Dataset link:

In [2]:
```
#https://www.kaggle.com/mirichoi0218/insurance
```

importing liabraries

In [1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
%matplotlib inline
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
```

In [6]:
```
x=pd.read_csv("C:\\Users\\user\\Downloads\\archive (3)\\insurance.csv")
```

In [7]:
```
x.head()
```

Out[7]:

	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 [9]:
```
## number of rows and columns
x.shape
```

Out[9]: (1338, 7)

In [10]:
```
# getting some informations about the dataset
x.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 [12]:
```
x.describe()
```

Out[12]:

	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 [13]:
```
x.isna().sum()
```

Out[13]:
```
age         0
sex         0
bmi         0
children    0
smoker      0
region      0
charges     0
dtype: int64
```

In [15]:
```
x.isnull().values.any()
```

Out[15]:
```
False
```

So we can say that There are no missing values.

so we have 3 categorical features

1.sex

2.smoker

3.Region

In [16]:
```
x['charges'].describe()
```

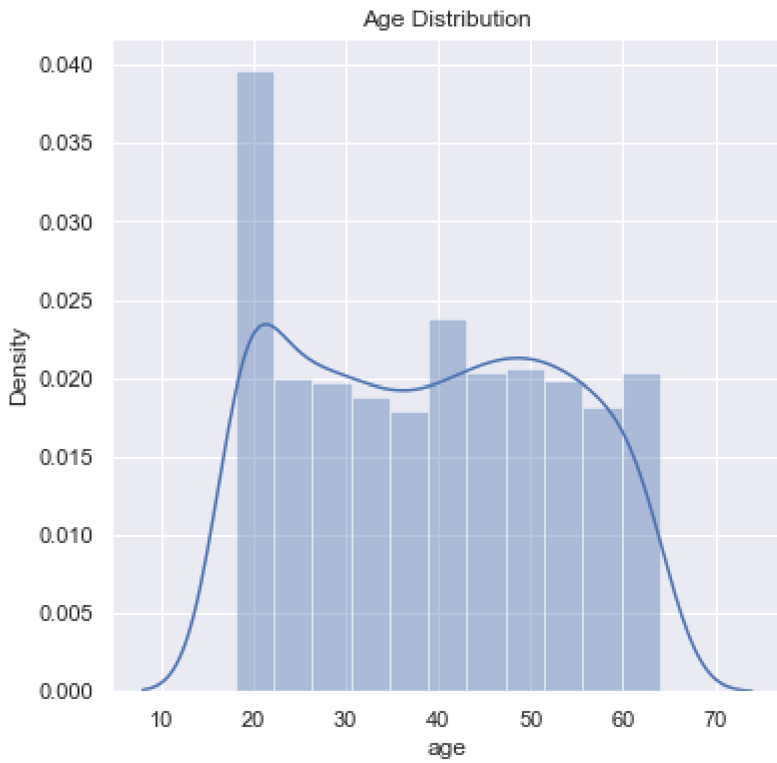
Out[16]:
```
count     1338.000000
mean     13270.422265
std      12110.011237
min       1121.873900
25%       4740.287150
50%       9382.033000
75%      16639.912515
max      63770.428010
Name: charges, dtype: float64
```

1.The minimum cost of an insurance is 1122

2.The maximum cost of an insurance is 63770

EDA:

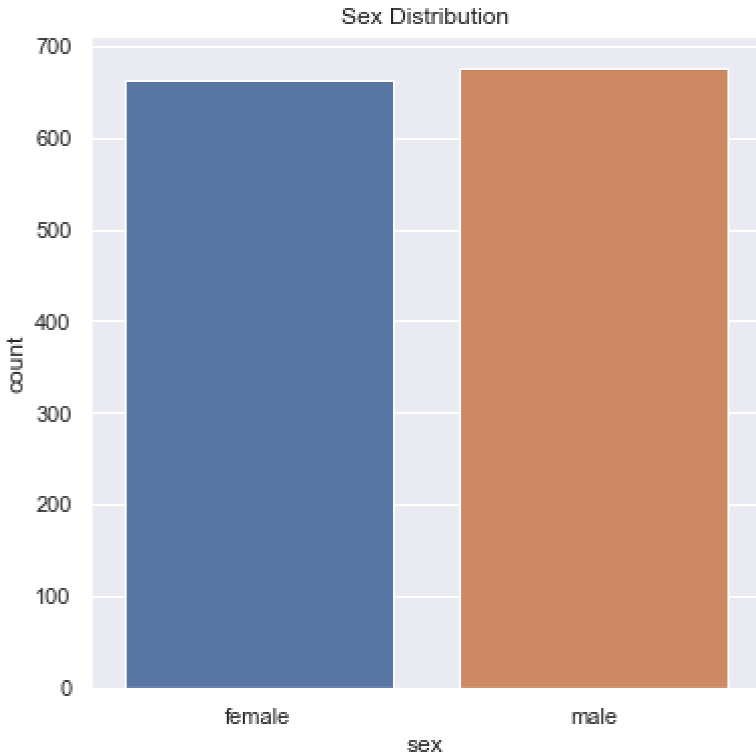
In [20]:
```
# distribution of age value
sns.set()
plt.figure(figsize=(6,6))
sns.distplot(x['age'])
plt.title('Age Distribution')
plt.show()
```



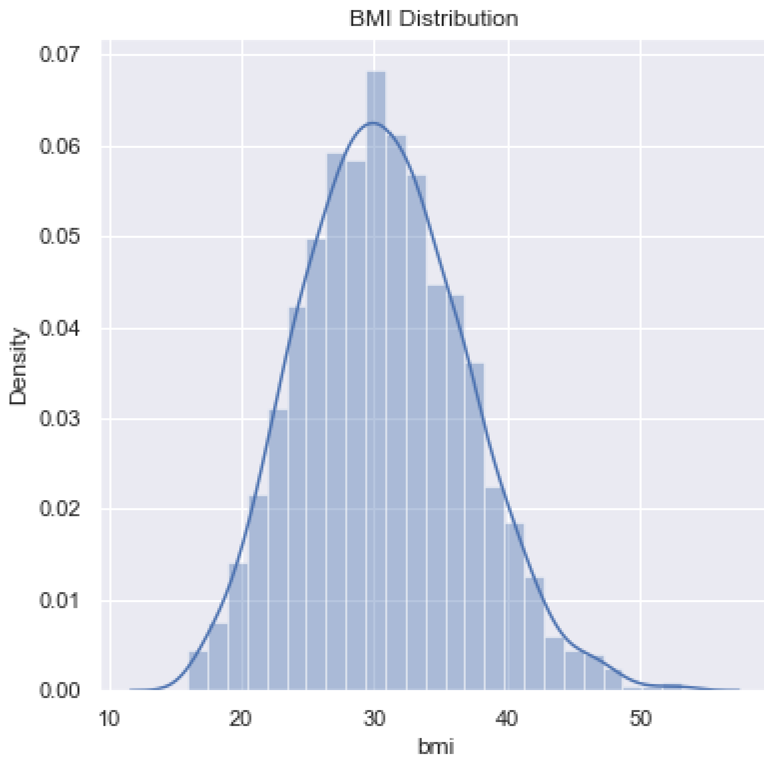
In [22]:
```
x['sex'].value_counts()
```

Out[22]:
```
male      676
female    662
Name: sex, dtype: int64
```

In [21]:
```
# Gender column
plt.figure(figsize=(6,6))
sns.countplot(x='sex', data=x)
plt.title('Sex Distribution')
plt.show()
```

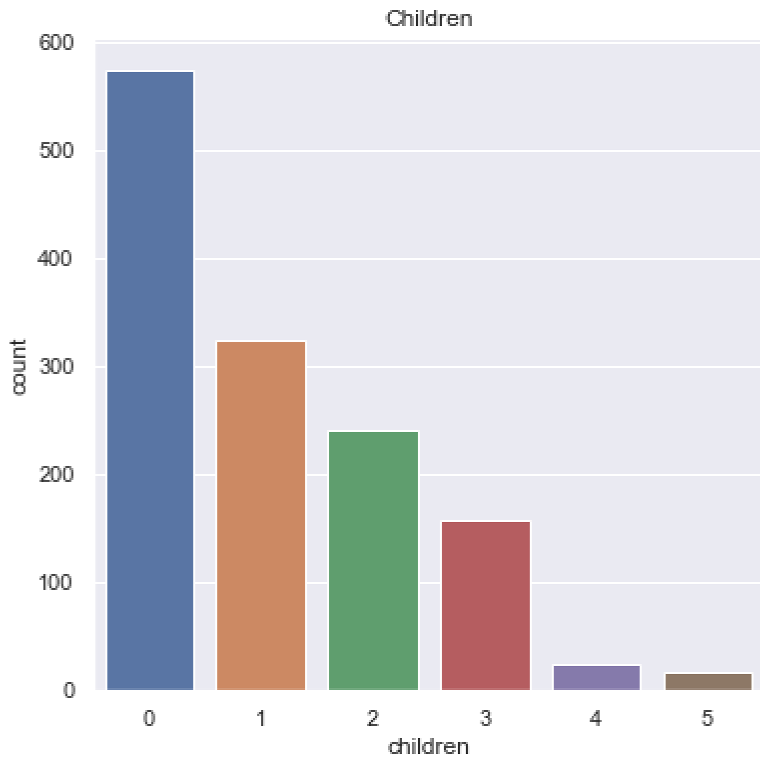


In [24]:
```
# bmi distribution
plt.figure(figsize=(6,6))
sns.distplot(x['bmi'])
plt.title('BMI Distribution')
plt.show()
```



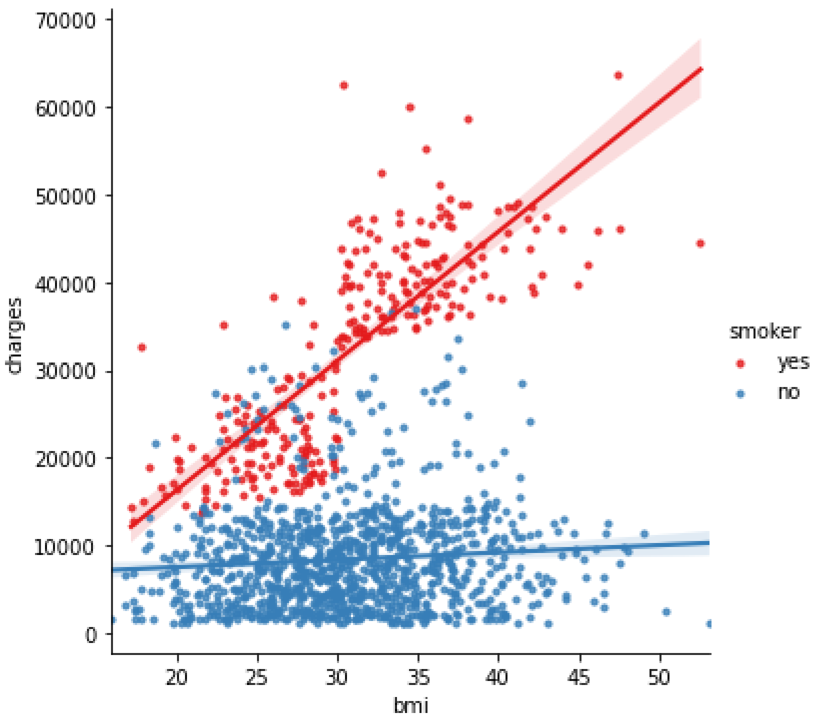
Normal BMI Range --> 18.5 to 24.9

In [25]:
```
# children column
plt.figure(figsize=(6,6))
sns.countplot(x='children', data=x)
plt.title('Children')
plt.show()
```



Let's analyze the medical insurance charges by age, bmi and children according to the smoking factor

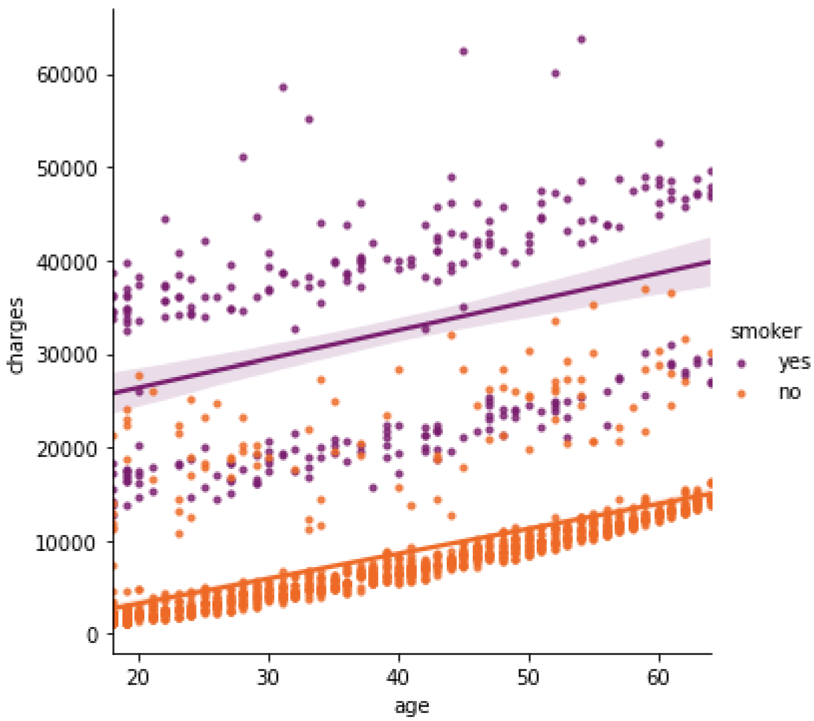
In [18]:
```
sns.lmplot( x='bmi',y='charges', data=x, hue='smoker', palette='Set1', scatter_kw
plt.show()
```



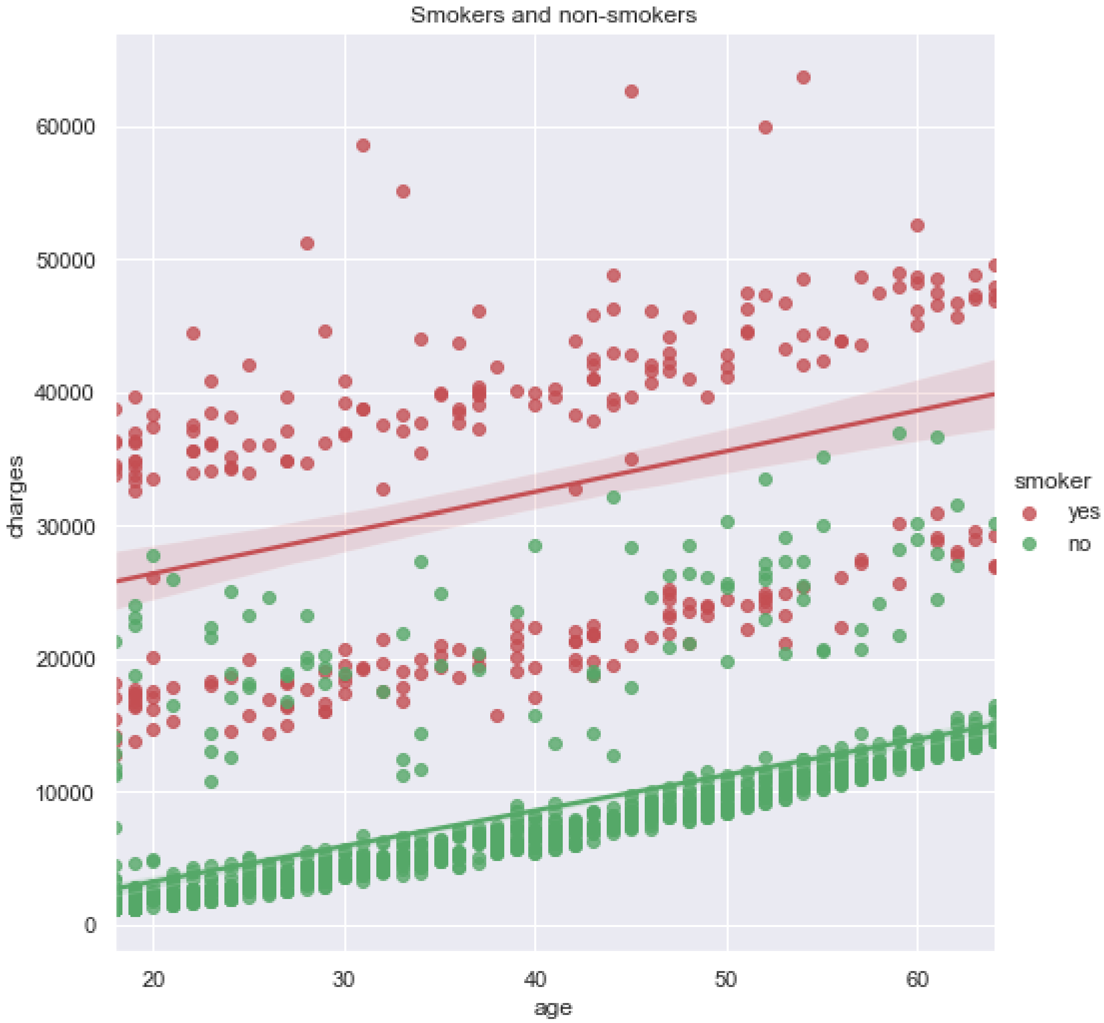
In [26]:
```
x['region'].value_counts()
```

Out[26]:
```
southeast    364
northwest    325
southwest    325
northeast    324
Name: region, dtype: int64
```

In [19]:
```
sns.lmplot(x='age', y='charges', hue='smoker', data=x, palette='inferno', scatter
plt.show()
```



In [29]:
```
#a relationship plot between age, smoker and charges for medical insurance
sns.lmplot(x="age", y="charges", hue="smoker", data=x, palette=dict(yes="r", no='
plt.title('Smokers and non-smokers')
plt.show()
```

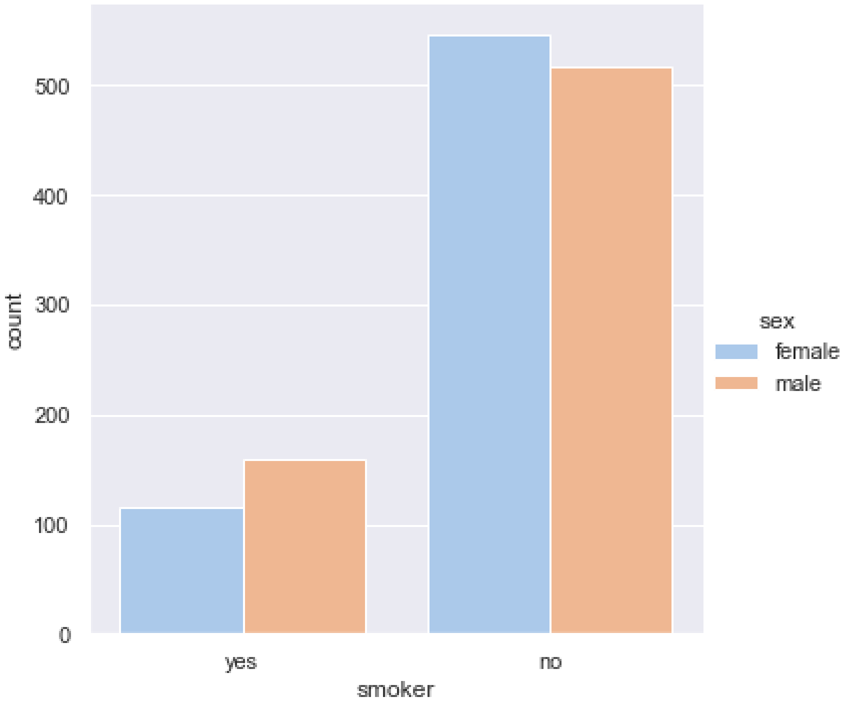


we can say smoking has the highest impact on the medical insurance costs.

While it seems obvious that the charges increase linearly with age, smoking appears to be the highest contributor to charges.

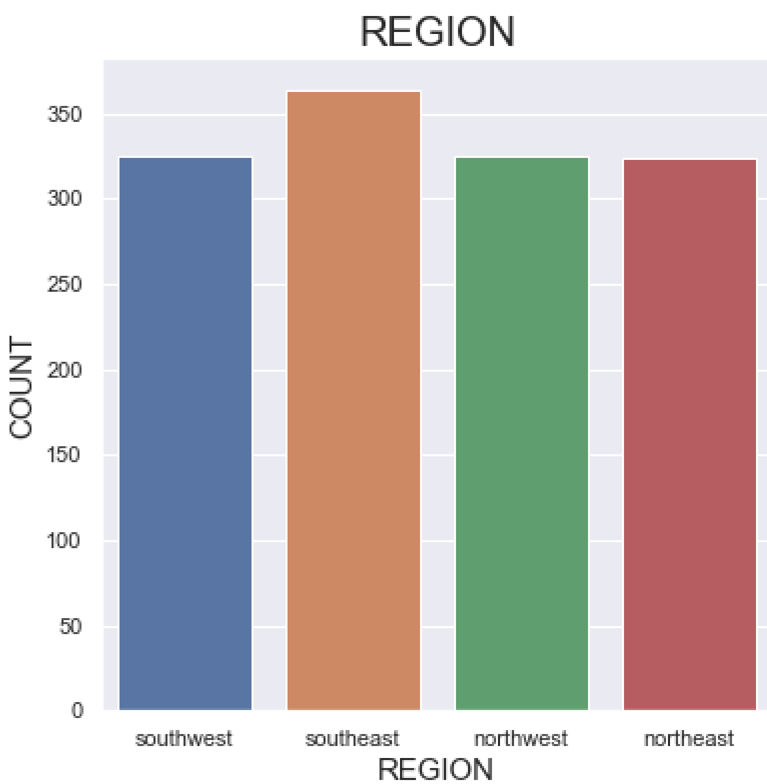
But cost is also increasing with age

In [27]:
```
#distribution of male and female in relation with smoking habit
sns.catplot(x="smoker", kind="count", hue = 'sex', data = x , palette='pastel');
plt.show()
```



the majority understands the downsides of smoking.

In [28]:
```
# region column
plt.figure(figsize=(6,6))
sns.countplot(x='region', data=x)
plt.title('REGION',fontdict={'fontsize': 20})
plt.xlabel('REGION',fontdict={'fontsize': 15})
plt.ylabel('COUNT',fontdict={'fontsize': 15})

plt.show()
```



Converting Categorical Features to Numerical

In [34]:
```
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()

le.fit(x.sex.drop_duplicates())
x.sex = le.transform(x.sex)

le.fit(x.smoker.drop_duplicates())
x.smoker = le.transform(x.smoker)

le.fit(x.region.drop_duplicates())
x.region = le.transform(x.region)

x.dtypes
```

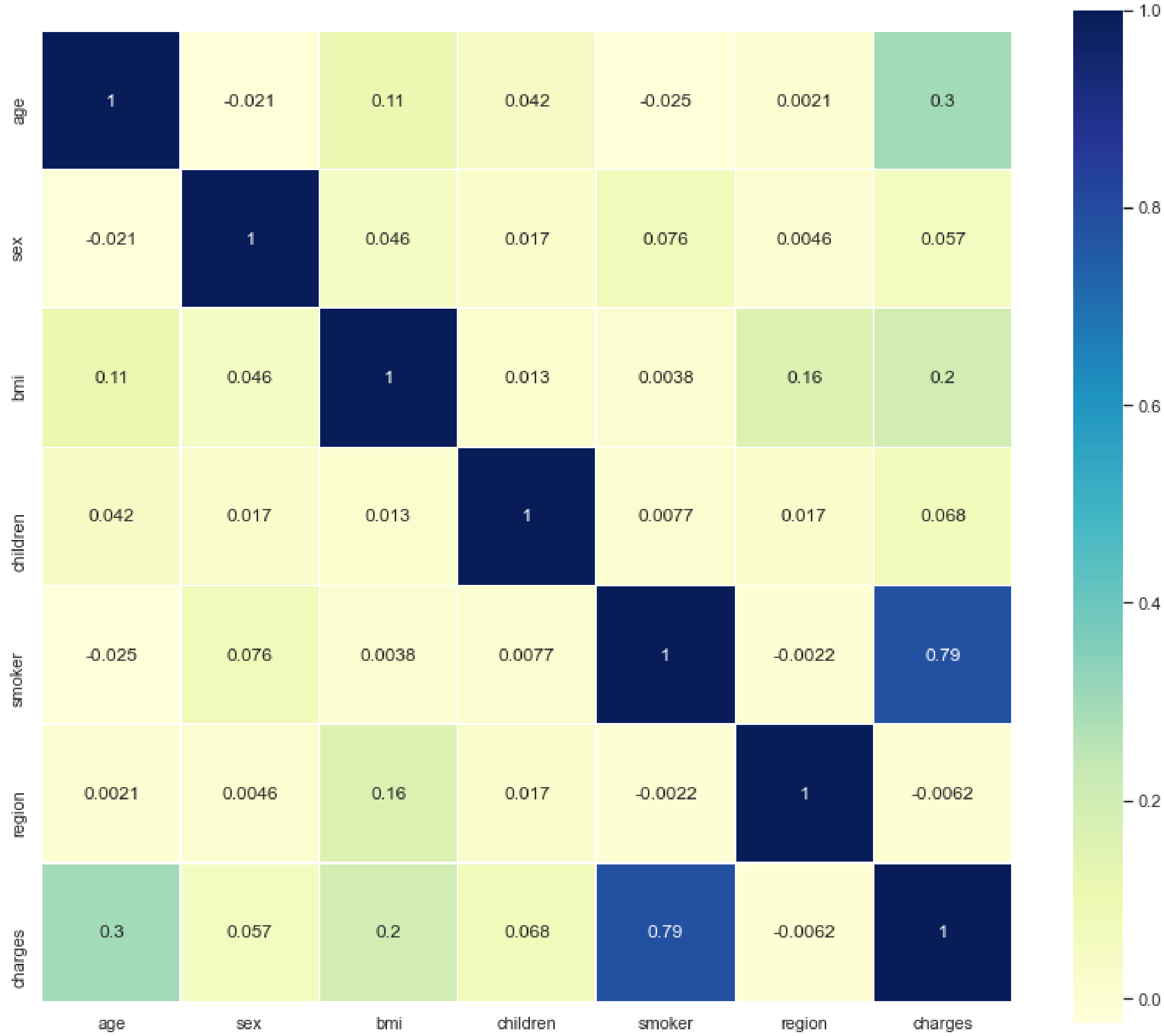
Out[34]:
```
age            int64
sex            int64
bmi          float64
children       int64
smoker         int64
region         int32
charges      float64
dtype: object
```

In [36]:
```
x.describe()
```

Out[36]:

	age	sex	bmi	children	smoker	region	charge
count	1338.000000	1338.000000	1338.000000	1338.000000	1338.000000	1338.000000	1338.00000
mean	39.207025	0.505232	30.663397	1.094918	0.204783	1.515695	13270.42226
std	14.049960	0.500160	6.098187	1.205493	0.403694	1.104885	12110.01123
min	18.000000	0.000000	15.960000	0.000000	0.000000	0.000000	1121.87390
25%	27.000000	0.000000	26.296250	0.000000	0.000000	1.000000	4740.28715
50%	39.000000	1.000000	30.400000	1.000000	0.000000	2.000000	9382.03300
75%	51.000000	1.000000	34.693750	2.000000	0.000000	2.000000	16639.91251
max	64.000000	1.000000	53.130000	5.000000	1.000000	3.000000	63770.42801

In [39]:
```
sns.set(color_codes=True)
plt.figure(figsize=(14, 12))
sns.heatmap(x.astype(float).corr(),
            linewidths=0.2,
            square=True,
            linecolor='white',
            annot=True,
            cmap="YlGnBu")
plt.show()
```



we have a co relation with the smoking,BMI and age

Splitting the data into Training data & Testing Data

In [45]:
```
from sklearn.linear_model import LinearRegression
from sklearn.ensemble import RandomForestRegressor
from sklearn.tree import DecisionTreeRegressor
from sklearn.svm import SVR
import xgboost as xgb

from sklearn.metrics import r2_score, mean_squared_error, accuracy_score, confusi
from sklearn.model_selection import cross_val_score, RandomizedSearchCV, GridSear
from sklearn.model_selection import train_test_split
```

In [46]:
```
X = x.drop(columns='charges', axis=1)
Y = x['charges']
X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size=0.2, random_s
```

In [47]:
```
print(X.shape, X_train.shape, X_test.shape)
```

```
(1338, 6) (1070, 6) (268, 6)
```

MODEL TRAINING

Linear regression

In [48]:
```
# Loading the Linear Regression model
regressor = LinearRegression()
```

In [49]:
```
regressor.fit(X_train, Y_train)
```

Out[49]:
```
LinearRegression()
```

In [50]:
```
regressor.fit(X_train, Y_train)

LinearRegression(copy_X=True, fit_intercept=True, n_jobs=None, normalize=False)
```

Out[50]:
```
LinearRegression()
```

In [54]:
```
# Training the model
from sklearn.linear_model import LinearRegression
regressor = LinearRegression()
regressor.fit(X_train, Y_train)
```

Out[54]:
```
LinearRegression()
```

In [56]:
```
y_predict = regressor.predict(X_test)
```

In [99]:
```
accuracy = regressor.score(X_test, Y_test)
print('Accuracy of linear reression model is = ', accuracy)
```

```
Accuracy of linear reression model is =  0.7445422986536503
```

Random forest

In [75]:
```
%%time
reg_rf = RandomForestRegressor()
parameters = { 'n_estimators':[200,600,1000],
             'max_features': ["auto"],
             'max_depth':[40,50,60],
             'min_samples_split': [5,7,9],
             'min_samples_leaf': [7,10,12],
             'criterion': ['mse']}

reg_rf_gscv = GridSearchCV(estimator=reg_rf, param_grid=parameters, cv=10, n_jobs
reg_rf_gscv = reg_rf_gscv.fit(X_train, Y_train)
```

```
Wall time: 7min 56s
```

In [76]:
```
reg_rf_gscv.best_score_, reg_rf_gscv.best_estimator_
```

Out[76]:
```
(0.8478159405315868,
 RandomForestRegressor(max_depth=60, min_samples_leaf=12, min_samples_split=9,
                       n_estimators=1000))
```

In [78]:
```
rf_reg = RandomForestRegressor(max_depth=60, min_samples_leaf=12, min_samples_spl
                      n_estimators=1000)
rf_reg.fit(X_train,Y_train)
```

Out[78]:
```
RandomForestRegressor(max_depth=60, min_samples_leaf=12, min_samples_split=9,
                      n_estimators=1000)
```

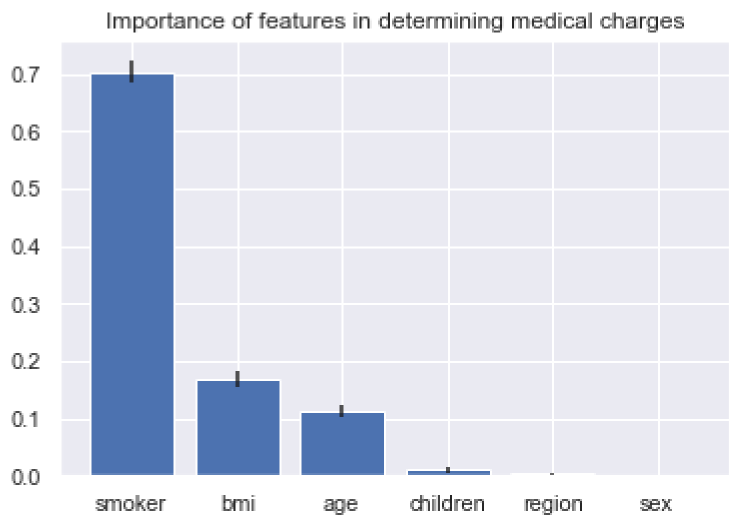
In [98]:
```
Accuracy = rf_reg.score(X_test, Y_test)
print(f'Accuracy : {Accuracy:.3}')
```

```
Accuracy : 0.866
```

In [104]:
```
importances = rf_reg.feature_importances_
std = np.std([tree.feature_importances_ for tree in rf_reg.estimators_], axis = 0

indices = np.argsort(importances)[::-1]
variables = ['age', 'sex','bmi', 'children','smoker','region']

imp_list = []
for value in range(X.shape[1]):
    variable = variables[indices[value]]
    imp_list.append(variable)
    print('%d.%s(%f)' % (value + 1, variable, importances[indices[value]]))

# Plotting the feature importances
plt.figure()
plt.title('Importance of features in determining medical charges')
plt.bar(imp_list, importances[indices], color = 'b', yerr = std[indices], align =
```

```
1.smoker(0.704242)
2.bmi(0.167949)
3.age(0.112480)
4.children(0.010170)
5.region(0.003980)
6.sex(0.001179)
```

Out[104]: <BarContainer object of 6 artists>



Best Algorithm:

Random Forest Regressor: 87%

In [106]:
```
import pickle

Pkl_Filename = "rf_tuned.pkl"

with open(Pkl_Filename, 'wb') as file:
    pickle.dump(rf_reg, file)
```

In [107]:
```
# Load the Model back from file
with open(Pkl_Filename, 'rb') as file:
    rf_tuned_loaded = pickle.load(file)
```

In [108]:
```
rf_tuned_loaded
```

Out[108]:
```
RandomForestRegressor(max_depth=60, min_samples_leaf=12, min_samples_split=9,
                      n_estimators=1000)
```

Building a Predictive System

In [111]:
```
#Predicting the Medical Charges
y_test_predic = rf_tuned_loaded.predict(X_test)

# Creating a dataframe for comparing the Actual Values with the Predicted Values
final_values = pd.DataFrame({'Actual values': Y_test, 'Predicted values': y_test_
final_values
```

Out[111]:

	Actual values	Predicted values
17	2395.17155	5061.405631
1091	11286.53870	12238.350428
273	9617.66245	12061.709672
270	1719.43630	3807.588128
874	8891.13950	9355.322550
...	...	...
232	1727.78500	2366.723892
323	11566.30055	12923.752597
1337	29141.36030	27165.371551
1066	8978.18510	10233.320927
966	23967.38305	23814.840072

268 rows × 2 columns

In [112]:
```
final_values.head(5)
```

Out[112]:

	Actual values	Predicted values
17	2395.17155	5061.405631
1091	11286.53870	12238.350428
273	9617.66245	12061.709672
270	1719.43630	3807.588128
874	8891.13950	9355.322550

In [113]:
```
final_values.tail()
```

Out[113]:

	Actual values	Predicted values
232	1727.78500	2366.723892
323	11566.30055	12923.752597
1337	29141.36030	27165.371551
1066	8978.18510	10233.320927
966	23967.38305	23814.840072

CONCLUSION

we can say random forest is the winner with 88% test accurecy.

Smoking is the greatest factor that affects medical cost charges.

In [ ]: