Importing Libraries

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

from sklearn.linear_model import LinearRegression
from sklearn.ensemble import RandomForestRegressor
from sklearn import svm
from sklearn.tree import DecisionTreeRegressor
from sklearn.model_selection import train_test_split
from sklearn.metrics import mean_squared_error
```

Loading Data

In [3]:
```
data = pd.read_csv(r'C:\Users\vamsi\Desktop\M.Tech\ML\19 Projects\medical_cost_da
```

In [4]:
```
data.head()
```

Out[4]:

	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 [5]:
```
data.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   bmi       1338 non-null   float64
 3   children  1338 non-null   int64  
 4   smoker    1338 non-null   object 
 5   region    1338 non-null   object 
 6   charges   1338 non-null   float64
dtypes: float64(2), int64(2), object(3)
memory usage: 73.3+ KB
```

In [6]:
```
data.describe()
```

Out[6]:

	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 [7]:
```
data.isnull().sum()
```

Out[7]:
```
age         0
sex         0
bmi         0
children    0
smoker      0
region      0
charges     0
dtype: int64
```

Categorical data

In [8]:
```
data.sex.unique()
```

Out[8]:
```
array(['female', 'male'], dtype=object)
```

In [9]:
```
data.smoker.unique()
```

Out[9]:
```
array(['yes', 'no'], dtype=object)
```

In [10]:
```
data.region.unique()
```

Out[10]:
```
array(['southwest', 'southeast', 'northwest', 'northeast'], dtype=object)
```

Label Encoding

In [11]:

```
from sklearn.preprocessing import LabelEncoder
#sex
le = LabelEncoder()
le.fit(data.sex.drop_duplicates())
data.sex = le.transform(data.sex)

# smoker or not
le.fit(data.smoker.drop_duplicates())
data.smoker = le.transform(data.smoker)

#region
le.fit(data.region.drop_duplicates())
data.region = le.transform(data.region)
```

Data Correlation

In [12]:

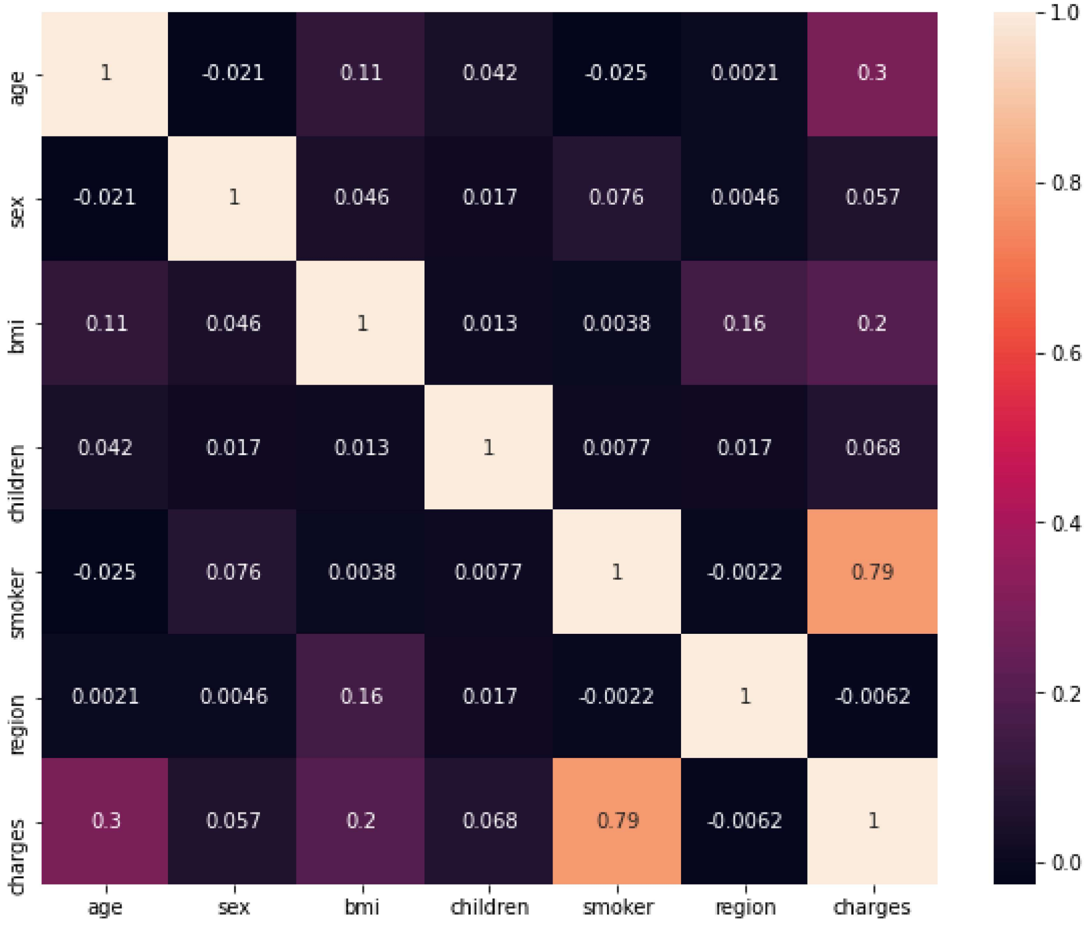
```
data.corr()['charges'].sort_values()
```

Out[12]:

```
region     -0.006208
sex         0.057292
children    0.067998
bmi         0.198341
age         0.299008
smoker      0.787251
charges     1.000000
Name: charges, dtype: float64
```

```
In [13]: f, ax = plt.subplots(figsize=(10, 8))
         corr = data.corr()
         sns.heatmap(corr, ax =ax, annot = True)
```

```
Out[13]: <AxesSubplot:>
```



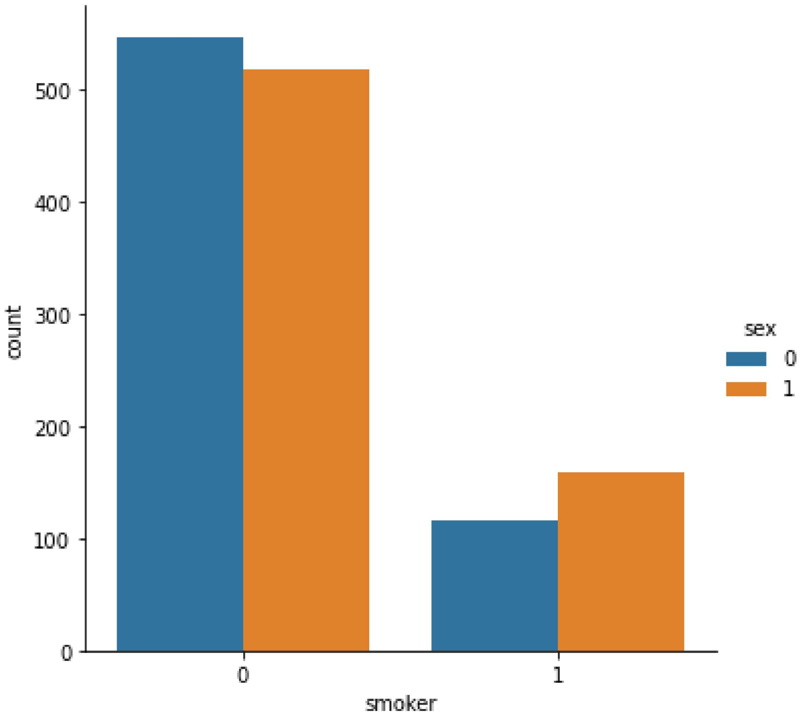
Clearly, a strong correlation is observed only with the fact of smoking the patient

Smoker Analysis

In [14]:
```
sns.factorplot(x="smoker", kind="count",hue = 'sex', data=data)
```

```
C:\Users\vamsi\anaconda3\lib\site-packages\seaborn\categorical.py:3704: UserWar
ning: The `factorplot` function has been renamed to `catplot`. The original nam
e will be removed in a future release. Please update your code. Note that the d
efault `kind` in `factorplot` (`'point'`) has changed `'strip'` in `catplot`.
  warnings.warn(msg)
```

Out[14]:
```
<seaborn.axisgrid.FacetGrid at 0x1ee05150520>
```



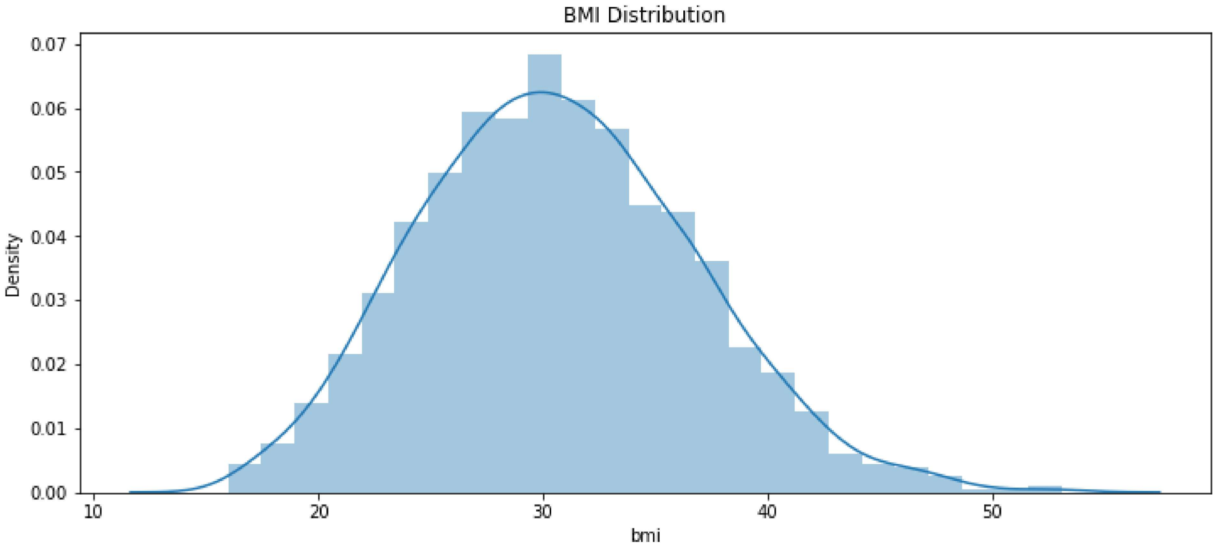
The total cost of treatment in men will be more than in women, given the impact of smoking.

BMI Analysis

In [15]:

```
plt.figure(figsize=(12,5))
plt.title("BMI Distribution")
ax = sns.distplot(data["bmi"])
```

```
C:\Users\vamsi\anaconda3\lib\site-packages\seaborn\distributions.py:2551: Futur
eWarning: `distplot` is a deprecated function and will be removed in a future v
ersion. Please adapt your code to use either `displot` (a figure-level function
with similar flexibility) or `histplot` (an axes-level function for histogram
s).
  warnings.warn(msg, FutureWarning)
```



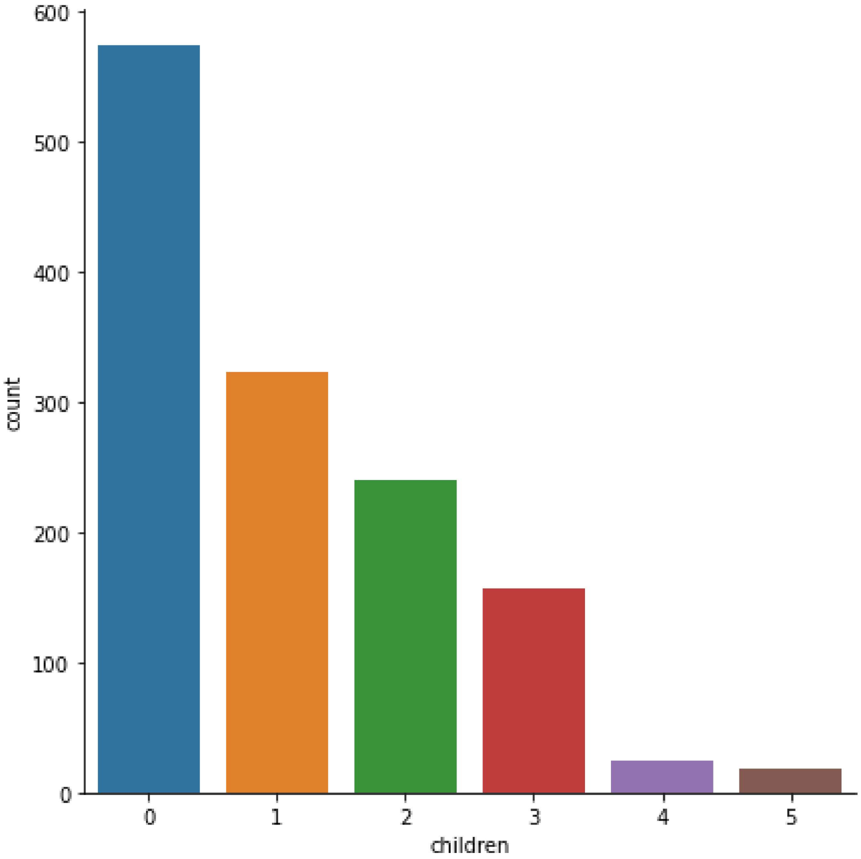
The average BMI in patients is 30.

Children Count Analysis

In [16]:
```
sns.factorplot(x="children", kind="count", data=data, size = 6)
```

```
C:\Users\vamsi\anaconda3\lib\site-packages\seaborn\categorical.py:3704: UserWar
ning: The `factorplot` function has been renamed to `catplot`. The original nam
e will be removed in a future release. Please update your code. Note that the d
efault `kind` in `factorplot` (`'point'`) has changed `'strip'` in `catplot`.
  warnings.warn(msg)
C:\Users\vamsi\anaconda3\lib\site-packages\seaborn\categorical.py:3710: UserWar
ning: The `size` parameter has been renamed to `height`; please update your cod
e.
  warnings.warn(msg, UserWarning)
```

Out[16]:
```
<seaborn.axisgrid.FacetGrid at 0x1ee0adb8370>
```



Most patients do not have children.

In [17]:
```
data.head()
```

Out[17]:

	age	sex	bmi	children	smoker	region	charges
0	19	0	27.900	0	1	3	16884.92400
1	18	1	33.770	1	0	2	1725.55230
2	28	1	33.000	3	0	2	4449.46200
3	33	1	22.705	0	0	1	21984.47061
4	32	1	28.880	0	0	1	3866.85520

Splitting Data

In [18]:
```
# training dataset and labels
x = data.drop(data.columns[[6, 5]], axis = 1)
y = data['charges']
```

In [19]:
```
x.head()
```

Out[19]:

	age	sex	bmi	children	smoker
0	19	0	27.900	0	1
1	18	1	33.770	1	0
2	28	1	33.000	3	0
3	33	1	22.705	0	0
4	32	1	28.880	0	0

In [21]:
```
# splitting into training and testing data
from sklearn.model_selection import train_test_split
xtrain, xtest, ytrain, ytest = train_test_split(x, y, test_size = 0.30, random_st
```

Feature Scaling

In [22]:
```
from sklearn.preprocessing import MinMaxScaler
sc_x = MinMaxScaler()
xtrain = sc_x.fit_transform(xtrain)
xtest = sc_x.fit_transform(xtest)
```

In [23]:
```
xtrain[0:2]
```

Out[23]:
```
array([[0.        , 0.        , 0.32970137, 0.        , 0.        ],
       [0.45652174, 0.        , 0.45305354, 0.        , 0.        ]])
```

ML Models

In [24]:

```
linear = LinearRegression()
dt = DecisionTreeRegressor()
svr = svm.SVR()
rf = RandomForestRegressor()
```

Training

In [25]:

```
linear.fit(xtrain, ytrain)
```

Out[25]:

```
LinearRegression()
```

In [26]:

```
dt.fit(xtrain, ytrain)
```

Out[26]:

```
DecisionTreeRegressor()
```

In [27]:

```
svr.fit(xtrain, ytrain)
```

Out[27]:

```
SVR()
```

In [28]:

```
rf.fit(xtrain, ytrain)
```

Out[28]:

```
RandomForestRegressor()
```

Prediction

In [29]:

```
y_pred_linear = linear.predict(xtest)
y_pred_dt = dt.predict(xtest)
y_pred_svr = svr.predict(xtest)
y_pred_rf = rf.predict(xtest)
```

RMSE Error

In [30]:

```
import math
error_linear = math.sqrt(mean_squared_error((y_pred_linear), ytest))
error_dt = math.sqrt(mean_squared_error(y_pred_dt, ytest))
error_svr = math.sqrt(mean_squared_error(y_pred_svr, ytest))
error_rf = math.sqrt(mean_squared_error(y_pred_rf, ytest))
```

In [31]:

```
print ("    Model           :     RMSE Error\n" )
print ("Linear Regression   : ", error_linear)
print ("Decision Tree       : ", error_dt)
print ("Support Vector      : ", error_svr)
print ("Random Forest       : ", error_rf)
```

```
    Model           :     RMSE Error

Linear Regression   :  5827.6103488260305
Decision Tree       :  7291.157424644265
Support Vector      :  13132.937356154958
Random Forest       :  5164.067609731632
```

In [ ]: