In this tutorial, I will utilize Kaggle dataset listing the insurance cost information of clients and the various factors affecting the cost in USA. I will use this dataset to develop a predictive model for estimating the annual insurance cost for the clients. We will conduct exploratory data analysis, visualization and preprocessing using pandas, matlplotlib and numpy. For model building, we will utilize **linear regression, polynomial regression, support vector regression, random forest regressor, dense neural networks and Xgboost regressor.** We will find the find the best model and hypertune the best model to improve the prediction accuracy. For model building we will utilize **scikit-learn, XGBoost and tensorflow** libraries.

Let's import all the libraries first.

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

Now let's read the insurance dataset using the pandas. The data can be read into a pandas DataFrame which can be used to extract all the important information about the dataset. The dataframe is a 2 dimensional where each row represents an observation and each column represents the features of the observation.

Similarly data from a single column can be read using the pandas Series class.

Exploratory data Analysis

In [2]:
```
data_path = "insurance.csv"  # data path
df = pd.read_csv(data_path)        # reading the datafile into a pandas dataf
```

Let's conduct some investigation of the dataset:

In [3]:
```
df.info() # Get some basic information about the dataset with all the columns
```

```
<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
```

There are 1338 rows and 7 columns. In this dataset, there are a total of 1338 insurance clients and associated 7 features. Let's take a look at the first 5 of them using df.head function

In [4]:
```
df.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

The dataset shows the age, sex, bmi, number of children, whether a smoker, living region and the insurance charges for the first 5 clients. We can also use df.columns to get the featuress and df.shape to get the size of this dataset.

In [5]:
```
print(f" The shape of the dataset is {df.shape}")
print(df.columns)
```

```
 The shape of the dataset is (1338, 7)
Index(['age', 'sex', 'bmi', 'children', 'smoker', 'region', 'charges'], dtype='
object')
```

Each column can be accessed via df["feature_name"]. Let's look at the age column and print 20 values

In [6]:
```
print(df["age"][:20])
```

```
0      19
1      18
2      28
3      33
4      32
5      31
```

```
6      46
7      37
8      37
9      60
10     25
11     62
12     23
13     56
14     27
15     19
16     52
17     23
18     56
19     30
Name: age, dtype: int64
```

When there are boolen data types, they can be converted to intiger data type using df["feature_name"].astype("int64"). In this case we don't have any boolean values. We can also use the other data types.

Let's use take a basics statistics of each numerical column: df.describe will give the non-null value count, mean, standard deviation, minimum, maximun and different percentile values. By default, the function will output information of all the numerical columns

In [7]:
```
df.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

Other categorical information statistics can be listed as follows

In [8]:
```
df.describe(include=["object", "bool", "category"])
```

Out[8]:

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

Here we can see that there are 2 unique categories for sex, 2 categories for smokers and 4 categories for the regions. Let's see what are those unique categories.

In [9]:
```
print(df["sex"].unique())
print(df["smoker"].unique())
print(df["region"].unique())
```

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

Let's see how much is the count for each of the catogories.

In [10]:
```
print(df["sex"].value_counts())
```

```
sex
male      676
female    662
Name: count, dtype: int64
```

In [11]:
```
print(df["smoker"].value_counts())
```

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

In [12]:
```
print(df["region"].value_counts())
```

```
region
southeast    364
southwest    325
northwest    325
northeast    324
Name: count, dtype: int64
```

Now let's do some sorting of the data by each column features. First let's sort the data by insurance charges in the descending order and take a look at the first 5 clients. Similary we can sort based on multiple features as well.

In [13]:
```
df.sort_values(by = ["charges"], ascending = [False]).head()
```

Out[13]:

	age	sex	bmi	children	smoker	region	charges
543	54	female	47.410	0	yes	southeast	63770.42801
1300	45	male	30.360	0	yes	southeast	62592.87309
1230	52	male	34.485	3	yes	northwest	60021.39897
577	31	female	38.095	1	yes	northeast	58571.07448
819	33	female	35.530	0	yes	northwest	55135.40209

In [14]:
```
df.sort_values(by = ["age","charges"], ascending = [True, False]).head()
```

Out[14]:

	age	sex	bmi	children	smoker	region	charges
803	18	female	42.240	0	yes	southeast	38792.68560
759	18	male	38.170	0	yes	southeast	36307.79830
161	18	female	36.850	0	yes	southeast	36149.48350
623	18	male	33.535	0	yes	northeast	34617.84065
57	18	male	31.680	2	yes	southeast	34303.16720

Let's print the min, max and mean of a feature column:

In [15]:
```
print(df["age"].min(), df["age"].max(), df["age"].mean(), df["age"].median())
```

```
18 64 39.20702541106129 39.0
```

Let's do some slicing of the data: Use df.loc while using feature names and iloc while using index values of rows and columns.

Interestingly loc will include the starting and last rows whereas the iloc will not include the last column index.

In [16]:
```
df.loc[0:3, "age": "region"]
```

Out[16]:

	age	sex	bmi	children	smoker	region
0	19	female	27.900	0	yes	southwest
1	18	male	33.770	1	no	southeast
2	28	male	33.000	3	no	southeast
3	33	male	22.705	0	no	northwest

In [17]:
```
df.iloc[0:3, 0:4]
```

Out[17]:

	age	sex	bmi	children
0	19	female	27.90	0
1	18	male	33.77	1
2	28	male	33.00	3

We can use df.apply function to apply a function in each column of the dataset. Let's look at the maximum values in each column.

In [18]:

```
df.apply(np.max)
```

Out[18]:
```
age                  64
sex                male
bmi               53.13
children              5
smoker              yes
region        southwest
charges     63770.42801
dtype: object
```

Now let's try to do some extraction of the values based on the categories. Let's look at people from north east who are female and aged > 40.

In [19]:
```
df[(df['sex'] == 'female') & (df['region'] == 'northeast') & (df['age'] > 40)
```

Out[19]:

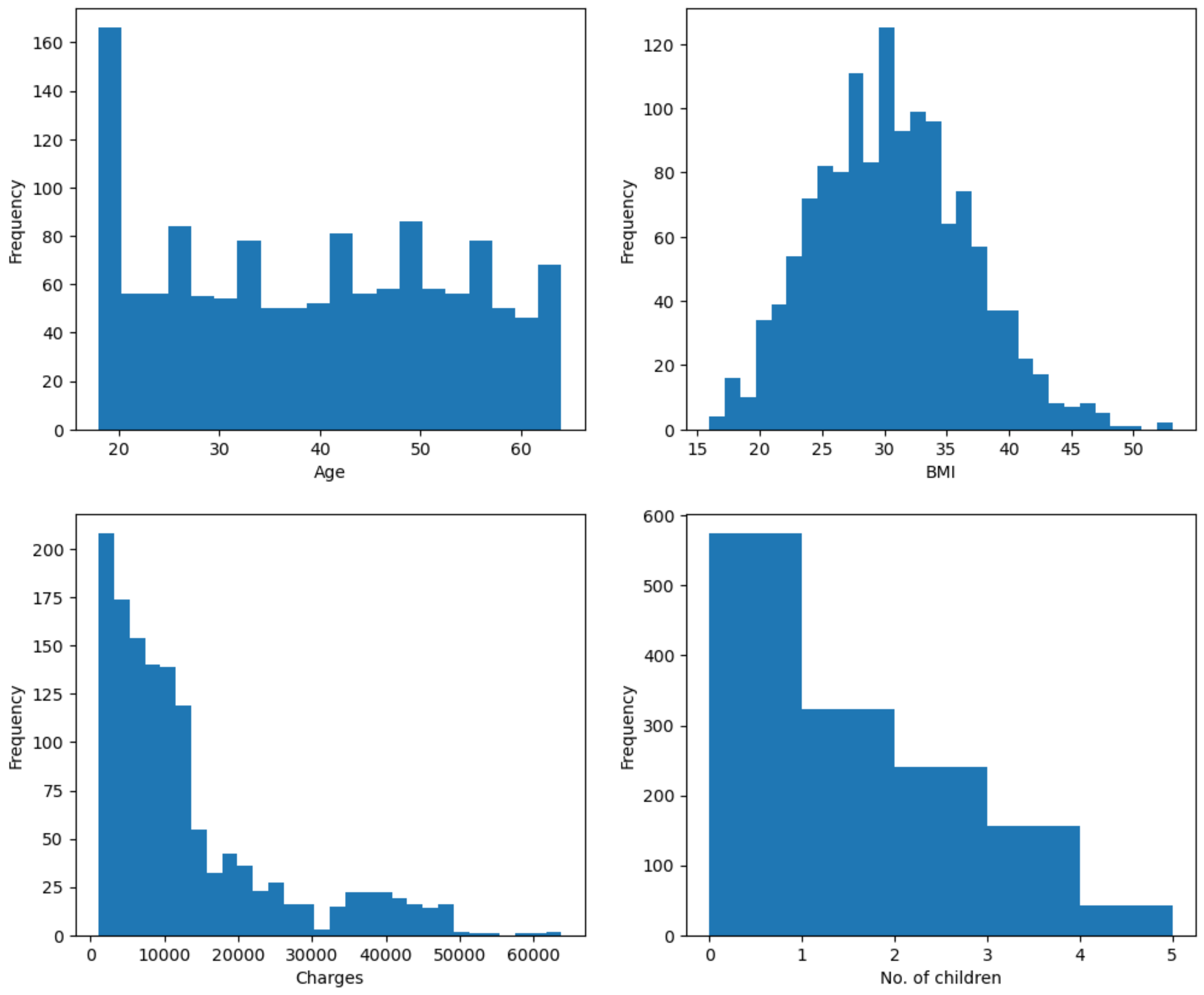
	age	sex	bmi	children	smoker	region	charges
16	52	female	30.780	1	no	northeast	10797.33620
20	60	female	36.005	0	no	northeast	13228.84695
26	63	female	23.085	0	no	northeast	14451.83515
56	58	female	31.825	2	no	northeast	13607.36875
81	45	female	38.285	0	no	northeast	7935.29115
...	...	...	...	...	...	...	...
1236	63	female	21.660	0	no	northeast	14449.85440
1259	52	female	23.180	0	no	northeast	10197.77220
1264	49	female	33.345	2	no	northeast	10370.91255
1285	47	female	24.320	0	no	northeast	8534.67180
1326	42	female	32.870	0	no	northeast	7050.02130

79 rows × 7 columns

Data Visualization

Now let's do some plotting to get an understanding of the data or to find any obvious correlations/patterns. For plotting let's use the matplotlib package for more flexibility. But we can alway use the df.plot for quick plotting as well.

In [20]:
```
fig = plt.figure(figsize = (12,10))

plt.subplot(2,2,1)
plt.hist(df['age'], bins = 20)
plt.xlabel("Age")
plt.ylabel("Frequency")

plt.subplot(2,2,2)
plt.hist(df['bmi'], bins = 30)
plt.hist(df['bmi'], bins = 30)
plt.xlabel("BMI")
plt.ylabel("Frequency")

plt.subplot(2,2,3)
plt.hist(df['charges'], bins = 30)
plt.xlabel("Charges")
plt.ylabel("Frequency")

plt.subplot(2,2,4)
plt.hist(df['children'], bins = 5)
plt.xlabel("No. of children")
plt.ylabel("Frequency")

plt.show()
```

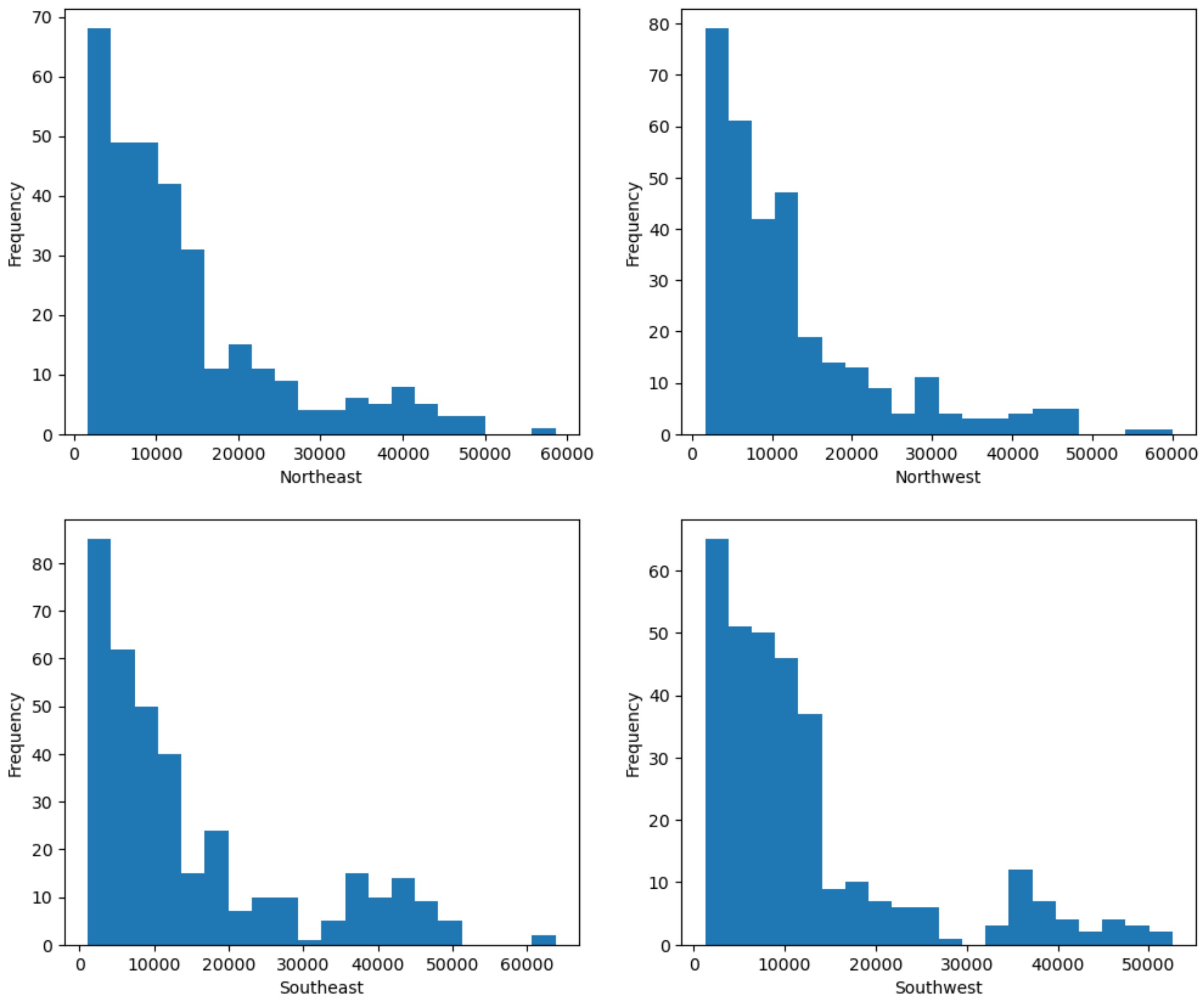


As we can see, the age distribution is mostly random and relatively there is a higher younger population in this dataset. A health BMI is between 18-25, 25-30 is overweight and above 30 is obese. Even though the distribution is more or less Gaussian, most of the population is overweight and obese. Most of the families have less than 10k annual charges and single children.

Now let's see how the charges vary as a function of various factors: let's look at region wise data:

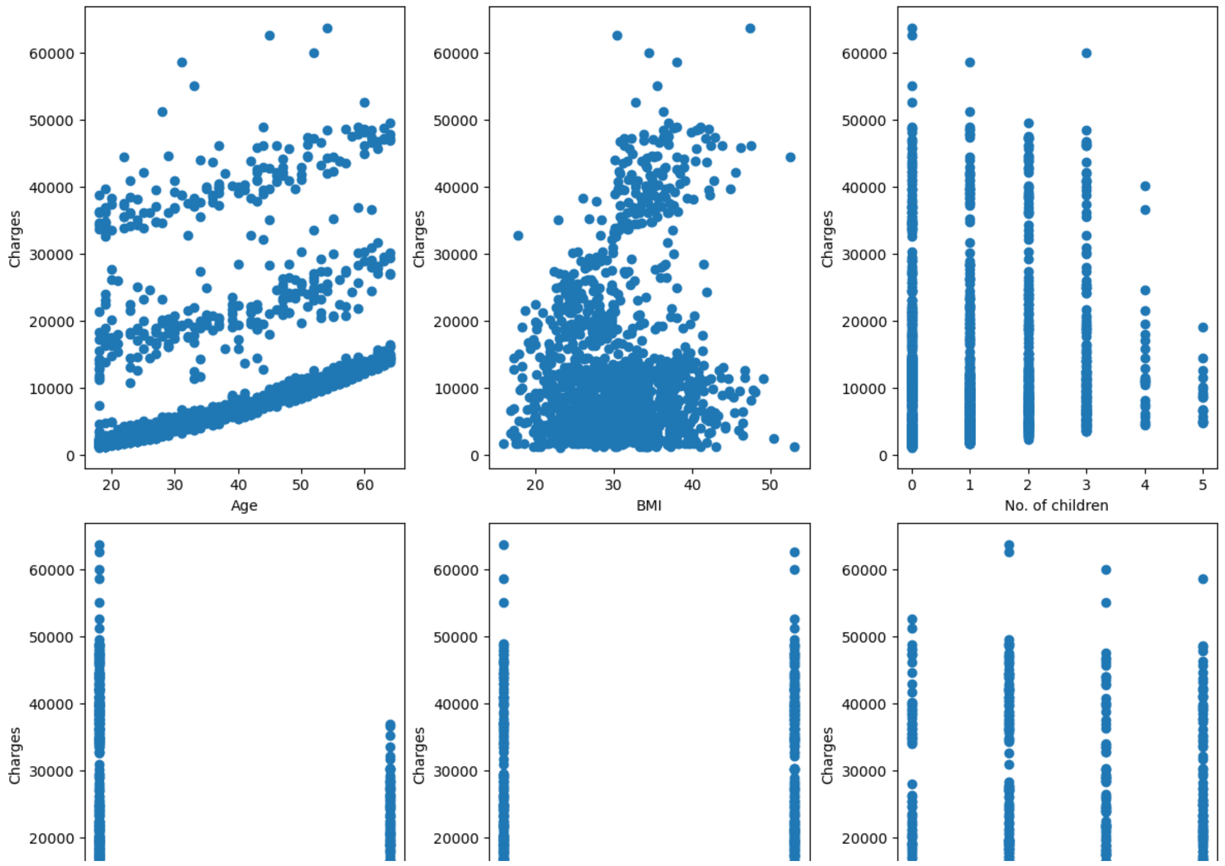
In [21]:

```python
fig = plt.figure(figsize = (12,10))

plt.subplot(2,2,1)
plt.hist(df[df['region'] == 'northeast']['charges'], bins = 20)
plt.xlabel("Northeast")
plt.ylabel("Frequency")

plt.subplot(2,2,2)
plt.hist(df[df['region'] == 'northwest']['charges'], bins = 20)
plt.xlabel("Northwest")
plt.ylabel("Frequency")

plt.subplot(2,2,3)
plt.hist(df[df['region'] == 'southeast']['charges'], bins = 20)
plt.xlabel("Southeast")
plt.ylabel("Frequency")

plt.subplot(2,2,4)
plt.hist(df[df['region'] == 'southwest']['charges'], bins = 20)
plt.xlabel("Southwest")
plt.ylabel("Frequency")

plt.show()
```



So here we do not see any correlation between regions and associated charges. Now let's compare the charges with other parameters:

In [22]:
```
fig = plt.figure(figsize = (12,10), constrained_layout = True)

plt.subplot(2,3,1)
plt.scatter(df['age'], df['charges'])
plt.xlabel("Age")
plt.ylabel("Charges")

plt.subplot(2,3,2)
plt.scatter(df['bmi'], df['charges'])
plt.xlabel("BMI")
plt.ylabel("Charges")

plt.subplot(2,3,3)
plt.scatter(df['children'], df['charges'])
plt.xlabel("No. of children")
plt.ylabel("Charges")

plt.subplot(2,3,4)
plt.scatter(df['smoker'], df['charges'])
plt.xlabel("Smoker")
plt.ylabel("Charges")

plt.subplot(2,3,5)
plt.scatter(df['sex'], df['charges'])
plt.xlabel("Sex")
plt.ylabel("Charges")

plt.subplot(2,3,6)
plt.scatter(df['region'], df['charges'])
plt.xlabel("Region")
plt.ylabel("Charges")
plt.show()
```

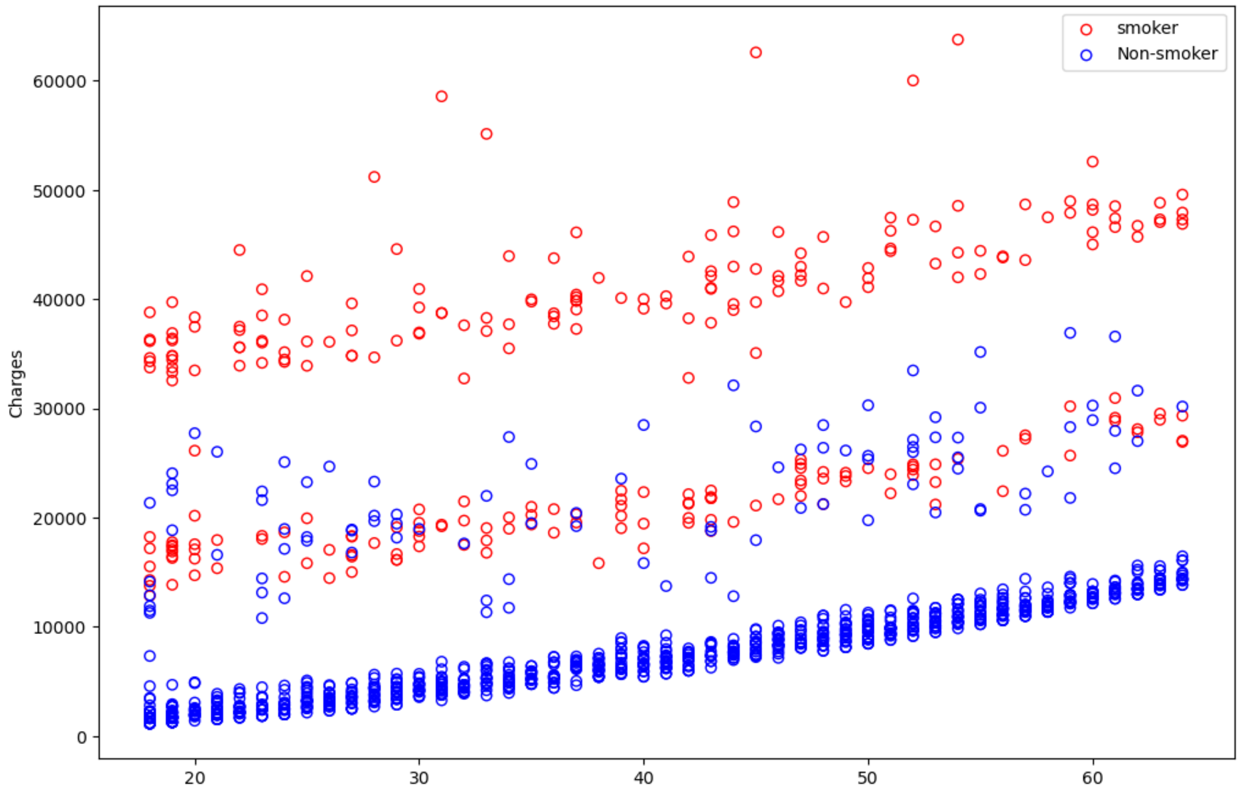


Here we see a clear correlation between insurance charge and the age of clients. As the age of client increases, the insurance cost increases. Also, it obvious that there are 3 distinct classes within the age category. Maybe there is a slight correlation between BMI and charges, however it is not a significant one. At the same time, it is work noticing that most of the overweight/obese individuals do not have high insurnce charges.

Insurance charges are higher for smokers compared to non-smokers. However, insurance charges does not seem to have a correlation with sex and region. But the insurance charges seems to lesser for clients with 5 children. It could be also due to a low population case as well.

Let's try to figure out the 3 distinct class of charges with in the age category. First let's see if there is a correlation between people who are smokers and not.

In [23]:
```
cond1 = df['smoker'] == 'yes'    # smoker
cond2 = df['smoker'] == 'no'     # non-smoker

fig = plt.figure(figsize = (12,8))
plt.scatter(df[cond1]['age'], df[cond1]['charges'], label = 'smoker', edgecol
plt.scatter(df[cond2]['age'], df[cond2]['charges'], label = 'Non-smoker', edg
plt.xlabel("Age")
plt.ylabel("Charges")
plt.legend()
plt.show()
```

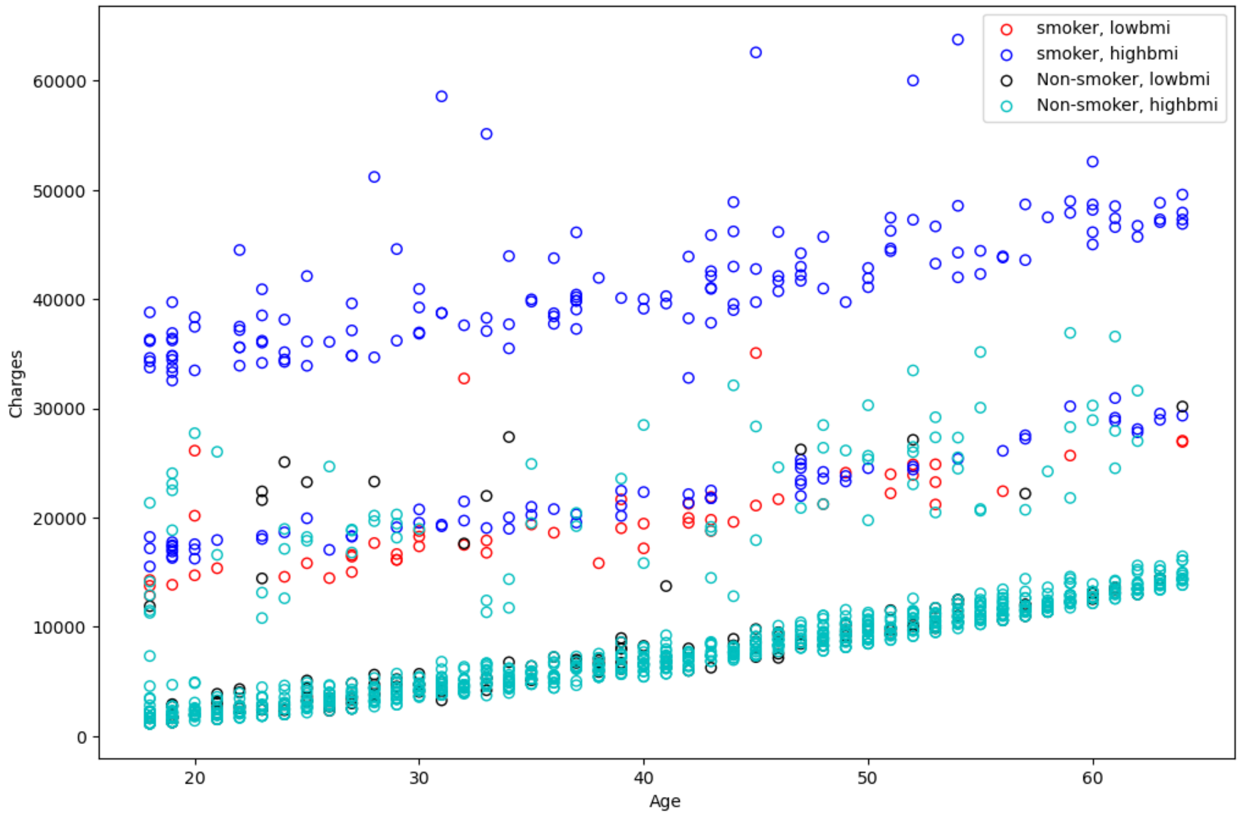


Age

There is a clear distinction between smokers and non-smokers. Non-smokers have lower insurance cost compared to smokers. However each smoker and non-smokers have distinct 2 class of charges. Let's try to find out the factor causing a split of charges like this? Is it BMI? Let's classify clients with bmi less than 25 and bmi greater than 25.

In [24]:
```
cond3 = df['bmi'] <= 25   # lowbmi
cond4 = df['bmi'] > 25  #highbmi

print(df[cond2 & cond4]['charges'].max())

fig = plt.figure(figsize = (12,8))
plt.scatter(df[cond1 & cond3]['age'], df[cond1 & cond3]['charges'], label = '
plt.scatter(df[cond1 & cond4]['age'], df[cond1 & cond4]['charges'], label = '

plt.scatter(df[cond2 & cond3]['age'], df[cond2 & cond3]['charges'], label = '
plt.scatter(df[cond2 & cond4]['age'], df[cond2 & cond4]['charges'], label = '

plt.xlabel("Age")
plt.ylabel("Charges")
plt.legend()
plt.show()
```

```
36910.60803
```

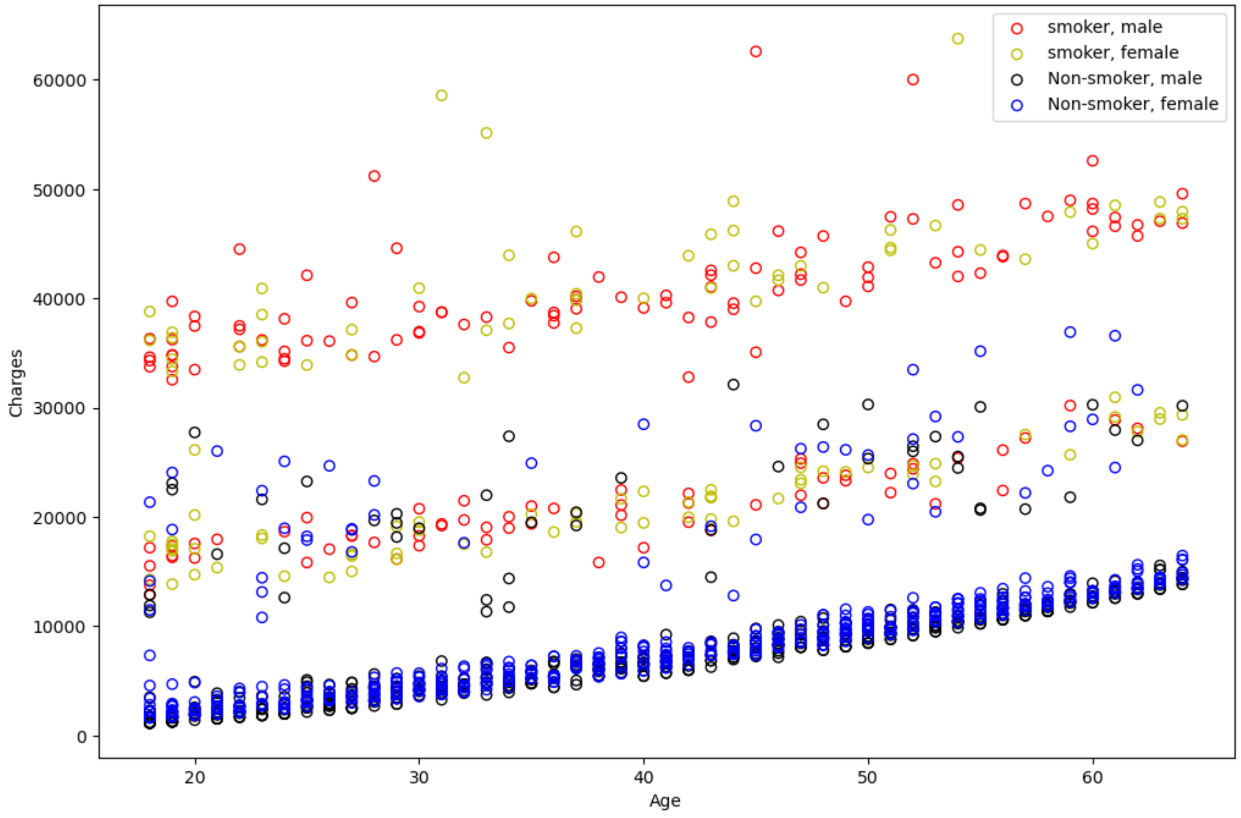


So BMI based classification does not make any sense. In addition, there are not clients who are smokers with low bmi which is interesting. Let's see if it has to do something with the sex of the individual.

In [25]:
```
cond5 = df['sex'] == 'male'
```

```
cond6 = df['sex'] == 'female'

fig = plt.figure(figsize = (12,8))
plt.scatter(df[cond1 & cond5]['age'], df[cond1 & cond5]['charges'], label = '
plt.scatter(df[cond1][cond6]['age'], df[cond1][cond6]['charges'], label = 'sm

plt.scatter(df[cond2 & cond5]['age'], df[cond2 & cond5]['charges'], label = '
plt.scatter(df[cond2 & cond6]['age'], df[cond2 & cond6]['charges'], label = '

plt.xlabel("Age")
plt.ylabel("Charges")
plt.legend()
plt.show()
```

```
/var/folders/c8/g5hp4hlx7dv6gv7n9zdg74rc0000gn/T/ipykernel_64447/2515681309.py:
6: UserWarning: Boolean Series key will be reindexed to match DataFrame index.
  plt.scatter(df[cond1][cond6]['age'], df[cond1][cond6]['charges'], label = 'sm
oker, female', edgecolors = 'y', facecolors = 'none')
/var/folders/c8/g5hp4hlx7dv6gv7n9zdg74rc0000gn/T/ipykernel_64447/2515681309.py:
6: UserWarning: Boolean Series key will be reindexed to match DataFrame index.
  plt.scatter(df[cond1][cond6]['age'], df[cond1][cond6]['charges'], label = 'sm
oker, female', edgecolors = 'y', facecolors = 'none')
```

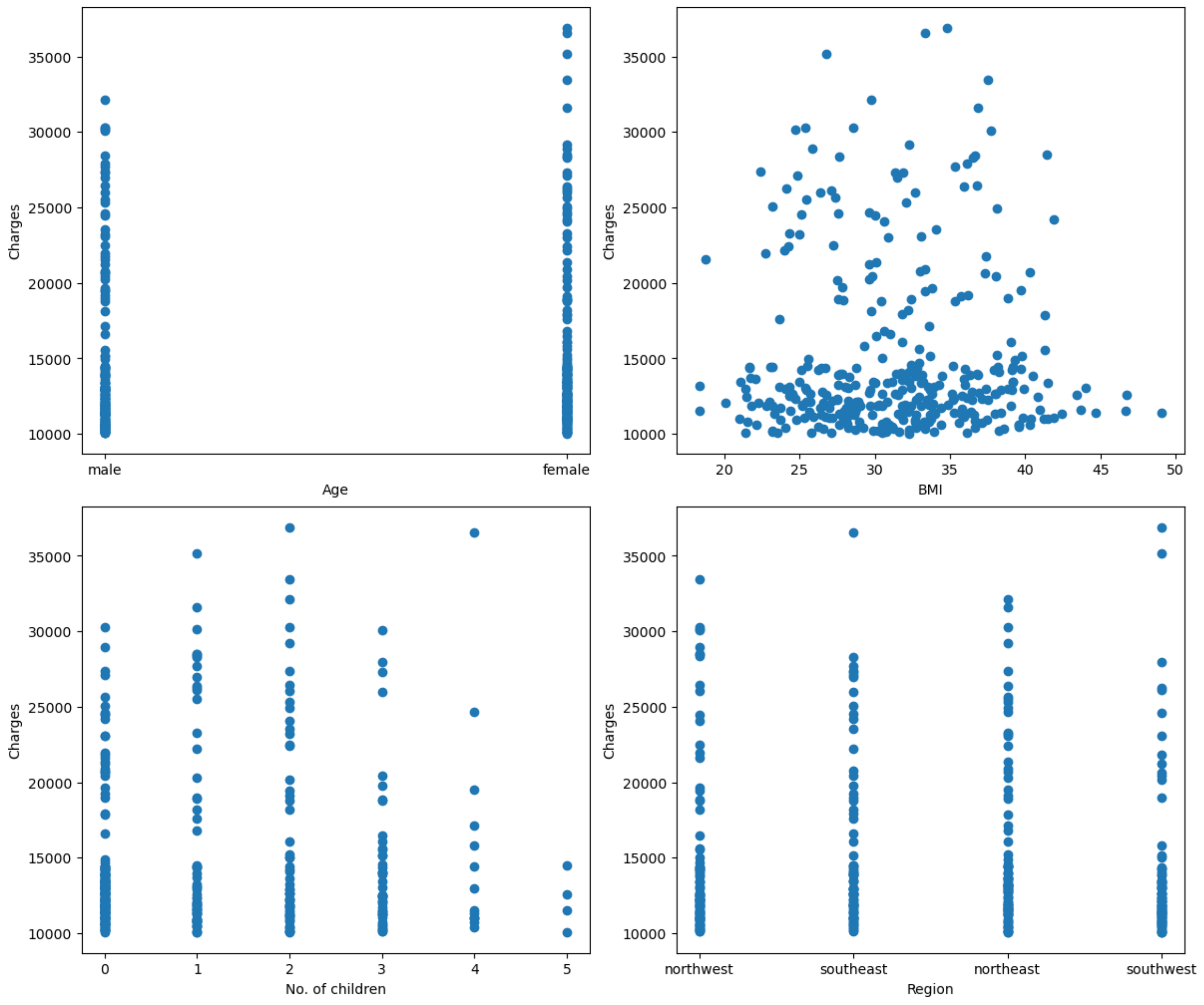


Sex is also not a distinct factor here. Let's taka a look at the non-smokers with insurance charges greater than 10000 and smokers with charges greater than 30000. The upper class in each smoker vs non-smoker category

In [26]:
```
data1 = df[(df['smoker'] == 'no') & (df['charges'] > 10000)]
data2 = df[(df['smoker'] == 'yes') & (df['charges'] > 30000)]
```

Let's look at the data1 case:

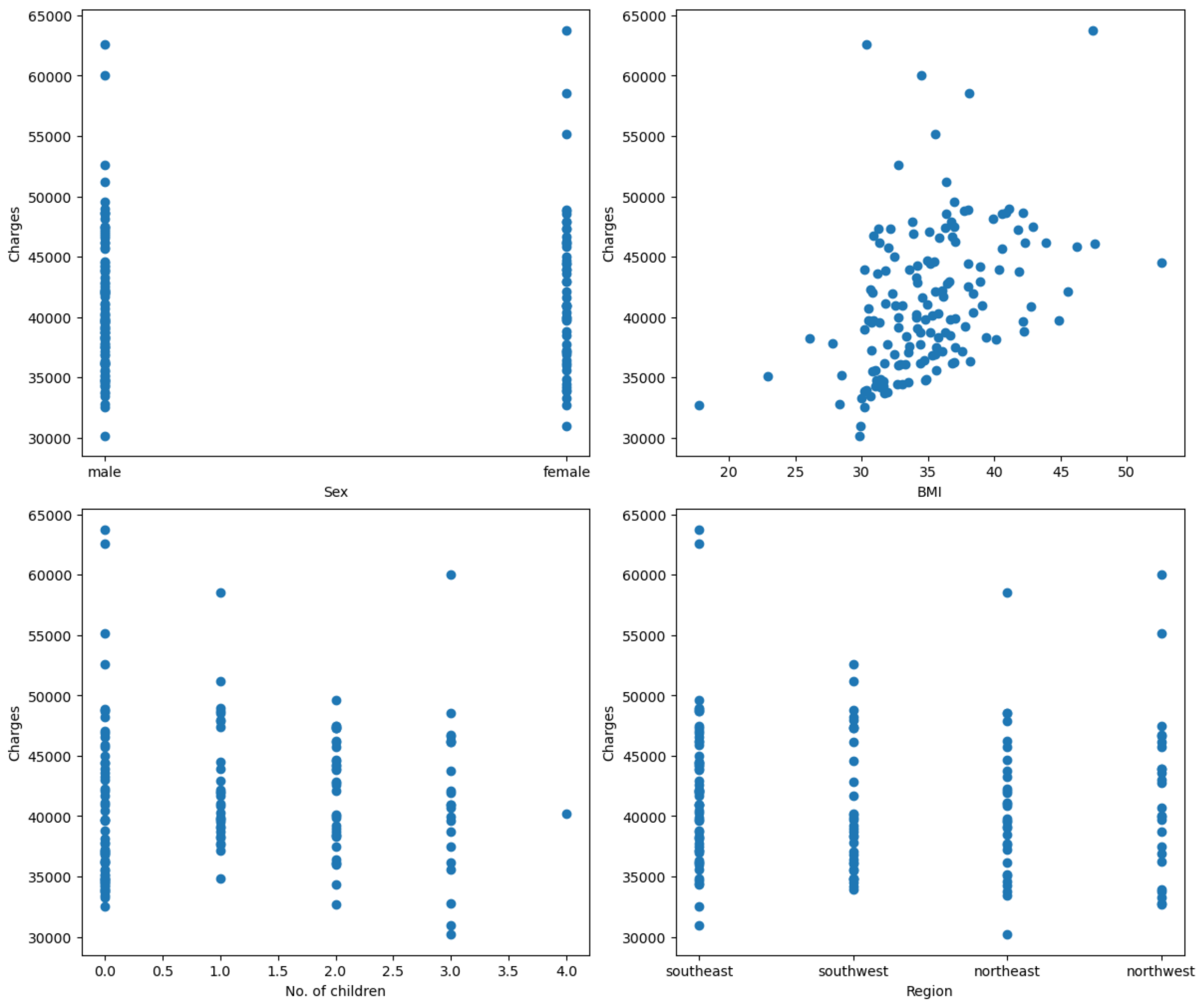
```
In [27]: fig = plt.figure(figsize = (12,10), constrained_layout = True)

         plt.subplot(2,2,1)
         plt.scatter(data1['sex'], data1['charges'])
         plt.xlabel("Age")
         plt.ylabel("Charges")

         plt.subplot(2,2,2)
         plt.scatter(data1['bmi'], data1['charges'])
         plt.xlabel("BMI")
         plt.ylabel("Charges")

         plt.subplot(2,2,3)
         plt.scatter(data1['children'], data1['charges'])
         plt.xlabel("No. of children")
         plt.ylabel("Charges")

         plt.subplot(2,2,4)
         plt.scatter(data1['region'], data1['charges'])
         plt.xlabel("Region")
         plt.ylabel("Charges")

         plt.show()
```



Now let's look at the data2 case:

In [28]:

```
fig = plt.figure(figsize = (12,10), constrained_layout = True)

plt.subplot(2,2,1)
plt.scatter(data2['sex'], data2['charges'])
plt.xlabel("Sex")
plt.ylabel("Charges")

plt.subplot(2,2,2)
plt.scatter(data2['bmi'], data2['charges'])
plt.xlabel("BMI")
plt.ylabel("Charges")

plt.subplot(2,2,3)
plt.scatter(data2['children'], data2['charges'])
plt.xlabel("No. of children")
plt.ylabel("Charges")

plt.subplot(2,2,4)
plt.scatter(data2['region'], data2['charges'])
plt.xlabel("Region")
plt.ylabel("Charges")

plt.show()
```



In the non-smoker class with high charges, there is smaller correlation between charges and bmi. Interestingly most of the non-smoker with high charges are **obese**. It looks like the 2 distinct class in smoker vs non-smokers could be due to a range of factors.

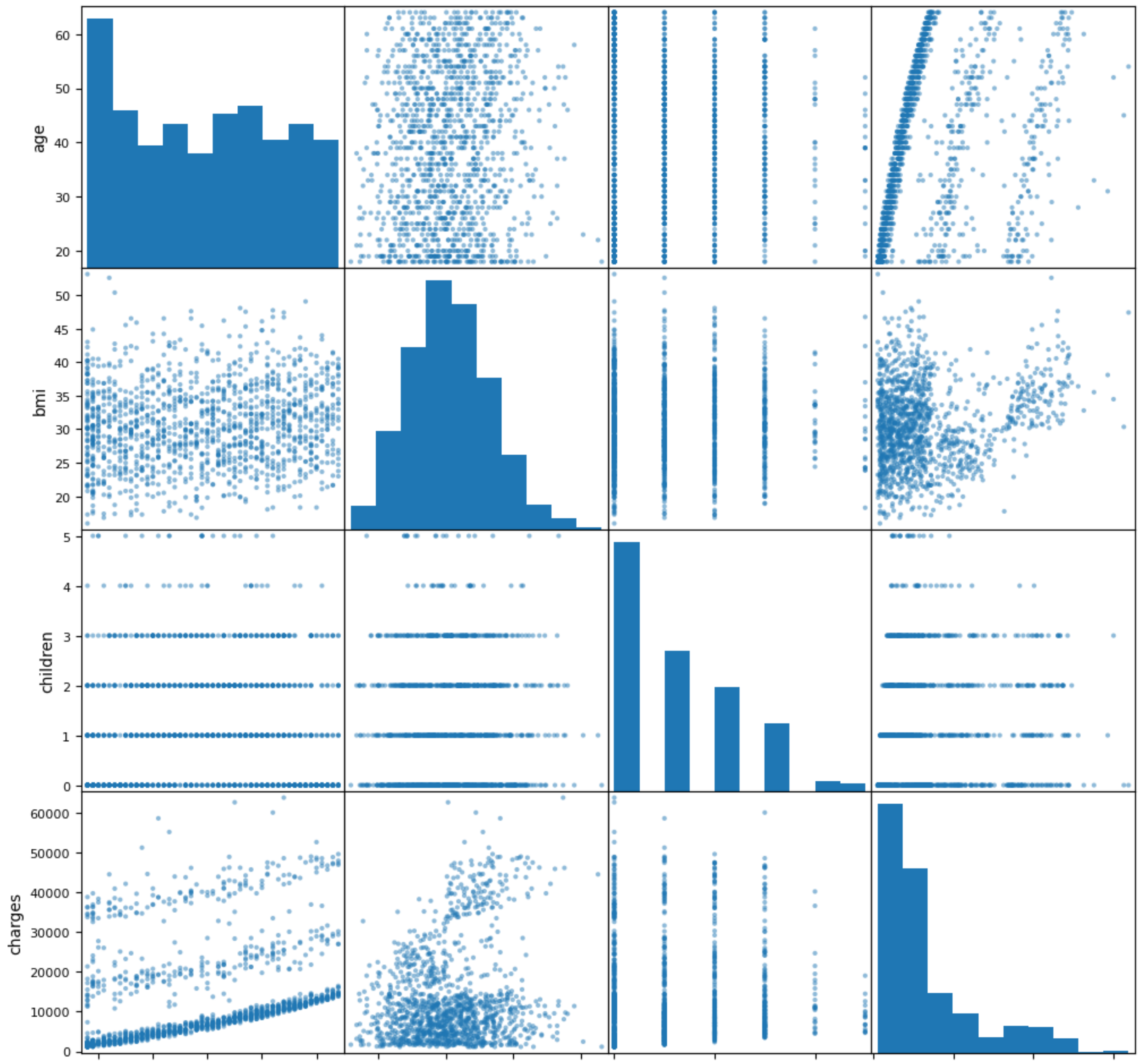
Let's looks for correlations using the corr() function.

In [29]:
```
corr_matrix = df.corr(numeric_only=True) #correlation matrix
corr_matrix['charges']  # correlation of parameters with charges
```

Out[29]:
```
age         0.299008
bmi         0.198341
children    0.067998
charges     1.000000
Name: charges, dtype: float64
```

The results are similar to what we already observed from the plots. We can directly make scatter matrix plot here.

In [30]:
```
from pandas.plotting import scatter_matrix
#attributes = ["age", "sysBP", "prevalentHyp", "diaBP", "glucose"]
scatter_matrix(df, figsize = (12,12))
plt.show()
```



Data preprocessing - cleaning, hot encoding and scaling

Now let's build a multivariate linear regression model to predict the insurace charges. Before building we need to clean the data and split it into training and test datasets. Let's do that.

In [31]:
```
# Check for null/NAN values in dataset
df.isnull().any()
```

Out[31]:
```
age         False
sex         False
bmi         False
children    False
smoker      False
region      False
charges     False
dtype: bool
```

In [32]:
```
# check for duplicate values
dup = df[df.duplicated()]

print("Duplicate Rows :")

# Print the resultant Dataframe
dup
```

```
Duplicate Rows :
```

Out[32]:

	age	sex	bmi	children	smoker	region	charges
581	19	male	30.59	0	no	northwest	1639.5631

In [33]:
```
# drop the duplicate rows
df = df.drop_duplicates()
```

In this dataset, we don't have any null values, so cleaning is not requried. But we have 3 categorical variables and most of the ML algorithms cannot feed cateogorical variables. We will use a technique called *one-hot encoding* to create a binary attribute for each category.

In [34]:
```
# let's use pandas get_dummies function to do the one-hot encoding
cat_variables = ['sex', 'smoker', 'region']
df_cod = pd.get_dummies(data = df,
                         prefix = cat_variables,
                         columns = cat_variables, dtype=int)
```

In [35]:
```
df_cod.info()
df_cod.head()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 1337 entries, 0 to 1337
Data columns (total 12 columns):
 #   Column            Non-Null Count  Dtype  
---  ------            --------------  -----  
 0   age               1337 non-null   int64  
 1   bmi               1337 non-null   float64
 2   children          1337 non-null   int64  
 3   charges           1337 non-null   float64
 4   sex_female        1337 non-null   int64  
 5   sex_male          1337 non-null   int64  
 6   smoker_no         1337 non-null   int64  
 7   smoker_yes        1337 non-null   int64  
 8   region_northeast  1337 non-null   int64  
 9   region_northwest  1337 non-null   int64  
 10  region_southeast  1337 non-null   int64  
 11  region_southwest  1337 non-null   int64  
dtypes: float64(2), int64(10)
memory usage: 135.8 KB
```

Out[35]:

	age	bmi	children	charges	sex_female	sex_male	smoker_no	smoker_yes
0	19	27.900	0	16884.92400	1	0	0	1
1	18	33.770	1	1725.55230	0	1	1	0
2	28	33.000	3	4449.46200	0	1	1	0
3	33	22.705	0	21984.47061	0	1	1	0
4	32	28.880	0	3866.85520	0	1	1	0

Now all the categorical values have been one hot encoded. Let's split the data into train, test and cross validatation dataset

In [36]:

```python
from sklearn.model_selection import train_test_split

# Split into train and test first
data_train, data_test = train_test_split(df_cod, test_size = 0.4, random_stat
# Split the test into test and validate again
data_test, data_val = train_test_split(data_test, test_size = 0.5, random_sta
print(f" Train data shape : {data_train.shape}, Test data shape : {data_test.
```

```
 Train data shape : (802, 12), Test data shape : (267, 12), Validation data sha
pe: (268, 12)
```

Let's extract the X and Y datasets from each of these cateogories:

In [37]:

```python
y_train = data_train['charges']
x_train = data_train.drop('charges', axis = 1)
print(x_train.head())

y_test = data_test['charges']
x_test = data_test.drop('charges', axis = 1)
print(x_test.head())

y_val = data_val['charges']
```

```
x_val = data_val.drop('charges', axis = 1)
print(y_val)
print(x_val.head())
```

```
     age     bmi  children  sex_female  sex_male  smoker_no  smoker_yes  \
25    59  27.720         3           1         0          1           0
336   60  25.740         0           0         1          1           0
47    28  34.770         0           1         0          1           0
106   19  28.400         1           1         0          1           0
994   27  20.045         3           1         0          0           1

     region_northeast  region_northwest  region_southeast  region_southwest
25                  0                 0                 1                 0
336                 0                 0                 1                 0
47                  0                 1                 0                 0
106                 0                 0                 0                 1
994                 0                 1                 0                 0
      age    bmi  children  sex_female  sex_male  smoker_no  smoker_yes  \
1240   52  41.80         2           0         1          0           1
639    56  33.66         4           0         1          1           0
583    32  23.65         1           1         0          1           0
611    38  34.80         2           1         0          1           0
1284   61  36.30         1           0         1          0           1

      region_northeast  region_northwest  region_southeast  region_southwest
1240                 0                 0                 1                 0
639                  0                 0                 1                 0
583                  0                 0                 1                 0
611                  0                 0                 0                 1
1284                 0                 0                 0                 1
1244     1135.94070
192      2137.65360
1221     6593.50830
716      9566.99090
244     29523.16560
           ...
56      13607.36875
362     13844.50600
567      7256.72310
575     12222.89830
282      4237.12655
Name: charges, Length: 268, dtype: float64
      age    bmi  children  sex_female  sex_male  smoker_no  smoker_yes  \
1244   18  33.33         0           0         1          1           0
192    25  25.74         0           0         1          1           0
1221   40  24.97         2           0         1          1           0
716    49  22.61         1           1         0          1           0
244    63  27.74         0           1         0          0           1

      region_northeast  region_northwest  region_southeast  region_southwest
1244                 0                 0                 1                 0
192                  0                 0                 1                 0
1221                 0                 0                 1                 0
716                  0                 1                 0                 0
244                  1                 0                 0                 0
```

Before modelling the data, we need to do scale all the features to get accurate results. This is to avoid biasing towards features with large range of values.

In [38]:
```
# standardization or z-score normalization
```

```
from sklearn.preprocessing import StandardScaler

scaler = StandardScaler()
x_train_norm = scaler.fit_transform(x_train) # Returns a numpy array and not

print(f"Age min and max before normalization: {x_train['age'].min(), x_train[
print(f"Age min and max after normalization: {x_train_norm[:,0].min(), x_trai

# similarly for validation and test dataset
x_val_norm = scaler.fit_transform(x_val)
x_test_norm = scaler.fit_transform(x_test)
```

```
Age min and max before normalization: (18, 64)
Age min and max after normalization: (-1.5137167128294682, 1.7729666471672798)
```

ML modelling

Linear Regression

Let's try to do a multivariate regression modelling for the data. For this we we will use a multivariate linear model

The model's prediction with multiple variables is given by the linear model:

$$f_{\mathbf{w},b}(\mathbf{x}) = w_0x_0 + w_1x_1 + \ldots + w_{n-1}x_{n-1} + b \tag{1}$$

or in vector notation:

$$f_{\mathbf{w},b}(\mathbf{x}) = \mathbf{w} \cdot \mathbf{x} + b \tag{2}$$

where $\cdot$ is a vector `dot product`

where

$$x_0, x_1 \ldots \ldots, x_n$$

are feature vectors and

$$w_0, \ldots \ldots w_b, b$$

are weight and bias parameters.

In order to conduct multivariate modelling, we use the SGDRegressor module from the scikit learn.

In [39]:
```
# Let's use the stochastic gradient descent regressor from Scikit Learn

from sklearn.linear_model import SGDRegressor

sgdr = SGDRegressor(max_iter=1000, alpha = 0.001) # setting the maximum itera
#sgdr = LinearRegression()
sgdr.fit(x_train_norm, y_train)
print(sgdr)
print(f"number of iterations completed: {sgdr.n_iter_}, number of weight upda
    print(f"number of iterations completed: {sgdr.n_iter_}, number of weight upda
```

```
SGDRegressor(alpha=0.001)
number of iterations completed: 14, number of weight updates: 11229.0
```

In [40]:
```
b_norm = sgdr.intercept_
w_norm = sgdr.coef_
print(f"model parameters:                    w: {w_norm}, b:{b_norm}")
```

```
model parameters:                    w: [ 3564.73276528  1982.39328734   518.867
58396    32.14937893
   -32.14937893 -4591.63677471  4591.63677471   292.33855625
   -60.40237412  -150.52103001   -70.14917312], b:[13036.88056322]
```

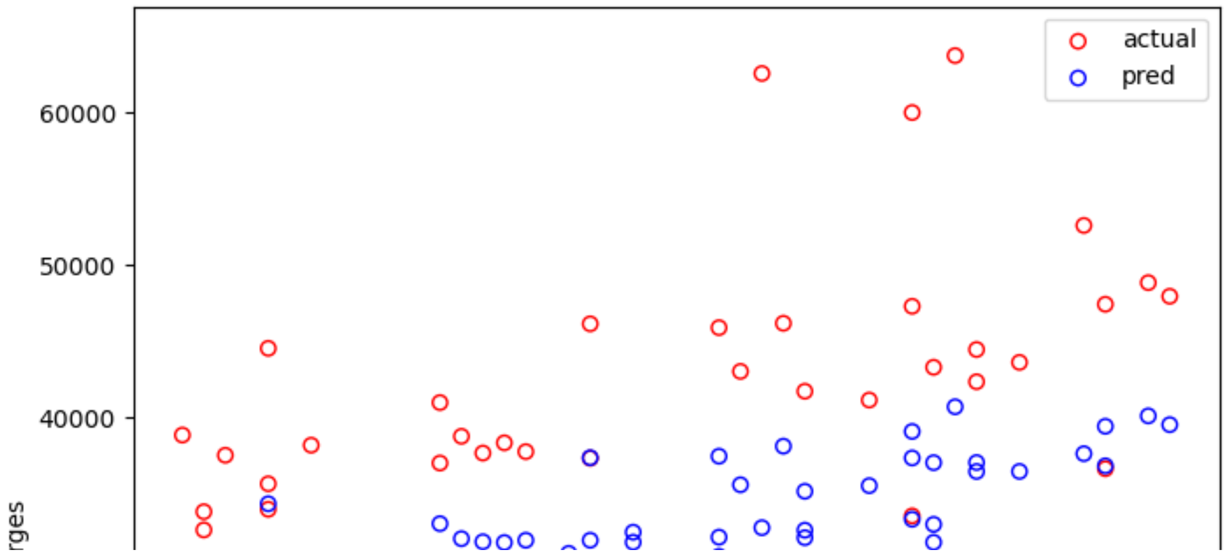
Now let's predict the results on training dataset using this model we developed and how it deviates from the actual insurance charges:

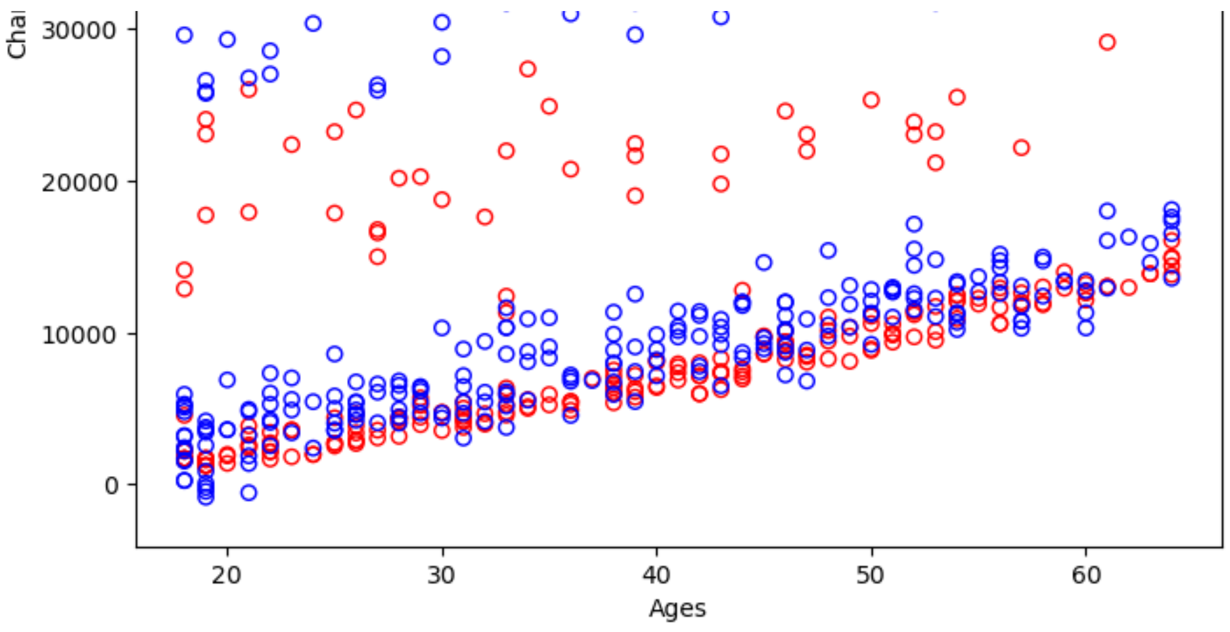
In [41]:
```
ypred_train_lsgd = sgdr.predict(x_train_norm) # predicted charges for train
ypred_val_lsgd = sgdr.predict(x_val_norm) # predicted charges for validation
ypred_test_lsgd = sgdr.predict(x_test_norm) # predicted charges for test

# calculated value using equation 2
y_calc_train = np.dot(x_train_norm, w_norm) + b_norm
```

Results from sgdr.predict and np.dot are the same. But some of these predicted insurance charges are negative which is indication of a poor model.

Now let's plot the actual charges and predicted charges for the test data to understand how good the model is.

In [42]:
```
fig = plt.figure(figsize = (8,8))
plt.scatter(x_test['age'], y_test, label = 'actual', edgecolors = 'red', face
plt.scatter(x_test['age'], ypred_test_lsgd, label = 'pred', edgecolors = 'blu
plt.xlabel('Ages')
plt.ylabel("Charges")
#plt.ylim(0,10000)
plt.legend()
plt.show()
```





It looks like the model is high bias/underfit as the predicted values are very different from the actual training set values. Let's calculate the root mean square error and R-squared values.

The root mean squared error (RMSE) basically calculates the square root of the mean of the squared residuals of samples. Also, we can calculate the R^2 value or coefficient of determination which would basically explain how much percentage of variance in the dependent (target variable) is explained by the independent variables (features).

The coefficient of determination (R2) = 1 - (SSR/TSR) where SSR = sum of squares of residuals and TSS = total sum of squares. An R2 value of 1 indicates good prediction and 0 indicated a poor model (Y independent of X).

In [43]:

```
from sklearn.metrics import mean_squared_error

#metrics for train data
rmse_lsgd_train = np.sqrt(mean_squared_error(y_train, ypred_train_lsgd))
R2_lsgd_train = sgdr.score(x_train_norm, y_train)

# metrics for validation data
rmse_lsgd_val = np.sqrt(mean_squared_error(y_val, ypred_val_lsgd))
R2_lsgd_val = sgdr.score(x_val_norm, y_val)

# metrics for test data
rmse_lsgd_test = np.sqrt(mean_squared_error(y_test, ypred_test_lsgd))
R2_lsgd_test = sgdr.score(x_test_norm, y_test)

print("Training:")
print(f" The root mean squared error: {rmse_lsgd_train}")
print(f" R2 value: {R2_lsgd_train}")

print("Validataion:")
print(f" The root mean squared error: {rmse_lsgd_val}")
print(f" R2 value: {R2_lsgd_val}")

print("Testing:")
print(f" The root mean squared error: {rmse_lsgd_test}")
print(f" R2 value: {R2_lsgd_test}")
```

```
Training:
 The root mean squared error: 5947.812971301977
 R2 value: 0.7357312239781457
Validataion:
 The root mean squared error: 5471.111517005788
 R2 value: 0.8110660195811252
Testing:
 The root mean squared error: 6838.290219396225
 R2 value: 0.7285834903187071
```

The results from the simple regression model are not bad. RMSE and R2 values of test and validation datasets looks reasonable compared to the training scores.

In some training examples, the the model does a good job. Let's try to add some polynomial features to see if the model does a better job. Let's make some more complex model.

Mulitvariate polyonomial regression

In [44]:

```
# Let's add some polynomial features
from sklearn.preprocessing import PolynomialFeatures

poly = PolynomialFeatures(degree = 3, include_bias=False) # using degree 3 po
x_train_mapped = poly.fit_transform(x_train)
x_train_mapped_norm = scaler.fit_transform(x_train_mapped)

x_val_mapped = poly.fit_transform(x_val)
x_val_mapped_norm = scaler.fit_transform(x_val_mapped)

x_test_mapped = poly.fit_transform(x_test)
x_test_mapped_norm = scaler.fit_transform(x_test_mapped)

print(x_train_mapped_norm.shape)
```

```
(802, 363)
```

We have 363 features instead of 11 features. Let's see how the model performs.

In [45]:

```
sgdr_poly = SGDRegressor(max_iter=1000, alpha = 0.1) # setting the maximum it
sgdr_poly.fit(x_train_mapped_norm, y_train)
print(sgdr_poly)
print(f"number of iterations completed: {sgdr_poly.n_iter_}, number of weight

# Fitted parameters
b_norm_poly = sgdr_poly.intercept_
w_norm_poly = sgdr_poly.coef_
#print(f"model parameters:   w: {w_norm_poly}, b:{b_norm_poly}")

# predicted charges
ypred_train_psgd = sgdr_poly.predict(x_train_mapped_norm) # predicted charges
ypred_val_psgd = sgdr_poly.predict(x_val_mapped_norm)
ypred_test_psgd = sgdr_poly.predict(x_test_mapped_norm)
```

```
SGDRegressor(alpha=0.1)
```

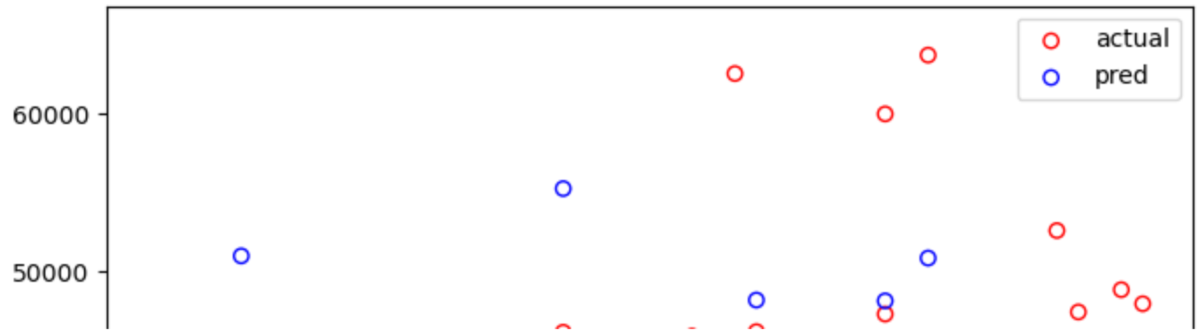
```
number of iterations completed: 23, number of weight updates: 18447.0
```

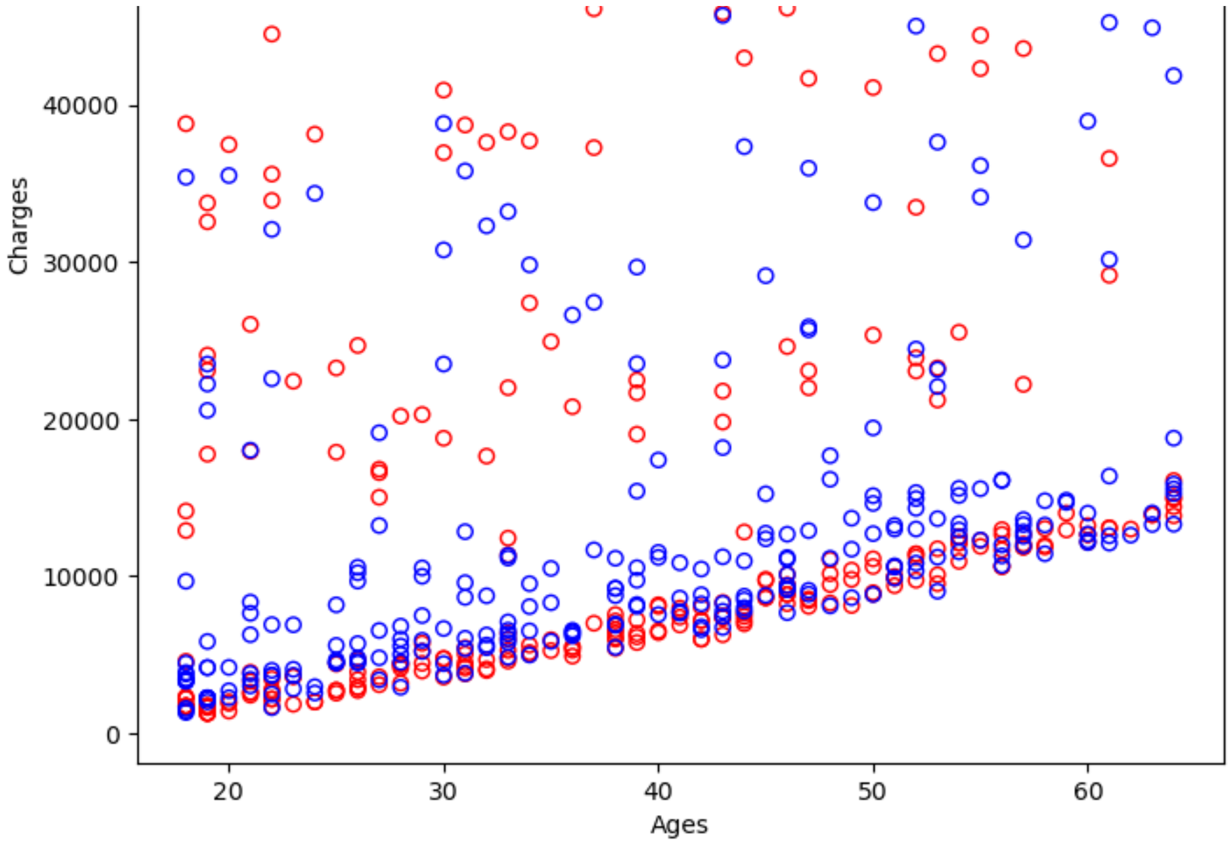
In [46]:
```
#metrics for train data
rmse_psgd_train = np.sqrt(mean_squared_error(y_train, ypred_train_psgd))
R2_psgd_train = sgdr_poly.score(x_train_mapped_norm, y_train)

# metrics for validation data
rmse_psgd_val = np.sqrt(mean_squared_error(y_val, ypred_val_psgd))
R2_psgd_val = sgdr_poly.score(x_val_mapped_norm, y_val)

# metrics for test data
rmse_psgd_test = np.sqrt(mean_squared_error(y_test, ypred_test_psgd))
R2_psgd_test = sgdr_poly.score(x_test_mapped_norm, y_test)

print("Training:")
print(f" The root mean squared error: {rmse_psgd_train}")
print(f" R2 value: {R2_psgd_train}")

print("Validataion:")
print(f" The root mean squared error: {rmse_psgd_val}")
print(f" R2 value: {R2_psgd_val}")

print("Testing:")
print(f" The root mean squared error: {rmse_psgd_test}")
print(f" R2 value: {R2_psgd_test}")
```

```
Training:
 The root mean squared error: 4812.5796483243585
 R2 value: 0.8269836657774282
Validataion:
 The root mean squared error: 4804.833027288717
 R2 value: 0.8542812153470754
Testing:
 The root mean squared error: 5997.253251013402
 R2 value: 0.7912406281123071
```

The RMSE and R2 values from the train, validation and test data using the polynomial model looks better than the corresponding values from the simple linear regression model.

In [47]:
```
fig = plt.figure(figsize = (8,8))
plt.scatter(x_test['age'], y_test, label = 'actual', edgecolors = 'red', face
plt.scatter(x_test['age'], ypred_test_psgd, label = 'pred', edgecolors = 'blu
plt.xlabel('Ages')
plt.ylabel("Charges")
#plt.ylim(0,10000)
plt.legend()
plt.show()
```





The polynomial model does a better job in the estimation of insurance charges compared to the linear model. The actual values and prediction values are close to each other for the test data even though they are not overlying. Even though this is a good model, it still require some more development to do a better job on the prediction.

Support Vector Regression (SVR)

Here we will use the widely use the SVR model for the insurance prediction. In the case of support vector regression, the model basically tries to fit a hyperplane to fit the data. Ideally we want all the data points inside a eta-insensitive tube surround the hyperplane with a radius eta. Or basically tries to find a function outputing values not deviating more than 'eta' from the actual values. The errors of points inside the tube will be disregarded and points outside the tube will be penalized in this process. The points outside the tube are called support vectors in this case.

One advantages of SVR, is that it can handle non-linear data pretty well. This is because SVR allows to fit a hyperpane in the higher dimensional feature space (through kernel trick) using the base features. Let's try the SVR for our prediction case now.

Here C is the regularization paramter (scales as 1/lamda). Higher the C, lower the reqularization and vice versa. Epsilon specifies the epsilon-tube radius within which no penalty is associated in the training loss function with points predicted within a distance epsilon from the actual value.

In [48]:
```
from sklearn.svm import SVR
```

```python
# Initiating the SVR
svr = SVR(kernel='linear', C=100, epsilon=0.1)

#fitting the data
svr.fit(x_train_norm, y_train)
```

Out[48]:
```
SVR(C=100, kernel='linear')
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.
On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.

In [49]:
```python
# predicted charges
ypred_train_svr = svr.predict(x_train_norm) # predicted charges from the mode
ypred_val_svr = svr.predict(x_val_norm)
ypred_test_svr = svr.predict(x_test_norm)

#metrics for train data
rmse_svr_train = np.sqrt(mean_squared_error(y_train, ypred_train_svr))
R2_svr_train = svr.score(x_train_norm, y_train)

# metrics for validation data
rmse_svr_val = np.sqrt(mean_squared_error(y_val, ypred_val_svr))
R2_svr_val = svr.score(x_val_norm, y_val)

# metrics for test data
rmse_svr_test = np.sqrt(mean_squared_error(y_test, ypred_test_svr))
R2_svr_test = svr.score(x_test_norm, y_test)

print("Training:")
print(f" The root mean squared error: {rmse_svr_train}")
print(f" R2 value: {R2_svr_train}")

print("Validataion:")
print(f" The root mean squared error: {rmse_svr_val}")
print(f" R2 value: {R2_svr_val}")

print("Testing:")
print(f" The root mean squared error: {rmse_svr_test}")
print(f" R2 value: {R2_svr_test}")
```

```
Training:
 The root mean squared error: 7244.46915483861
 R2 value: 0.6079473613581137
Validataion:
 The root mean squared error: 7585.297876628681
 R2 value: 0.6368348042660665
Testing:
 The root mean squared error: 8743.19774423167
 R2 value: 0.5563077875142073
```

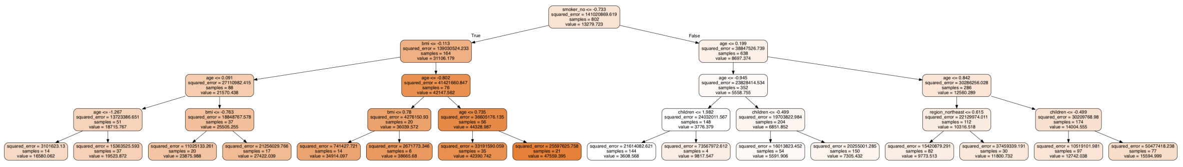
The RMSE and R2 score for testing is lesser for SVR compared to polynomial regression. Upon trying linear kernel, polynomial filter kernels with degrees upto 4, radial basis function kernel and sigmoid kernel, the linear kernel seems to be producing the best RMSE and R2 score.

Decision Tree (DT) Regressor

Now let's try a DT regressor for this problem. In the case of DT, the splitting of feature will be using thresholds which will maximize the reduction of the variance. i.e., the difference (variance of root node - (left fraction * variance of left split + right fraction * variance of right split). The "squared_error" for the mean squared error, which is equal to variance reduction as feature selection criterion and minimizes the L2 loss using the mean of each terminal node

In [61]:
```python
from sklearn.tree import DecisionTreeRegressor,export_graphviz

# DT regressor
dt = DecisionTreeRegressor(criterion='squared_error', max_depth=5, random_sta
dt.fit(x_train_norm, y_train)

# tree visualization
# Getting a list of the feature names
feat_names = list(x_train.columns)

# using export_graphviz() for writing down the tree into a dot format
export_graphviz(
            dt,
out_file="dt.dot",
feature_names=feat_names,
rounded=True,
filled=True,
impurity=True
)
```

Let's take a look at the DT from fitting on the training data.



Now let's test the RMSE and R2 scores on all the datasets.

In [62]:
```python
# predicted charges
ypred_train_dt = dt.predict(x_train_norm) # predicted charges from the model
ypred_val_dt = dt.predict(x_val_norm)
ypred_test_dt = dt.predict(x_test_norm)

#metrics for train data
rmse_dt_train = np.sqrt(mean_squared_error(y_train, ypred_train_dt))
R2_dt_train = dt.score(x_train_norm, y_train)

# metrics for validation data
rmse_dt_val = np.sqrt(mean_squared_error(y_val, ypred_val_dt))
R2_dt_val = dt.score(x_val_norm, y_val)

# metrics for test data
rmse_dt_test = np.sqrt(mean_squared_error(y_test, ypred_test_dt))
R2_dt_test = dt.score(x_test_norm, y_test)

print("Training:")
print(f" The root mean squared error: {rmse_dt_train}")
print(f" R2 value: {R2_dt_train}")

print("Validation:")
print(f" The root mean squared error: {rmse_dt_val}")
print(f" R2 value: {R2_dt_val}")

print("Testing:")
print(f" The root mean squared error: {rmse_dt_test}")
print(f" R2 value: {R2_dt_test}")
```

```
Training:
 The root mean squared error: 4044.6917764087475
 R2 value: 0.8777913040477071
Validation:
 The root mean squared error: 3894.0439367489207
 R2 value: 0.9042892686106055
Testing:
 The root mean squared error: 5805.334129405968
 R2 value: 0.8043879312342002
```

The metrics of have improved for the DT regression compared to polynomial regression. Before we move on, let's try the DT on the feature engineered dataset with polynomial features as well.

In [70]:

```
# DT regressor for feature engineered dataset
dtp = DecisionTreeRegressor(criterion='squared_error', max_depth=5, random_st
dtp.fit(x_train_mapped_norm, y_train)


# predicted charges
ypred_train_dtp = dtp.predict(x_train_mapped_norm) # predicted charges from t
ypred_val_dtp = dtp.predict(x_val_mapped_norm)
ypred_test_dtp = dtp.predict(x_test_mapped_norm)

#metrics for train data
rmse_dtp_train = np.sqrt(mean_squared_error(y_train, ypred_train_dtp))
R2_dtp_train = dtp.score(x_train_mapped_norm, y_train)

# metrics for validation data
rmse_dtp_val = np.sqrt(mean_squared_error(y_val, ypred_val_dtp))
R2_dtp_val = dtp.score(x_val_mapped_norm, y_val)

# metrics for test data
rmse_dtp_test = np.sqrt(mean_squared_error(y_test, ypred_test_dtp))
R2_dtp_test = dtp.score(x_test_mapped_norm, y_test)

print("Training:")
print(f" The root mean squared error: {rmse_dtp_train}")
print(f" R2 value: {R2_dtp_train}")

print("Validation:")
print(f" The root mean squared error: {rmse_dtp_val}")
print(f" R2 value: {R2_dtp_val}")

print("Testing:")
print(f" The root mean squared error: {rmse_dtp_test}")
print(f" R2 value: {R2_dtp_test}")
```

```
Training:
 The root mean squared error: 3900.0759304604458
 R2 value: 0.8863740909908884
Validation:
 The root mean squared error: 5103.833499237489
 R2 value: 0.8355810250243827
Testing:
 The root mean squared error: 6818.903642370411
 R2 value: 0.7301202424128873
```

DT seems to be giving good results on the original dataset rather than the feature engineered dataset with polynomial features.

Random Forest (RF) Regression

The RF regression will use an ensemble of trees rather than a single DT. During the feature split, rather than using all the features, RF will use a subset of features and select the best feature among the subset for splitting the samples. Let's see how random forest performs for this regression task.

In [63]:
```
from sklearn.ensemble import RandomForestRegressor

rf = RandomForestRegressor(n_estimators=128, criterion='squared_error', max_d
rf.fit(x_train_norm, y_train)
```

Out[63]:
```
RandomForestRegressor(max_depth=5, max_features='sqrt', max_samples=50
0,
                      n_estimators=128)
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.
On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.

In [64]:
```
# predicted charges
ypred_train_rf = rf.predict(x_train_norm) # predicted charges from the model
ypred_val_rf = rf.predict(x_val_norm)
ypred_test_rf = rf.predict(x_test_norm)

#metrics for train data
rmse_rf_train = np.sqrt(mean_squared_error(y_train, ypred_train_rf))
R2_rf_train = rf.score(x_train_norm, y_train)

# metrics for validation data
rmse_rf_val = np.sqrt(mean_squared_error(y_val, ypred_val_rf))
R2_rf_val = rf.score(x_val_norm, y_val)

# metrics for test data
rmse_rf_test = np.sqrt(mean_squared_error(y_test, ypred_test_rf))
R2_rf_test = rf.score(x_test_norm, y_test)

print("Training:")
print(f" The root mean squared error: {rmse_rf_train}")
print(f" R2 value: {R2_rf_train}")
print("Validation:")
print(f" The root mean squared error: {rmse_rf_val}")
print(f" R2 value: {R2_rf_val}")

print("Testing:")
print(f" The root mean squared error: {rmse_rf_test}")
print(f" R2 value: {R2_rf_test}")
```

```
Training:
 The root mean squared error: 4435.535582038425
 R2 value: 0.8530317980587319
Validation:
 The root mean squared error: 4585.050371068288
 R2 value: 0.8673072598427082
Testing:
 The root mean squared error: 6120.891360705613
 R2 value: 0.7825444246601169
```

The RF, R2 and RMSE has gone down below the metrics from the single DT. Let's try the random forest on the dataset feature engineered with polynomial features. This is interesting.

In [65]:
```
# random forest trained with feature engineered polyonomial features
rfp = RandomForestRegressor(n_estimators=128, criterion='squared_error', max_
rfp.fit(x_train_mapped_norm, y_train)
```

Out[65]:
```
RandomForestRegressor(max_depth=5, max_features='sqrt', max_samples=50
0,
                      n_estimators=128)
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.
On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.

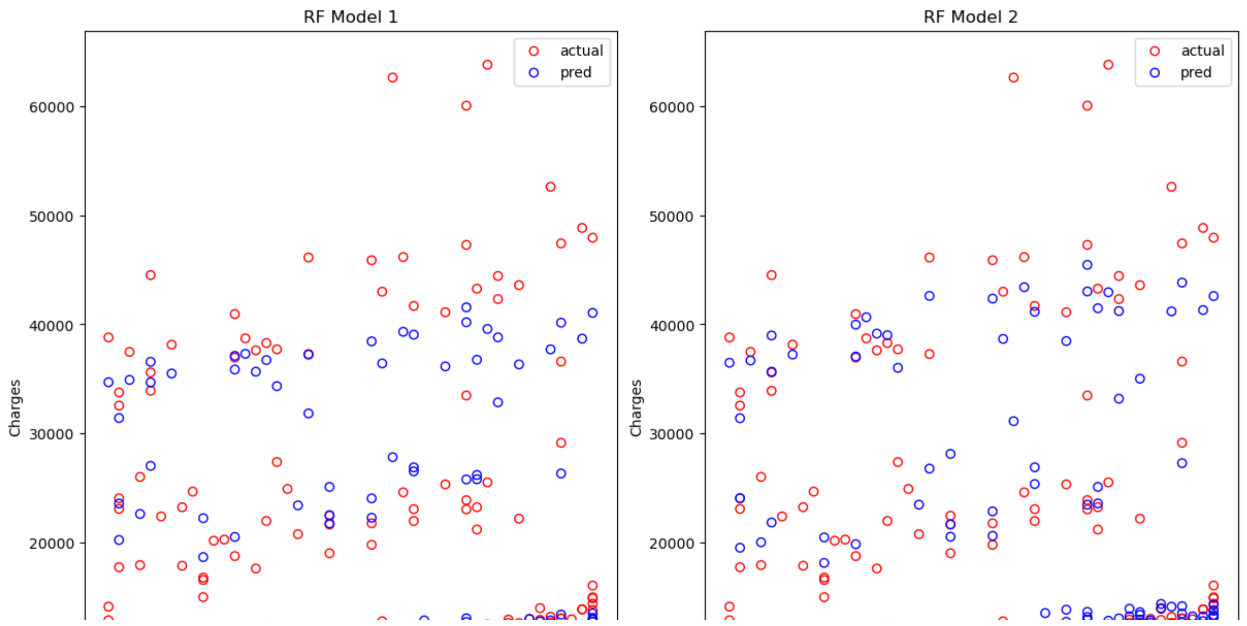
In [66]:
```
# predicted charges
ypred_train_rfp = rfp.predict(x_train_mapped_norm) # predicted charges from t
ypred_val_rfp = rfp.predict(x_val_mapped_norm)
ypred_test_rfp = rfp.predict(x_test_mapped_norm)

#metrics for train data
rmse_rfp_train = np.sqrt(mean_squared_error(y_train, ypred_train_rfp))
R2_rfp_train = rfp.score(x_train_mapped_norm, y_train)

# metrics for validation data
rmse_rfp_val = np.sqrt(mean_squared_error(y_val, ypred_val_rfp))
R2_rfp_val = rfp.score(x_val_mapped_norm, y_val)

# metrics for test data
rmse_rfp_test = np.sqrt(mean_squared_error(y_test, ypred_test_rfp))
R2_rfp_test = rfp.score(x_test_mapped_norm, y_test)

print("Training:")
print(f" The root mean squared error: {rmse_rf_train}")
print(f" R2 value: {R2_rfp_train}")

print("Validation:")
print(f" The root mean squared error: {rmse_rf_val}")
print(f" R2 value: {R2_rfp_val}")

print("Testing:")
print(f" The root mean squared error: {rmse_rf_test}")
print(f" R2 value: {R2_rfp_test}")
```

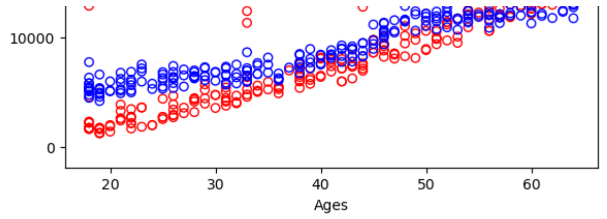
```
Training:
 The root mean squared error: 4435.535582038425
 R2 value: 0.8831464862006457
Validation:
 The root mean squared error: 4585.050371068288
 R2 value: 0.8927852086459744
Testing:
 The root mean squared error: 6120.891360705613
 R2 value: 0.8035219129450712
```

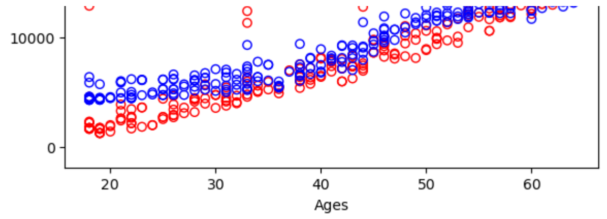
The metrics on RF model trained on data with polynomial features are slightly better than the original data. However, the differences are not remarkable. The results are more similar to the DT model. Now let's see the how the plots of insurance charges wrt age looks now with second RF model.

In [67]:

```
fig, axs = plt.subplots(1,2, figsize = (12,8), constrained_layout=True)
axs[0].scatter(x_test['age'], y_test, label = 'actual', edgecolors = 'red', f
axs[0].scatter(x_test['age'], ypred_test_rf, label = 'pred', edgecolors = 'bl
axs[0].set_xlabel('Ages')
axs[0].set_ylabel("Charges")
axs[0].set_title("RF Model 1")
#plt.ylim(0,10000)
axs[0].legend()

axs[1].scatter(x_test['age'], y_test, label = 'actual', edgecolors = 'red', f
axs[1].scatter(x_test['age'], ypred_test_rfp, label = 'pred', edgecolors = 'b
axs[1].set_xlabel('Ages')
axs[1].set_ylabel("Charges")
axs[1].set_title("RF Model 2")
#plt.ylim(0,10000)
axs[1].legend()
plt.show()
```







In both of these models, even though the predictions becomes closer for the scattered points at the top, the blue and red points kind diverge for the lowest insurance charges below 10000. At the same time, polynomial models do a a better job in predicting insurance cost below 10000.

XGBoost Regression

Let's try the XGBoost regression which is a powerful and efficient implementation of gradient boosting for regression and classification tasks. As the name sounds, this is an extreme version of the gradient boosting, with with advanced engineering techniques to enhance performance and efficiency. The idea is to use several weak learners to form a strong learner. Each tree learns from the mistakes of the previous tree in a sequential manner. The algorithm starts with an initial prediction, then boosted trees will fit on the residuals(mistake of the previous tree) and this process goes on untill the maximum number of trees are reached or residuals becomes smaller than the threshold. The total prediction would be sum of initial prediciton and scaled contribution from rest of the trees.

Advantages of xgboost over a normal gradient boost includes

1. Fast and efficient implemnetaion: Parallel tree construction, Out-of-core computation to handle large datasets, Cache awareness (optimized data structures)
2. Regularization to prevent overfitting and generalization
3. Tree Pruning: Rather than pre-pruning with a fixed depth, it grows the complete tree and prune branches backwards (from the leaves) which don't improve performance.
4. Handles missing data
5. Uses first and second order gradient descent for accurate optimization.
6. weighted quantile sketch to better split the data, handle sparse data, Inbuilt cross validatation and better hyperparameter tuning.

We will utilize the xgboost library for this purpose and see how it performs. Since the RF performs better on the feature engineered dataset, let's use the same for the xgboost regression as well.

In [68]:
```
from xgboost import XGBRegressor

# learning rate = scaled contribution of residuals from each tree.
xgb = XGBRegressor(n_estimators=128, max_depth=4, objective='reg:squarederror
xgb.fit(x_train_mapped_norm, y_train)
```

Out[68]:
```
XGBRegressor(base_score=None, booster=None, callbacks=None,
             colsample_bylevel=None, colsample_bynode=None,
             colsample_bytree=None, device=None, early_stopping_rounds
```

```
                 colsample_bytree=None, device=None, early_stopping_rounds
=None,
                 enable_categorical=False,
                 eval_metric=<function mean_squared_error at 0x7fa158fc455
0>,
                 feature_types=None, gamma=None, grow_policy=None,
                 importance_type=None, interaction_constraints=None,
                 learning_rate=0.1, max_bin=None, max_cat_threshold=None,
                 max_cat_to_onehot=None, max_delta_step=None, max_depth=4,
                 max_leaves=None, min_child_weight=None, missing=nan,
                 monotone_constraints=None, multi_strategy=None, n_estimat
ors=128,
                 n_jobs=None, num_parallel_tree=None, random_state=None, .
..)
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.
On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.

In [69]:

```
# predicted charges
ypred_train_xgb = xgb.predict(x_train_mapped_norm) # predicted charges from t
ypred_val_xgb = xgb.predict(x_val_mapped_norm)
ypred_test_xgb = xgb.predict(x_test_mapped_norm)

#metrics for train data
rmse_xgb_train = np.sqrt(mean_squared_error(y_train, ypred_train_xgb))
R2_xgb_train = xgb.score(x_train_mapped_norm, y_train)

# metrics for validation data
rmse_xgb_val = np.sqrt(mean_squared_error(y_val, ypred_val_xgb))
R2_xgb_val = xgb.score(x_val_mapped_norm, y_val)

# metrics for test data
rmse_xgb_test = np.sqrt(mean_squared_error(y_test, ypred_test_xgb))
R2_xgb_test = xgb.score(x_test_mapped_norm, y_test)

print("Training:")
print(f" The root mean squared error: {rmse_xgb_train}")
print(f" R2 value: {R2_xgb_train}")

print("Validation:")
print(f" The root mean squared error: {rmse_xgb_val}")
print(f" R2 value: {R2_xgb_val}")

print("Testing:")
print(f" The root mean squared error: {rmse_xgb_test}")
print(f" R2 value: {R2_xgb_test}")
```

```
Training:
 The root mean squared error: 2294.4813798082478
 R2 value: 0.9606721394596172
Validation:
 The root mean squared error: 7137.46924116155
 R2 value: 0.6784507954584006
Testing:
 The root mean squared error: 8187.727768694638
 R2 value: 0.6108939410888659
```

Even though the xgboost model is doing pretty well for the training and validation, it does not perform well compared to the random forest model. Many times, the RF model seems to perform well on smaller datasets compared to Xgboost. Similiarly xgboost have been observed to perform well in larger datasets with intricate relationships.

Dense Neural Networks

Let's try a DNN model as well to see if it can perform better than the RF model.

In [103…

```
# load the tensorflow libraries
import tensorflow as tf
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense, Flatten, Input

print(x_train_norm.shape[1:])

# Let's build the model
tf.random.set_seed(42) # Set the random seed to get same reproducable results
dnn = Sequential([
        Input(shape = x_train_mapped_norm.shape[1:]),
        Dense(50, activation="relu", name = 'layer1'),
        Dense(25, activation="relu", name = 'layer2'),
        Dense(15, activation="relu", name = 'layer3'),
        Dense(5, activation="relu", name = 'layer4'),
        Dense(1, activation="linear", name = 'output')
])
dnn.summary()
```

```
(11,)
Model: "sequential_7"
_________________________________________________________________
 Layer (type)                Output Shape              Param #   
=================================================================
 layer1 (Dense)              (None, 50)                18200     
                                                                 
 layer2 (Dense)              (None, 25)                1275      
                                                                 
 layer3 (Dense)              (None, 15)                390       
                                                                 
 layer4 (Dense)              (None, 5)                 80        
                                                                 
 output (Dense)              (None, 1)                 6         
                                                                 
=================================================================
Total params: 19,951
Trainable params: 19,951
Non-trainable params: 0
_________________________________________________________________
```

In [104…

```
dnn.compile(optimizer = tf.keras.optimizers.Adam(learning_rate = 1e-3), loss
               metrics = ["mse"]) # setting the mean square error(mse) for lo
dnn.fit(x_train_mapped_norm, y_train, batch_size=32, epochs=40, validation_da
```

```
Epoch 1/40
26/26 [==============================] - 0s 4ms/step - loss: 304166624.0000 - m
se: 304166624.0000 - val_loss: 339795872.0000 - val_mse: 339795872.0000
```

```
Epoch 2/40
26/26 [==============================] - 0s 2ms/step - loss: 304108032.0000 - m
se: 304108032.0000 - val_loss: 339663296.0000 - val_mse: 339663296.0000
Epoch 3/40
26/26 [==============================] - 0s 2ms/step - loss: 303804576.0000 - m
se: 303804576.0000 - val_loss: 338986656.0000 - val_mse: 338986656.0000
Epoch 4/40
26/26 [==============================] - 0s 1ms/step - loss: 302377376.0000 - m
se: 302377376.0000 - val_loss: 335735136.0000 - val_mse: 335735136.0000
Epoch 5/40
26/26 [==============================] - 0s 2ms/step - loss: 296115776.0000 - m
se: 296115776.0000 - val_loss: 323497536.0000 - val_mse: 323497536.0000
Epoch 6/40
26/26 [==============================] - 0s 1ms/step - loss: 275985920.0000 - m
se: 275985920.0000 - val_loss: 288592928.0000 - val_mse: 288592928.0000
Epoch 7/40
26/26 [==============================] - 0s 1ms/step - loss: 227068832.0000 - m
se: 227068832.0000 - val_loss: 216471680.0000 - val_mse: 216471680.0000
Epoch 8/40
26/26 [==============================] - 0s 1ms/step - loss: 146663088.0000 - m
se: 146663088.0000 - val_loss: 115078824.0000 - val_mse: 115078824.0000
Epoch 9/40
26/26 [==============================] - 0s 1ms/step - loss: 65791540.0000 - ms
e: 65791540.0000 - val_loss: 46931464.0000 - val_mse: 46931464.0000
Epoch 10/40
26/26 [==============================] - 0s 1ms/step - loss: 40833304.0000 - ms
e: 40833304.0000 - val_loss: 35473800.0000 - val_mse: 35473800.0000
Epoch 11/40
26/26 [==============================] - 0s 1ms/step - loss: 36784272.0000 - ms
e: 36784272.0000 - val_loss: 34670228.0000 - val_mse: 34670228.0000
Epoch 12/40
26/26 [==============================] - 0s 1ms/step - loss: 34560816.0000 - ms
e: 34560816.0000 - val_loss: 32676624.0000 - val_mse: 32676624.0000
Epoch 13/40
26/26 [==============================] - 0s 1ms/step - loss: 33391202.0000 - ms
e: 33391202.0000 - val_loss: 32719256.0000 - val_mse: 32719256.0000
Epoch 14/40
26/26 [==============================] - 0s 1ms/step - loss: 32348430.0000 - ms
e: 32348430.0000 - val_loss: 30445476.0000 - val_mse: 30445476.0000
Epoch 15/40
26/26 [==============================] - 0s 1ms/step - loss: 31498838.0000 - ms
e: 31498838.0000 - val_loss: 29564076.0000 - val_mse: 29564076.0000
Epoch 16/40
26/26 [==============================] - 0s 1ms/step - loss: 30913096.0000 - ms
e: 30913096.0000 - val_loss: 28875498.0000 - val_mse: 28875498.0000
Epoch 17/40
26/26 [==============================] - 0s 1ms/step - loss: 30276332.0000 - ms
e: 30276332.0000 - val_loss: 28252606.0000 - val_mse: 28252606.0000
Epoch 18/40
26/26 [==============================] - 0s 1ms/step - loss: 29796978.0000 - ms
e: 29796978.0000 - val_loss: 28406770.0000 - val_mse: 28406770.0000
Epoch 19/40
26/26 [==============================] - 0s 1ms/step - loss: 29404360.0000 - ms
e: 29404360.0000 - val_loss: 27747448.0000 - val_mse: 27747448.0000
Epoch 20/40
26/26 [==============================] - 0s 2ms/step - loss: 29158324.0000 - ms
e: 29158324.0000 - val_loss: 28383544.0000 - val_mse: 28383544.0000
Epoch 21/40
26/26 [==============================] - 0s 1ms/step - loss: 28665254.0000 - ms
e: 28665254.0000 - val_loss: 27262354.0000 - val_mse: 27262354.0000
Epoch 22/40
26/26 [==============================] - 0s 1ms/step - loss: 28296646.0000 - ms
```

```
26/26 [==============================] - 0s 1ms/step - loss: 28296646.0000 - ms
e: 28296646.0000 - val_loss: 27034888.0000 - val_mse: 27034888.0000
Epoch 23/40
26/26 [==============================] - 0s 1ms/step - loss: 28023196.0000 - ms
e: 28023196.0000 - val_loss: 27519536.0000 - val_mse: 27519536.0000
Epoch 24/40
26/26 [==============================] - 0s 1ms/step - loss: 27798002.0000 - ms
e: 27798002.0000 - val_loss: 27064538.0000 - val_mse: 27064538.0000
Epoch 25/40
26/26 [==============================] - 0s 1ms/step - loss: 27431256.0000 - ms
e: 27431256.0000 - val_loss: 25740038.0000 - val_mse: 25740038.0000
Epoch 26/40
26/26 [==============================] - 0s 1ms/step - loss: 27293638.0000 - ms
e: 27293638.0000 - val_loss: 25867656.0000 - val_mse: 25867656.0000
Epoch 27/40
26/26 [==============================] - 0s 1ms/step - loss: 27038608.0000 - ms
e: 27038608.0000 - val_loss: 25810278.0000 - val_mse: 25810278.0000
Epoch 28/40
26/26 [==============================] - 0s 1ms/step - loss: 27022400.0000 - ms
e: 27022400.0000 - val_loss: 24975326.0000 - val_mse: 24975326.0000
Epoch 29/40
26/26 [==============================] - 0s 1ms/step - loss: 26637770.0000 - ms
e: 26637770.0000 - val_loss: 25701732.0000 - val_mse: 25701732.0000
Epoch 30/40
26/26 [==============================] - 0s 1ms/step - loss: 26363076.0000 - ms
e: 26363076.0000 - val_loss: 25102908.0000 - val_mse: 25102908.0000
Epoch 31/40
26/26 [==============================] - 0s 1ms/step - loss: 26368556.0000 - ms
e: 26368556.0000 - val_loss: 25264996.0000 - val_mse: 25264996.0000
Epoch 32/40
26/26 [==============================] - 0s 1ms/step - loss: 26070116.0000 - ms
e: 26070116.0000 - val_loss: 25167252.0000 - val_mse: 25167252.0000
Epoch 33/40
26/26 [==============================] - 0s 1ms/step - loss: 25942912.0000 - ms
e: 25942912.0000 - val_loss: 24911514.0000 - val_mse: 24911514.0000
Epoch 34/40
26/26 [==============================] - 0s 1ms/step - loss: 25688020.0000 - ms
e: 25688020.0000 - val_loss: 24531636.0000 - val_mse: 24531636.0000
Epoch 35/40
26/26 [==============================] - 0s 1ms/step - loss: 25653042.0000 - ms
e: 25653042.0000 - val_loss: 24324834.0000 - val_mse: 24324834.0000
Epoch 36/40
26/26 [==============================] - 0s 1ms/step - loss: 25436724.0000 - ms
e: 25436724.0000 - val_loss: 24232622.0000 - val_mse: 24232622.0000
Epoch 37/40
26/26 [==============================] - 0s 1ms/step - loss: 25650104.0000 - ms
e: 25650104.0000 - val_loss: 24288452.0000 - val_mse: 24288452.0000
Epoch 38/40
26/26 [==============================] - 0s 1ms/step - loss: 25255602.0000 - ms
e: 25255602.0000 - val_loss: 24503816.0000 - val_mse: 24503816.0000
Epoch 39/40
26/26 [==============================] - 0s 1ms/step - loss: 25056802.0000 - ms
e: 25056802.0000 - val_loss: 24188002.0000 - val_mse: 24188002.0000
Epoch 40/40
26/26 [==============================] - 0s 1ms/step - loss: 25069964.0000 - ms
e: 25069964.0000 - val_loss: 24422162.0000 - val_mse: 24422162.0000
```

Out[104…

```
<keras.callbacks.History at 0x7fa18a7f12e0>
```

In [105…

```python
from sklearn.metrics import r2_score

# predicted charges
# predicted charges
ypred_train_dnn = dnn.predict(x_train_mapped_norm) # predicted charges from t
ypred_val_dnn = dnn.predict(x_val_mapped_norm)
ypred_test_dnn = dnn.predict(x_test_mapped_norm)

#metrics for train data
rmse_dnn_train = np.sqrt(mean_squared_error(y_train, ypred_train_dnn))
R2_dnn_train = r2_score(y_train, ypred_train_dnn)

# metrics for validation data
rmse_dnn_val = np.sqrt(mean_squared_error(y_val, ypred_val_dnn))
R2_dnn_val = r2_score(y_val, ypred_val_dnn)

# metrics for test data
rmse_dnn_test = np.sqrt(mean_squared_error(y_test, ypred_test_dnn))
R2_dnn_test = r2_score(y_test, ypred_test_dnn)

print("Training:")
print(f" The root mean squared error: {rmse_dnn_train}")
print(f" R2 value: {R2_dnn_train}")

print("Validation:")
print(f" The root mean squared error: {rmse_dnn_val}")
print(f" R2 value: {R2_dnn_val}")

print("Testing:")
print(f" The root mean squared error: {rmse_dnn_test}")
print(f" R2 value: {R2_dnn_test}")
```

```
26/26 [==============================] - 0s 496us/step
9/9 [==============================] - 0s 577us/step
9/9 [==============================] - 0s 600us/step
Training:
 The root mean squared error: 4970.888472908932
 R2 value: 0.8154137764570799
Validation:
 The root mean squared error: 4941.878078508421
 R2 value: 0.8458501900689064
Testing:
 The root mean squared error: 6073.668241133427
 R2 value: 0.7858868521798337
```

If we can put all our results on test dataset with original/ having polynomial features using different models.

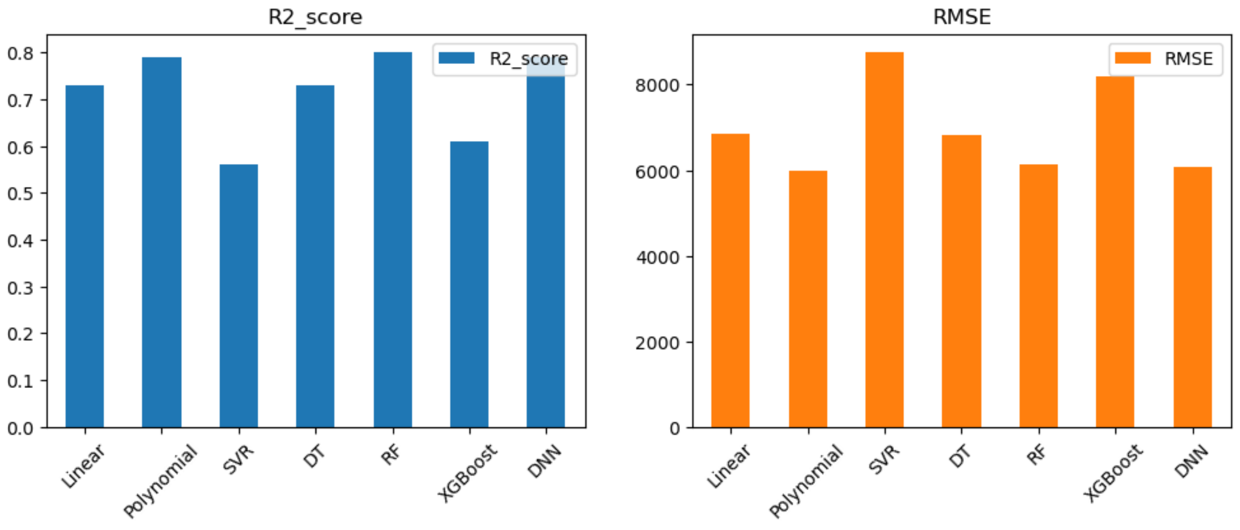
Model	R2 score	RMSE
Linear	0.73	6838.29
Polynomial	0.79	5997.25
SVR	0.56	8743.19
DT	0.73	6818.90
RF	0.80	6120.89
XGBoost	0.61	8187.72
DNN	0.79	6073.66

Below is a bar plot of the R2 score and RMSE of different models for better visualization

Below is a bar plot of the R2 score and RMSE of different models for better visualization.

In [130…
```
d = {'R2_score':[0.73, 0.79, 0.56, 0.73, 0.80, 0.61, 0.79],
     'RMSE': [6838.29, 5997.25, 8743.19, 6818.90, 6120.89, 8187.72, 6073.66]}
ind = ['Linear', 'Polynomial', 'SVR', 'DT', 'RF', 'XGBoost', 'DNN']
res = pd.DataFrame(d, index = ind)
res.plot.bar(rot=45, subplots=True, layout=(1,2), figsize=(12,4))
```

Out[130…
```
array([[<Axes: title={'center': 'R2_score'}>,
        <Axes: title={'center': 'RMSE'}>]], dtype=object)
```

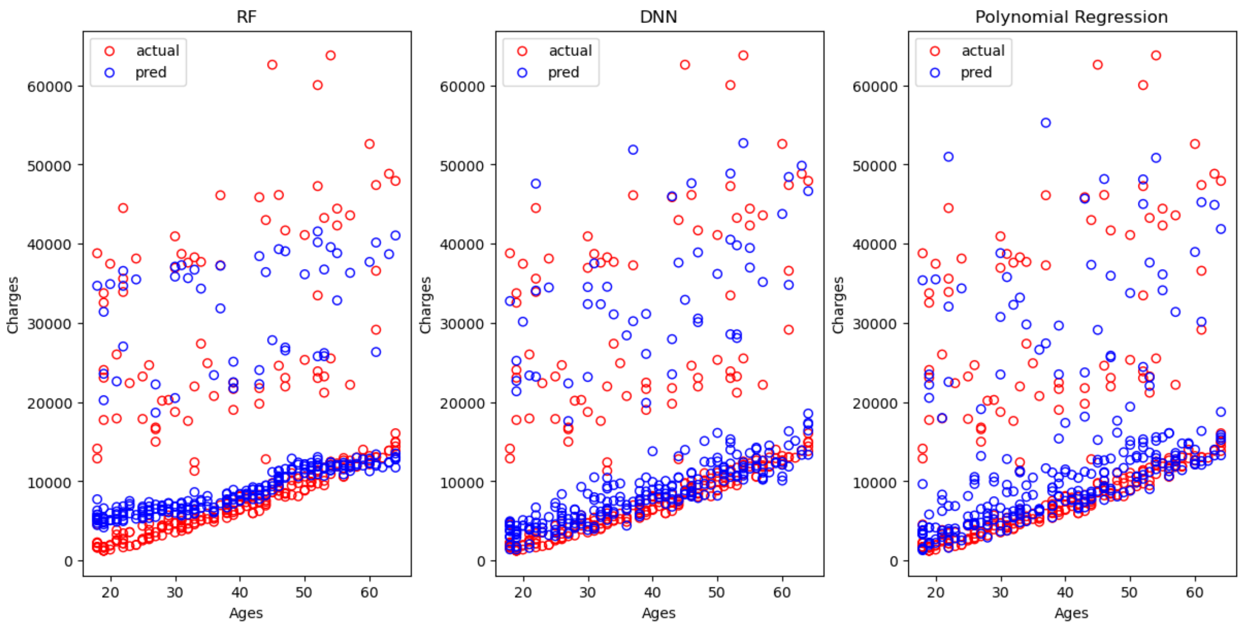


If we look at the above plot, performance of Polynomial, RF and DNN are very similar. At the same time, we can rule out the DT, Xgboost models. Also the SVR and linear regression models utilized the original data have lower metric scores as well.

Let's see how the prediction charges vs age looks like for the polynomial regression, RF and DNN models.

In [108…
```
fig, axs = plt.subplots(1,3, figsize = (12,6), constrained_layout=True)
axs[0].scatter(x_test['age'], y_test, label = 'actual', edgecolors = 'red', f
axs[0].scatter(x_test['age'], ypred_test_rf, label = 'pred', edgecolors = 'bl
axs[0].set_xlabel('Ages')
axs[0].set_ylabel("Charges")
axs[0].set_title("RF")
#plt.ylim(0,10000)
axs[0].legend()

axs[1].scatter(x_test['age'], y_test, label = 'actual', edgecolors = 'red', f
axs[1].scatter(x_test['age'], ypred_test_dnn, label = 'pred', edgecolors = 'b
axs[1].set_xlabel('Ages')
axs[1].set_ylabel("Charges")
axs[1].set_title("DNN")
#plt.ylim(0,10000)
axs[1].legend()

axs[2].scatter(x_test['age'], y_test, label = 'actual', edgecolors = 'red', f
axs[2].scatter(x_test['age'], ypred_test_psgd, label = 'pred', edgecolors = '
axs[2].set_xlabel('Ages')
axs[2].set_ylabel("Charges")
axs[2].set_title("Polynomial Regression")
#plt.ylim(0,10000)
```

```
axs[2].legend()
plt.show()
```



Conclusion

If we look at both the predictions of low and high insurance charges, DNN seems to doing the best job for low insurance charges and RF seems to doing a better job in predicting high insurance charges. Polynomial prediction has little more deviation from the actual values at both high and low charges.

From our modeling procedure, we should use DNN model if we want better accuracy for the lower charge prediction (< 15,000 dollars) and RF model for better accuracy at high charge prediction (> 15,000 dollars).