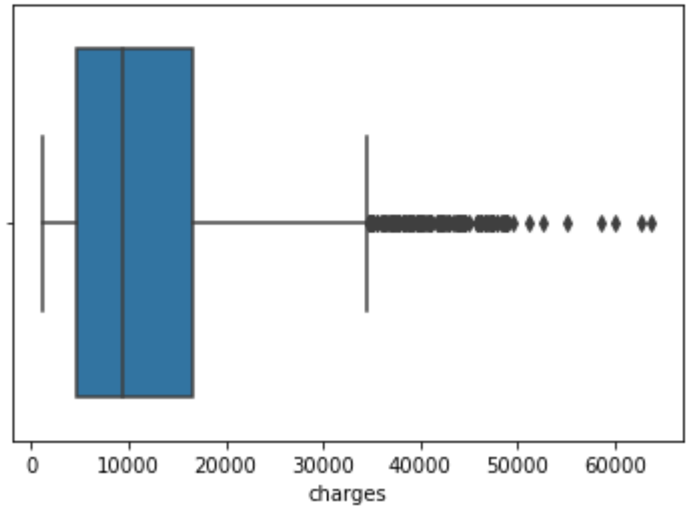
```
age         0
sex         0
bmi         0
children    0
smoker      0
region      0
charges     0
dtype: int64
```

In [10]:

```
# Understanding about some columns first.
#sns.set_theme(style="whitegrid")
sns.boxplot(medi['charges'])
```

Out[10]:

```
<AxesSubplot:xlabel='charges'>
```

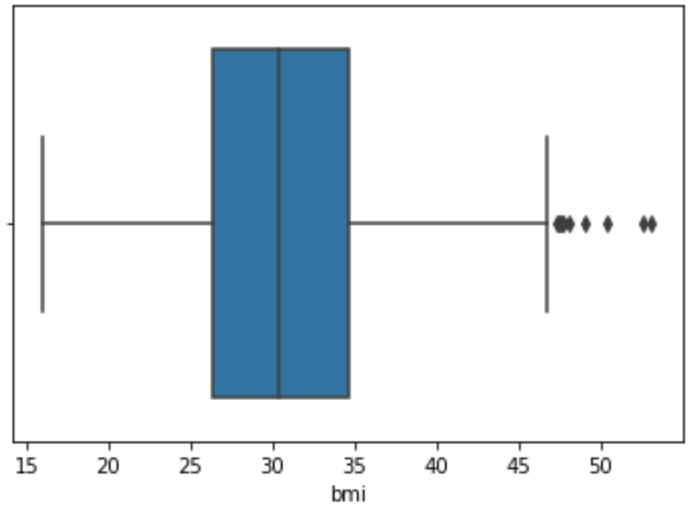


In [11]:

```
sns.boxplot(medi['bmi'])
```

Out[11]:

```
<AxesSubplot:xlabel='bmi'>
```



In [12]:

```
medi[['sex','age']].groupby('sex').agg(['mean','count'])
```

Out[12]:

	age	
	mean	**count**

sex		
female	39.503021	662
male	38.917160	676

In [13]:

```
medi['smoker'].value_counts()
```

Out[13]:

```
no     1064
yes     274
Name: smoker, dtype: int64
```

In [14]:

```
medi[['sex','children']].groupby('sex').agg(['mean'])
```

Out[14]:

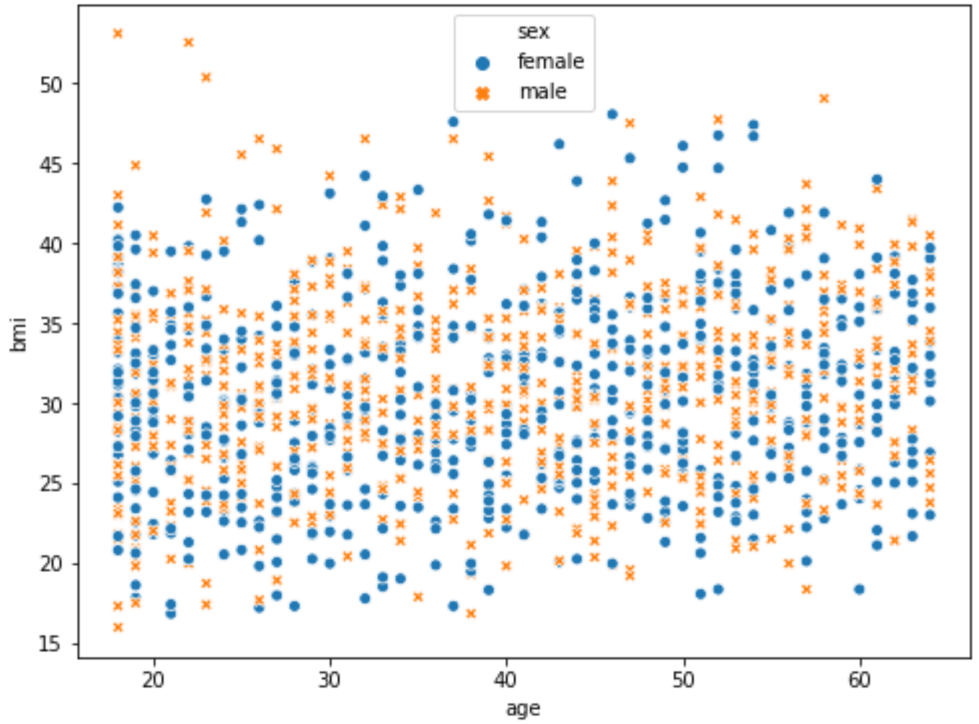
	children
	mean
sex	
female	1.074018
male	1.115385

In [15]:

```
plt.figure(figsize=(8, 6))
sns.scatterplot(data=medi, x="age", y="bmi", hue="sex", style="sex")
```

Out[15]:

```
<AxesSubplot:xlabel='age', ylabel='bmi'>
```

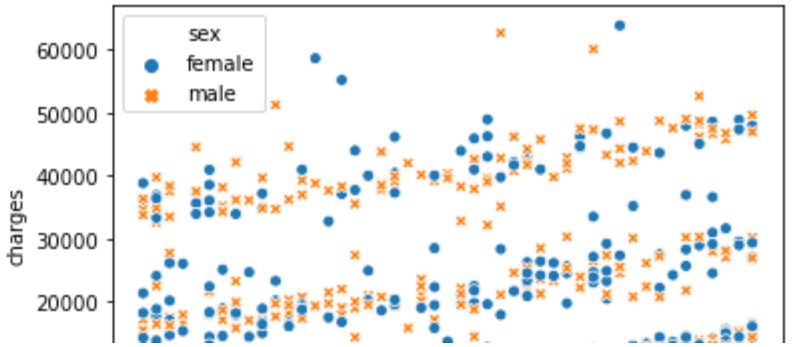


In [16]:

```
sns.scatterplot(data=medi, x="age", y="charges", hue="sex", style="sex")
```

Out[16]:

```
<AxesSubplot:xlabel='age', ylabel='charges'>
```

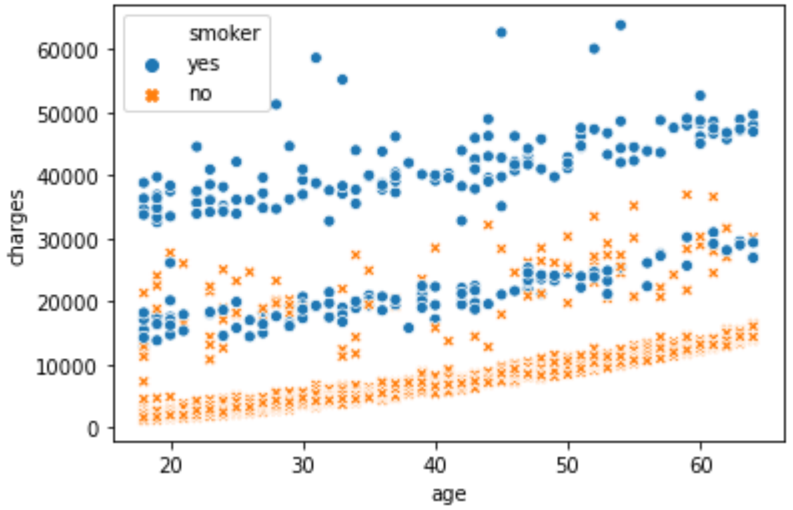


In [17]:

```
sns.scatterplot(data=medi, x="age", y="charges", hue="smoker", style="smoker")
```

Out[17]:

```
<AxesSubplot:xlabel='age', ylabel='charges'>
```



In [18]:

```
# First removing outlier values:

medi = medi[medi['bmi'] < 47]
# medi = medi[medi['charges'] < 25000]

medi.shape
```

Out[18]:

```
(1329, 7)
```

In [19]:

```
# Finding categorical data:

medi['smoker'].value_counts()
```

Out[19]:

```
no      1058
yes      271
Name: smoker, dtype: int64
```

In [20]:

```
medi['region'].value_counts()
```

Out[20]:

```
southeast    357
northwest    325
southwest    324
northeast    323
Name: region, dtype: int64
```

In [21]:

```
medi['sex'].value_counts()
```

Out[21]:

```
male      670
female    659
Name: sex, dtype: int64
```

In [22]:

```python
from sklearn.preprocessing import LabelEncoder

def label_encoded(feat):
    le = LabelEncoder()
    le.fit(feat)
    print(feat.name,le.classes_)
    return le.transform(feat)
```

In [23]:

```python
name_list = ['sex', 'smoker', 'region']

for name in name_list:
  medi[name] = label_encoded(medi[name])

medi.head(3)
```

```
sex ['female' 'male']
smoker ['no' 'yes']
region ['northeast' 'northwest' 'southeast' 'southwest']
```

Out[23]:

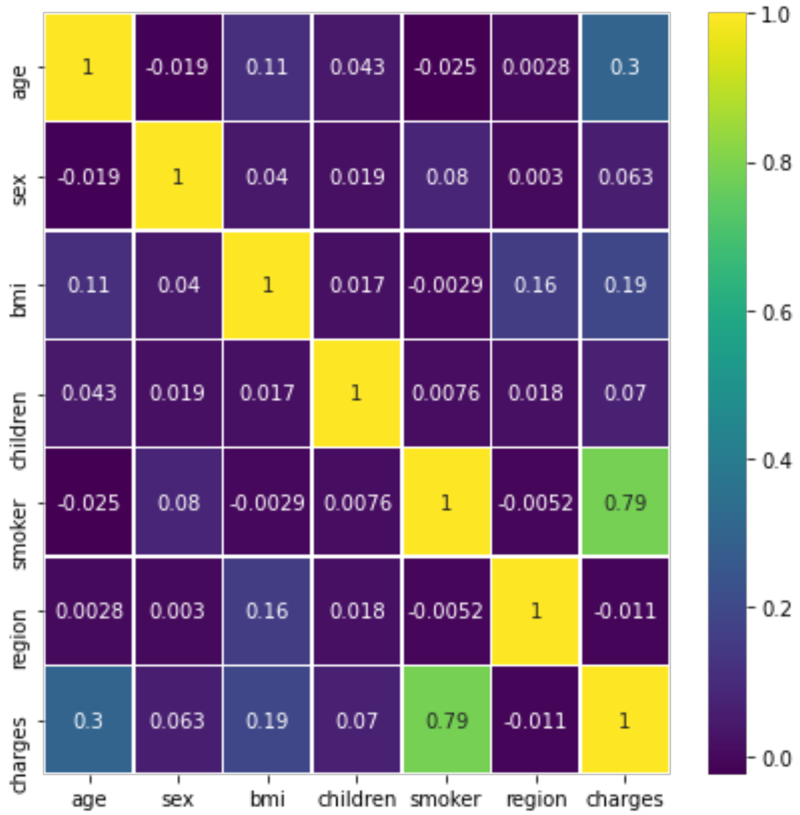
	age	sex	bmi	children	smoker	region	charges
0	19	0	27.90	0	1	3	16884.9240
1	18	1	33.77	1	0	2	1725.5523
2	28	1	33.00	3	0	2	4449.4620

In [25]:

```python
plt.figure(figsize=(7,7))
sns.heatmap(medi.corr(),annot=True,cmap='viridis',linewidths=.5)
```

Out[25]:

```
<AxesSubplot:>
```



In [26]:

```
y = medi['charges']
X = medi.drop(['charges'], axis = 1)
```

In [27]:

```
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.ensemble import RandomForestRegressor
```

In [28]:

```
Xtrain, Xtest, ytrain, ytest = train_test_split(X, y, test_size=0.2, random_state = 42)
```

In [29]:

```
random_model = RandomForestRegressor(n_estimators=250, n_jobs = -1)
```

In [30]:

```
#Fit
random_model.fit(Xtrain, ytrain)

y_pred = random_model.predict(Xtest)

#Checking the accuracy
random_model_accuracy = round(random_model.score(Xtrain, ytrain)*100,2)
print(round(random_model_accuracy, 2), '%')
```

```
97.61 %
```

In [31]:

```
random_model_accuracy1 = round(random_model.score(Xtest, ytest)*100,2)
print(round(random_model_accuracy1, 2), '%')
```

```
83.11 %
```

In [33]:

```
# Save the trained model as a pickle string.
import pickle

saved_model = pickle.dump(random_model, open('C:/Users/HP/Documents/GitHub/medical_cost/Medical.pickle','wb'))
```

In [ ]: