In [ ]:

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

Merging the data sets

In [ ]:

```
df_1 = pd.read_csv('Hospitalisation details.csv')
df_2 = pd.read_excel('Names.xlsx')
df_3 = pd.read_csv('Medical Examinations.csv')
```

In [ ]:

```
semi_comp = pd.merge(df_1, df_2, on='Customer ID')
```

In [ ]:

```
complete = pd.merge(semi_comp, df_3, on = 'Customer ID')
complete.head()
```

Out[ ]:

	Customer ID	year	month	date	children	charges	Hospital tier	City tier	State ID	name	BMI	HBA
0	Id2335	1992	Jul	9	0	563.84	tier - 2	tier - 3	R1013	German, Mr. Aaron K	17.58	4
1	Id2334	1992	Nov	30	0	570.62	tier - 2	tier - 1	R1013	Rosendahl, Mr. Evan P	17.60	4
2	Id2333	1993	Jun	30	0	600.00	tier - 2	tier - 1	R1013	Albano, Ms. Julie	16.47	6
3	Id2332	1992	Sep	13	0	604.54	tier - 3	tier - 3	R1013	Riveros Gonzalez, Mr. Juan D. Sr.	17.70	6
4	Id2331	1998	Jul	27	0	637.26	tier - 3	tier - 3	R1013	Brietzke, Mr. Jordan	22.34	5

EDA and Feature Engineering

In [ ]:

```
complete.shape
```

Out[ ]:

```
(2335, 17)
```

In [ ]:

```
complete.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 2335 entries, 0 to 2334
Data columns (total 17 columns):
 #   Column                 Non-Null Count  Dtype  
---  ------                 --------------  -----  
 0   Customer ID            2335 non-null   object 
 1   year                   2335 non-null   object 
 2   month                  2335 non-null   object 
 3   date                   2335 non-null   int64  
 4   children               2335 non-null   int64  
 5   charges                2335 non-null   float64
 6   Hospital tier          2335 non-null   object 
 7   City tier              2335 non-null   object 
 8   State ID               2335 non-null   object 
 9   name                   2335 non-null   object 
 10  BMI                    2335 non-null   float64
 11  HBA1C                  2335 non-null   float64
 12  Heart Issues           2335 non-null   object 
 13  Any Transplants        2335 non-null   object 
 14  Cancer history         2335 non-null   object 
 15  NumberOfMajorSurgeries 2335 non-null   object 
 16  smoker                 2335 non-null   object 
dtypes: float64(3), int64(2), object(12)
memory usage: 328.4+ KB
```

In [ ]:

```
complete.describe()
```

Out[ ]:

	date	children	charges	BMI	HBA1C
count	2335.000000	2335.000000	2335.000000	2335.000000	2335.000000
mean	15.563597	1.025696	13529.918034	30.972649	6.578998
std	8.720508	1.234754	11898.654299	8.742095	2.228731
min	1.000000	0.000000	563.840000	15.010000	4.000000
25%	8.000000	0.000000	5084.010000	24.600000	4.900000
50%	15.000000	0.000000	9630.910000	30.400000	5.810000
75%	23.000000	2.000000	16912.295000	36.300000	7.955000
max	30.000000	5.000000	63770.430000	55.050000	12.000000

Checking for Null Values

In [ ]:

```
complete.isnull().sum()
```

Out[ ]:

```
Customer ID               0
year                      0
month                     0
date                      0
children                  0
charges                   0
Hospital tier             0
City tier                 0
State ID                  0
name                      0
BMI                       0
HBA1C                     0
Heart Issues              0
Any Transplants           0
Cancer history            0
NumberOfMajorSurgeries    0
smoker                    0
dtype: int64
```

In [ ]:

```
complete
```

Out[ ]:

	Customer ID	year	month	date	children	charges	Hospital tier	City tier	State ID	name	BMI
0	Id2335	1992	Jul	9	0	563.84	tier - 2	tier - 3	R1013	German, Mr. Aaron K	17.580
1	Id2334	1992	Nov	30	0	570.62	tier - 2	tier - 1	R1013	Rosendahl, Mr. Evan P	17.600
2	Id2333	1993	Jun	30	0	600.00	tier - 2	tier - 1	R1013	Albano, Ms. Julie	16.470
3	Id2332	1992	Sep	13	0	604.54	tier - 3	tier - 3	R1013	Riveros Gonzalez, Mr. Juan D. Sr.	17.700
4	Id2331	1998	Jul	27	0	637.26	tier - 3	tier - 3	R1013	Brietzke, Mr. Jordan	22.340
...	...	...	...	...	...	...	...	...	...	...	...
2330	Id5	1989	Jun	19	0	55135.40	tier - 1	tier - 2	R1012	Kadala, Ms. Kristyn	35.530
2331	Id4	1991	Jun	6	1	58571.07	tier - 1	tier - 3	R1024	Osborne, Ms. Kelsey	38.095
2332	Id3	1970	?	11	3	60021.40	tier - 1	tier - 1	R1012	Lu, Mr. Phil	34.485
2333	Id2	1977	Jun	8	0	62592.87	tier - 2	tier - 3	R1013	Lehner, Mr. Matthew D	30.360
2334	Id1	1968	Oct	12	0	63770.43	tier - 1	tier - 3	R1013	Hawks, Ms. Kelly	47.410

2335 rows × 17 columns

Identifying unique values

In [ ]:

```
complete.nunique()
```

Out[ ]:

```
Customer ID               2335
year                        48
month                        8
date                        30
children                     6
charges                   2331
Hospital tier                4
City tier                    4
State ID                    17
name                      2335
BMI                       1335
HBA1C                      667
Heart Issues                 2
Any Transplants              2
Cancer history               2
NumberOfMajorSurgeries       4
smoker                       3
dtype: int64
```

In [ ]:

```
complete['smoker'].unique()
```

Out[ ]:

```
array(['No', 'yes', '?'], dtype=object)
```

In [ ]:

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

Out[ ]:

```
No      1845
yes      488
?          2
Name: smoker, dtype: int64
```

In [ ]:

```
complete[complete['smoker'] == '?']
```

Out[ ]:

	Customer ID	year	month	date	children	charges	Hospital tier	City tier	State ID	name	BMI
1700	Id635	2004	Jul	17	0	15518.18	tier - 2	tier - 3	R1015	Bruns, Mr. Zachary T	25.175
1775	Id560	1994	Jul	1	3	17663.14	tier - 1	tier - 3	R1013	Pearlman, Mr. Oz	23.980

In [ ]:

```
complete['NumberOfMajorSurgeries'].value_counts()
```

Out[ ]:

```
No major surgery    1074
1                    965
2                    274
3                     22
Name: NumberOfMajorSurgeries, dtype: int64
```

In [ ]:

```
complete['smoker'].replace('?','No', inplace=True )# I replaced it with the most co
complete['smoker'].value_counts()
```

Out[ ]:

```
No      1847
yes      488
Name: smoker, dtype: int64
```

Dealing with State information Given: The most important states to work with are R1011,R1012,R1013

To not loose a lot of information I will create Bins to categorize the states

In [ ]:
```
specific_char = '?'

# Loop through columns
for col in complete.columns:
    if complete[col].dtype == 'object':
        if specific_char in complete[col].values:
            mode_value = complete[col].mode().iloc[0]
            complete[col] = complete[col].replace(specific_char, mode_value)
```

In [ ]:
```
for col in complete.columns:
    if complete[col].dtype == 'int':
        if specific_char in complete[col].values:
            mode_value = complete[col].mean().iloc[0]
            complete[col] = complete[col].replace(specific_char, mode_value)
```

In [ ]:
```
for col in complete.columns:
    if complete[col].dtype == 'float64':
        if specific_char in complete[col].values:
            mode_value = complete[col].mean().iloc[0]
            complete[col] = complete[col].replace(specific_char, mode_value)
```

In [ ]:
```
complete['State ID'].value_counts()
```

Out[ ]:
```
R1013    614
R1012    575
R1011    574
R1024    160
R1026     84
R1021     70
R1016     64
R1025     40
R1023     38
R1017     36
R1019     26
R1022     14
R1014     13
R1015     12
R1018      9
R1020      6
Name: State ID, dtype: int64
```

In [ ]:
```
states = ['R1013', 'R1012','R1011']

for i in complete['State ID'].values:
    if i == 'R1013':
        continue
    if i == 'R1012':
        continue
    if i == 'R1011':
        continue
    else:
        complete['State ID'].replace(i,'R0000', inplace= True)
complete['State ID'].value_counts()
```

Out[ ]:
```
R1013    614
R1012    575
R1011    574
R0000    572
Name: State ID, dtype: int64
```

In [ ]:
```
complete['State ID'] = complete['State ID'].map({
                            'R1013': 0,
                            'R1012': 1,
                            'R1011': 2,
                            'R0000': 3
})
```

In [ ]:
```
complete['State ID'].value_counts()
```

Out[ ]:
```
0    614
1    575
2    574
3    572
Name: State ID, dtype: int64
```

Cleaning Major of Surgeries since it has numbers and strings

In [ ]:
```
complete['NumberOfMajorSurgeries'].value_counts()
```

Out[ ]:
```
No major surgery    1074
1                    965
2                    274
3                     22
Name: NumberOfMajorSurgeries, dtype: int64
```

Numer of major Surgery

No major Surgery = 0

In [ ]:
```
complete['NumberOfMajorSurgeries'] = complete['NumberOfMajorSurgeries'].map({
                            '1': 1,
                            '2': 2,
                            '3': 3,
                            'No major surgery': 0
})
complete['NumberOfMajorSurgeries']
```

Out[ ]:

```
0       1
1       1
2       1
3       1
4       1
       ..
2330    0
2331    0
2332    2
2333    0
2334    0
Name: NumberOfMajorSurgeries, Length: 2335, dtype: int64
```

In [ ]:

```python
complete['NumberOfMajorSurgeries'].value_counts()
```

Out[ ]:

```
0    1074
1     965
2     274
3      22
Name: NumberOfMajorSurgeries, dtype: int64
```

Addressing Age

In [ ]:

```python
complete.head(1)
```

Out[ ]:

	Customer ID	year	month	date	children	charges	Hospital tier	City tier	State ID	name	BMI	HBA1C
0	Id2335	1992	Jul	9	0	563.84	tier - 2	tier - 3	0	German, Mr. Aaron K	17.58	4.51

In [ ]:

```python
for i in complete['year'].values:
    str_yr = str(i)
    if len(str_yr) == 4:
        complete['year'] = complete['year'].replace(i, (2023.0 - float(str_yr)))
    else:
        continue
```

In [ ]:

```python
complete['year'].min(), complete['year'].max()
```

Out[ ]:

```
(19.0, 65.0)
```

In [ ]:

```python
complete['age_gap'] =pd.cut(pd.to_numeric(complete['year']),
                                          bins= (19,35,45,55,66),
                                          labels=['19-35','36-45','46-55','56-55'])
```

In [ ]:

```python
complete['age_gap'].value_counts()
```

Out[ ]:

```
19-35    850
46-55    531
36-45    477
56-55    377
Name: age_gap, dtype: int64
```

Adding Gender to our dataset

```
In [ ]: complete.columns
```

```
Out[ ]: Index(['Customer ID', 'year', 'month', 'date', 'children', 'charges',
               'Hospital tier', 'City tier', 'State ID', 'name', 'BMI', 'HBA1C',
               'Heart Issues', 'Any Transplants', 'Cancer history',
               'NumberOfMajorSurgeries', 'smoker', 'age_gap'],
              dtype='object')
```

```
In [ ]: complete['name']
```

```
Out[ ]: 0                       German, Mr.  Aaron K
        1                     Rosendahl, Mr.  Evan P
        2                         Albano, Ms.  Julie
        3         Riveros Gonzalez, Mr.  Juan D. Sr.
        4                      Brietzke, Mr.  Jordan
                                 ...
        2330                    Kadala, Ms.  Kristyn
        2331                    Osborne, Ms.  Kelsey
        2332                           Lu, Mr.  Phil
        2333                  Lehner, Mr.  Matthew D
        2334                       Hawks, Ms.  Kelly
        Name: name, Length: 2335, dtype: object
```

```
In [ ]: import re
        complete['gender']  = complete['name'].str.extract(r'(Mr\.|Ms\.|Mrs\.)')
        complete.columns
```

```
Out[ ]: Index(['Customer ID', 'year', 'month', 'date', 'children', 'charges',
               'Hospital tier', 'City tier', 'State ID', 'name', 'BMI', 'HBA1C',
               'Heart Issues', 'Any Transplants', 'Cancer history',
               'NumberOfMajorSurgeries', 'smoker', 'age_gap', 'gender'],
              dtype='object')
```

```
In [ ]: complete['gender'].value_counts()
```

```
Out[ ]: Mr.     1165
        Ms.     1028
        Mrs.     142
        Name: gender, dtype: int64
```

Male: 0

Female: 1

```
In [ ]: complete['gender'] = complete['gender'].map({
                                'Mr.': 0,
                                'Ms.':1,
                                'Mrs.':1
        })
```

```
In [ ]: complete['gender'].value_counts().sum()
```

```
Out[ ]: 2335
```

```
In [ ]: complete.head(1)
```

Out[ ]:

	Customer ID	year	month	date	children	charges	Hospital tier	City tier	State ID	name	BMI	HBA1C
0	Id2335	31.0	Jul	9	0	563.84	tier - 2	tier - 3	0	German, Mr. Aaron K	17.58	4.51

Other features I believe we should map or discard

In [ ]:

```python
complete = complete.drop(columns=['month', 'date','Customer ID'])
```

In [ ]:

```python
complete = complete.drop(columns='name')
complete.columns
```

Out[ ]:

```
Index(['year', 'children', 'charges', 'Hospital tier', 'City tier', 'State ID',
       'BMI', 'HBA1C', 'Heart Issues', 'Any Transplants', 'Cancer history',
       'NumberOfMajorSurgeries', 'smoker', 'age_gap', 'gender'],
      dtype='object')
```

In [ ]:

```python
complete['Hospital tier'].value_counts()
```

Out[ ]:

```
tier - 2    1338
tier - 3     693
tier - 1     304
Name: Hospital tier, dtype: int64
```

In [ ]:

```python
complete['Hospital tier'] = complete['Hospital tier'].map({
                        'tier - 1': 1,
                        'tier - 2' :2,
                        'tier - 3': 3
})
```

In [ ]:

```python
complete['Hospital tier'].value_counts()
```

Out[ ]:

```
2    1338
3     693
1     304
Name: Hospital tier, dtype: int64
```

In [ ]:

```python
complete.columns
```

Out[ ]:

```
Index(['year', 'children', 'charges', 'Hospital tier', 'City tier', 'State ID',
       'BMI', 'HBA1C', 'Heart Issues', 'Any Transplants', 'Cancer history',
       'NumberOfMajorSurgeries', 'smoker', 'age_gap', 'gender'],
      dtype='object')
```

In [ ]:

```python
complete['City tier'].value_counts()
```

Out[ ]:

```
tier - 2    809
tier - 3    794
tier - 1    732
Name: City tier, dtype: int64
```

```
In [ ]: complete['City tier'] = complete['City tier'].map({
                                'tier - 1': 1,
                                'tier - 2' :2,
                                'tier - 3': 3
        })
```

```
In [ ]: complete['City tier'].value_counts()
```

```
Out[ ]: 2    809
        3    794
        1    732
        Name: City tier, dtype: int64
```

Heart Issues

No = 0 Yes = 1

```
In [ ]: complete['Heart Issues'].value_counts()
```

```
Out[ ]: No     1409
        yes     926
        Name: Heart Issues, dtype: int64
```

```
In [ ]: complete['Heart Issues'] = complete['Heart Issues'].map({
                                'No': 0,
                                'yes': 1
        })
```

```
In [ ]: complete['Heart Issues'].value_counts()
```

```
Out[ ]: 0    1409
        1     926
        Name: Heart Issues, dtype: int64
```

Any Transplants

No = 0 Yes = 1

```
In [ ]: complete['Any Transplants'].value_counts()
```

```
Out[ ]: No     2191
        yes     144
        Name: Any Transplants, dtype: int64
```

```
In [ ]: complete['Any Transplants'] = complete['Any Transplants'].map({
                                'No': 0,
                                'yes': 1
        })
```

```
In [ ]: complete['Any Transplants'].value_counts()
```

```
Out[ ]: 0    2191
        1     144
        Name: Any Transplants, dtype: int64
```

```
In [ ]: complete.head(1)
```

Out[ ]:

	year	children	charges	Hospital tier	City tier	State ID	BMI	HBA1C	Heart Issues	Any Transplants	Cancer history	Num
0	31.0	0	563.84	2	3	0	17.58	4.51	0	0	No	

Cancer History

No = 0 Yes = 1

In [ ]:

```
complete['Cancer history'].value_counts()
```

Out[ ]:

```
No     1944
Yes     391
Name: Cancer history, dtype: int64
```

In [ ]:

```
complete['Cancer history'] = complete['Cancer history'].map({
                        'No': 0,
                        'Yes': 1
})
```

In [ ]:

```
complete['Cancer history'].value_counts()
```

Out[ ]:

```
0    1944
1     391
Name: Cancer history, dtype: int64
```

Smoker

No = 0 Yes = 1

In [ ]:

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

Out[ ]:

```
No     1847
yes     488
Name: smoker, dtype: int64
```

In [ ]:

```
complete['smoker'] = complete['smoker'].map({
                        'No': 0,
                        'yes': 1
})
```

In [ ]:

```
complete['smoker'].value_counts().sum()
```

Out[ ]:

```
2335
```

In [ ]:

```
complete.head(5)
```

Out[ ]:

	year	children	charges	Hospital tier	City tier	State ID	BMI	HBA1C	Heart Issues	Any Transplants	Cancer history	Num
0	31.0	0	563.84	2	3	0	17.58	4.51	0	0	0	
1	31.0	0	570.62	2	1	0	17.60	4.39	0	0	0	
2	30.0	0	600.00	2	1	0	16.47	6.35	0	0	1	
3	31.0	0	604.54	3	3	0	17.70	6.28	0	0	0	
4	25.0	0	637.26	3	3	0	22.34	5.57	0	0	0	

In [ ]:

```
complete['children'].value_counts()
```

Out[ ]:

```
0    1189
1     379
3     378
2     346
4      25
5      18
Name: children, dtype: int64
```

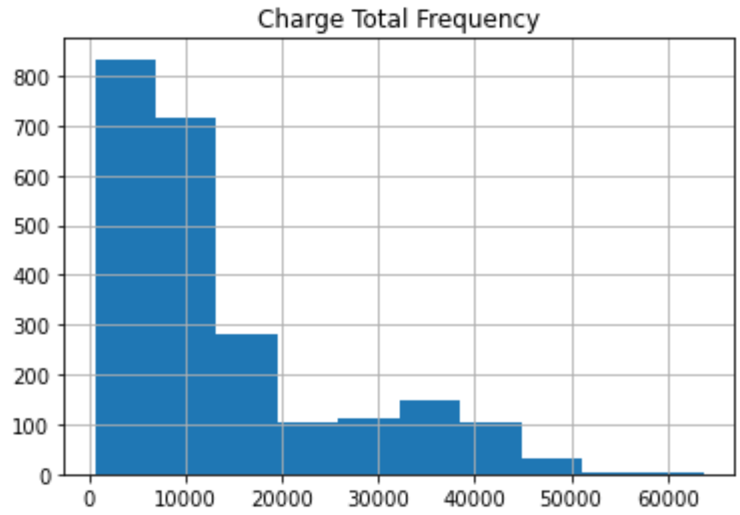
EDA

In [ ]:

```
complete['charges'].hist()
plt.title('Charge Total Frequency')
```

Out[ ]:

```
Text(0.5, 1.0, 'Charge Total Frequency')
```

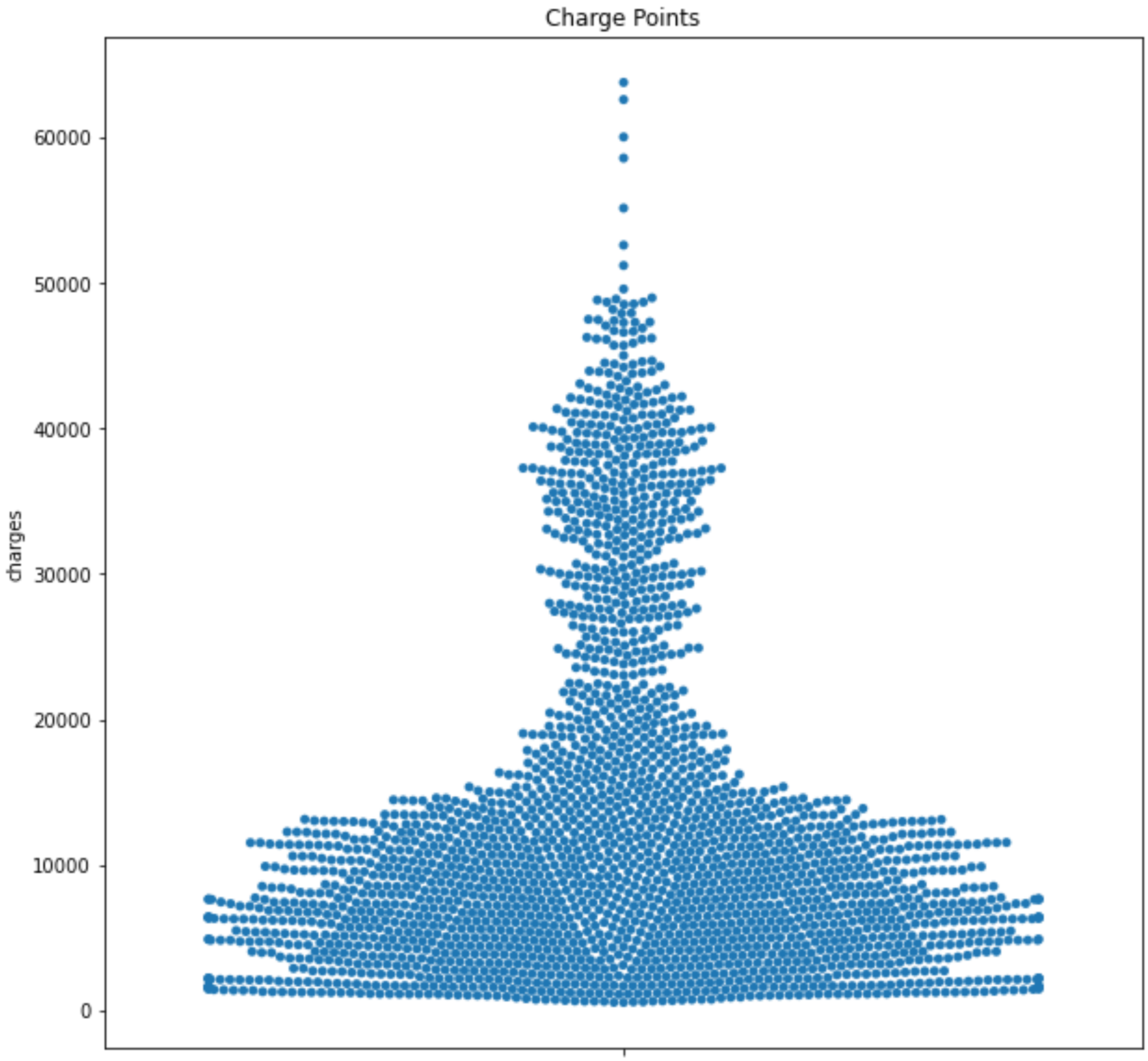


In [ ]:

```
plt.figure(figsize=(10,10))
sns.swarmplot(data= complete, y = complete['charges'], hue = complete['gender'])
plt.title('Charge Points')
```

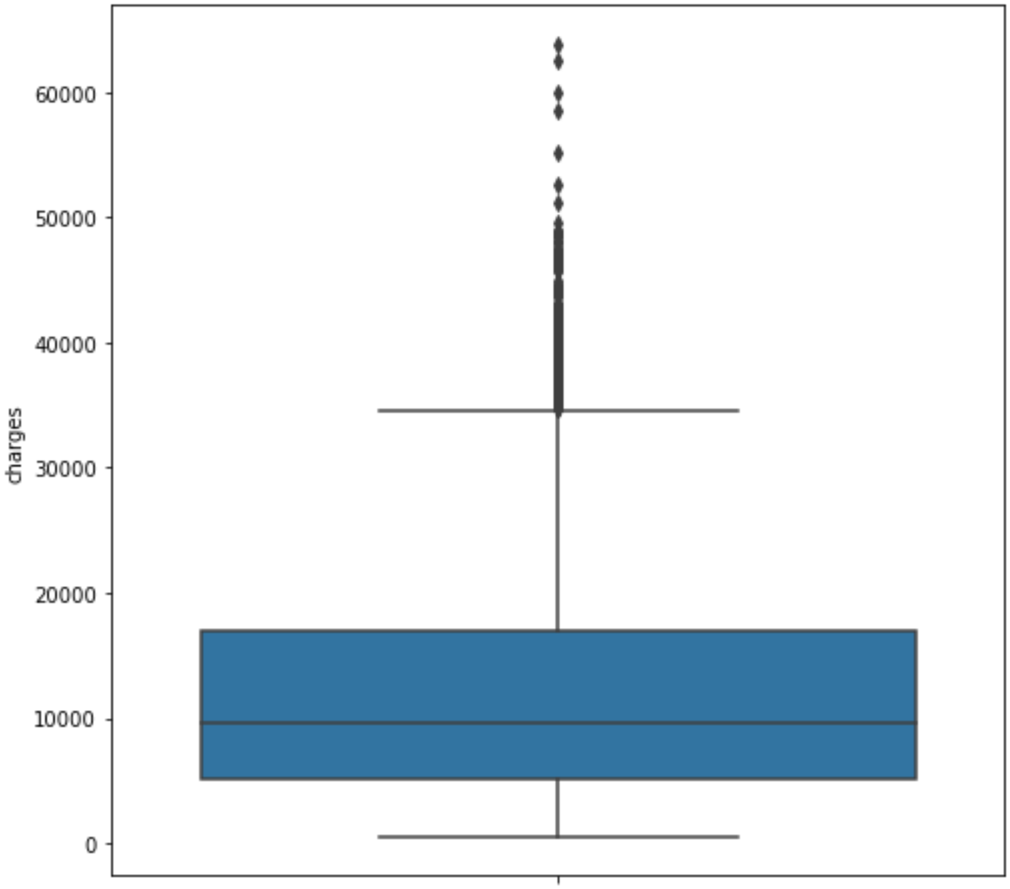
Out[ ]:

```
Text(0.5, 1.0, 'Charge Points')
```



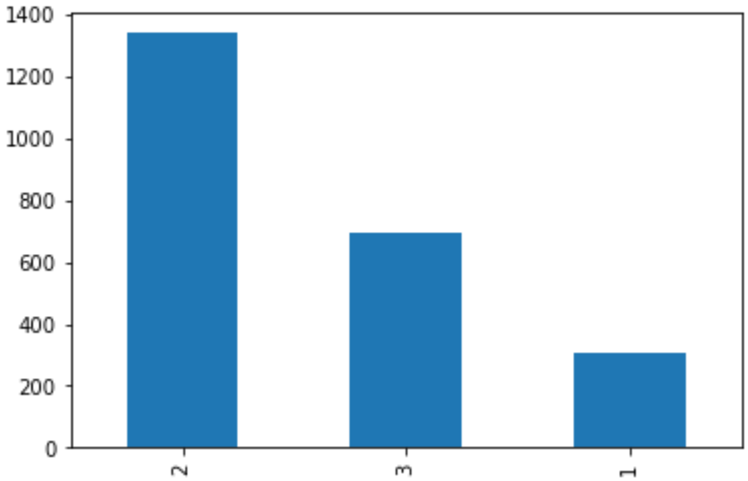
```
In [ ]: plt.figure(figsize=(8,8))
        sns.boxplot(y =complete['charges'])
```

```
Out[ ]: <AxesSubplot:ylabel='charges'>
```



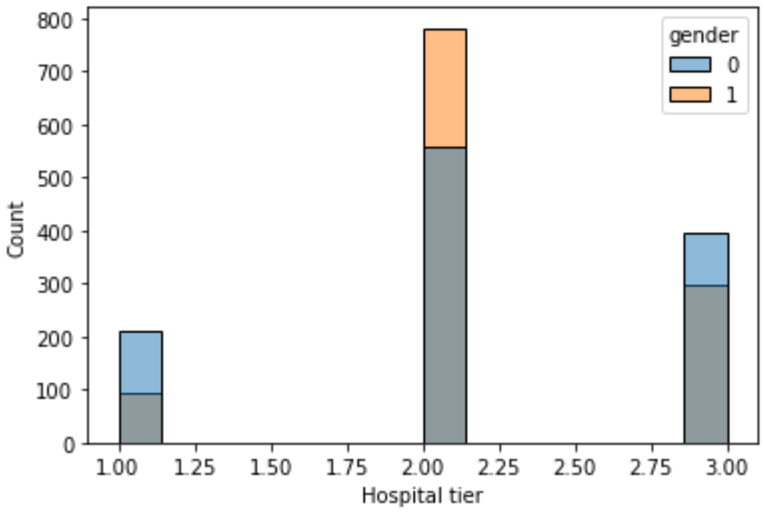
In [ ]:
```
complete['Hospital tier'].value_counts().plot(kind = 'bar')
```

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



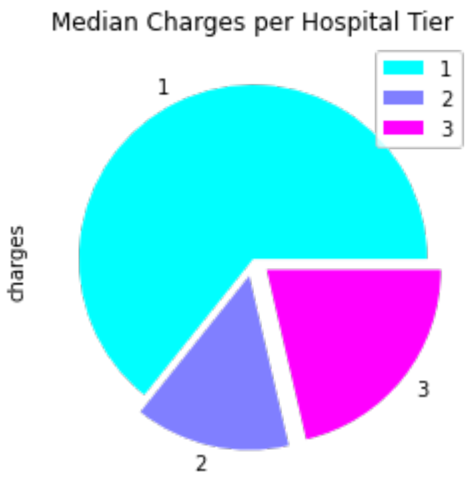
In [ ]:
```
sns.histplot(data= complete, x = 'Hospital tier', hue= 'gender')
```

Out[ ]:
```
<AxesSubplot:xlabel='Hospital tier', ylabel='Count'>
```



We see that Tier 2 Hosptitals has more Female patients than Tier 1 and 3 but Tier 1 and 3 had more Male patients in general

In [ ]:
```
explode = (0, 0.1, .1)
complete.groupby('Hospital tier')['charges'].median().plot(kind ='pie', colormap= '
plt.show();
```



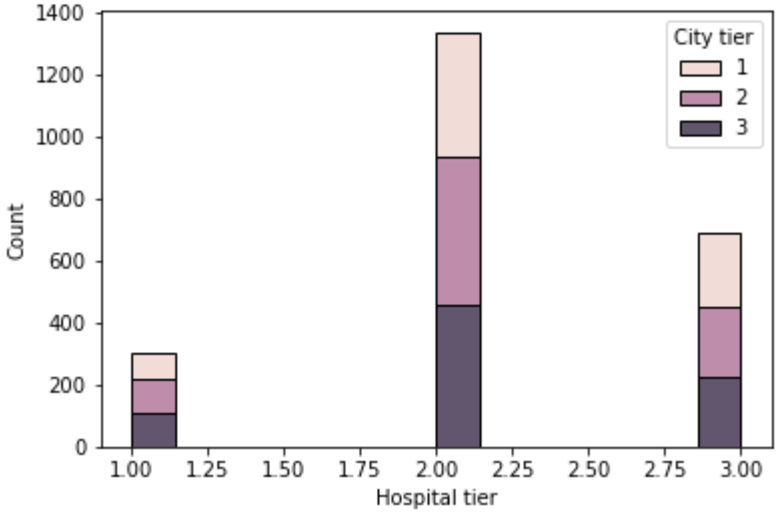
We see that the media charge at the Tier 1 hospital was the largest in comparison to the other two Hospitals

In [ ]:
```
complete.columns
```

Out[ ]:
```
Index(['year', 'children', 'charges', 'Hospital tier', 'City tier', 'State ID',
       'BMI', 'HBA1C', 'Heart Issues', 'Any Transplants', 'Cancer history',
       'NumberOfMajorSurgeries', 'smoker', 'age_gap', 'gender'],
      dtype='object')
```

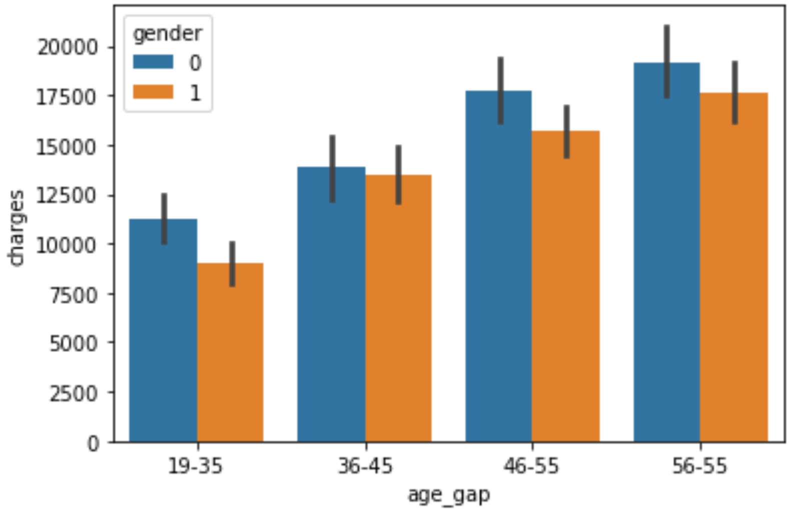
In [ ]:
```
sns.histplot( x=complete["Hospital tier"], hue= complete['City tier'], multiple= 's
```

Out[ ]:
```
<AxesSubplot:xlabel='Hospital tier', ylabel='Count'>
```



```
In [ ]: sns.barplot(data= complete,x=complete['age_gap'], y = complete['charges'], hue= com
```

```
Out[ ]: <AxesSubplot:xlabel='age_gap', ylabel='charges'>
```



Statistics

```
In [ ]: complete.groupby('Hospital tier')['charges'].mean()
```

```
Out[ ]: Hospital tier
        1    30129.198586
        2    11865.268767
        3     9462.269307
        Name: charges, dtype: float64
```

Hospital Hypothesis testing

H_0 = The average hospitalization cost for three type of hospitals are not significantly different

In [ ]:

```
hosp_1 = complete[complete['Hospital tier'] == 1]['charges']
hosp_2 = complete[complete['Hospital tier'] == 2]['charges']
hosp_3 = complete[complete['Hospital tier'] == 3]['charges']
```

In [ ]:

```
import scipy.stats as stats

F, p = stats.f_oneway(hosp_1, hosp_2,hosp_3)

print("F-statistic:", F)
print("p-value:", p)
```

```
F-statistic: 498.3038399629512
p-value: 6.505496697290111e-181
```

In [ ]:

```
alpha = 0.05
if p < alpha:
    print("Reject null hypothesis: The average hospitalization costs are significan
else:
    print("Fail to reject null hypothesis: We can't say that the average hospitaliz
```

```
Reject null hypothesis: The average hospitalization costs are significantly differe
nt.
```

City Hypothesis Testing

H_0 = The average hospitalization cost for the three types of citites are not significantly different

In [ ]:

```
city_1 = complete[complete['City tier'] == 1]['charges']
city_2 = complete[complete['City tier'] == 2]['charges']
city_3 = complete[complete['City tier'] == 3]['charges']
```

In [ ]:

```
F, p = stats.f_oneway(city_1, city_2,city_3)

print("F-statistic:", F)
print("p-value:", p)
```

```
F-statistic: 1.3921799249729778
p-value: 0.24873941194436716
```

In [ ]:

```
alpha = 0.05
if p < alpha:
    print("Reject null hypothesis: The average hospitalization costs in the three c
else:
    print("Fail to reject null hypothesis: We can't say that the average hospitaliz
```

```
Fail to reject null hypothesis: We can't say that the average hospitalization costs
in the three cities are significantly different.
```

Smoker Analysis

H_0 = The average hospitalization cost for smokers is not significantly different from the average cost for nonsmokers

Non-smoker = 0

In [ ]:

```
smoker_0= complete[complete['smoker'] == 0]['charges']
smoker_1= complete[complete['smoker'] == 1]['charges']
```

In [ ]:

```
F, p = stats.f_oneway(smoker_0, smoker_1)

print("F-statistic:", F)
print("p-value:", p)
```

```
F-statistic: 5516.158096563916
p-value: 0.0
```

In [ ]:

```
alpha = 0.05
if p < alpha:
    print("Reject null hypothesis: The average hospitalization costs for smoker and
else:
    print("Fail to reject null hypothesis: We can't say that the average hospitaliz
```

```
Reject null hypothesis: The average hospitalization costs for smoker and non-smoker
are significantly different.
```

Testing if heart isues and smoking are independent

In [ ]:

```
complete.columns
```

Out[ ]:

```
Index(['year', 'children', 'charges', 'Hospital tier', 'City tier', 'State ID',
       'BMI', 'HBA1C', 'Heart Issues', 'Any Transplants', 'Cancer history',
       'NumberOfMajorSurgeries', 'smoker', 'age_gap', 'gender'],
      dtype='object')
```

In [ ]:

```
cont_tab = pd.crosstab(complete['smoker'],complete['Heart Issues'])
cont_tab
```

Out[ ]:

Heart Issues	**0**	**1**
smoker		
0	1112	735
1	297	191

In [ ]:

```
from scipy.stats import chi2_contingency

chi2_score,p,dof,ex_fre  = chi2_contingency(cont_tab)
p
```

Out[ ]:

```
0.8328787488420707
```

In [ ]:

```
alpha = 0.05
if p < alpha:
    print("Reject null hypothesis: Smoking and heart issues are dependent.")
else:
    print("Fail to reject null hypothesis: Smoking and heart issues are independent
```

```
Fail to reject null hypothesis: Smoking and heart issues are independent.
```

Machine Learning

In [ ]:

```
complete.head(5)
```

Out[ ]:

	year	children	charges	Hospital tier	City tier	State ID	BMI	HBA1C	Heart Issues	Any Transplants	Cancer history	Num
0	31.0	0	563.84	2	3	0	17.58	4.51	0	0	0	
1	31.0	0	570.62	2	1	0	17.60	4.39	0	0	0	
2	30.0	0	600.00	2	1	0	16.47	6.35	0	0	1	
3	31.0	0	604.54	3	3	0	17.70	6.28	0	0	0	
4	25.0	0	637.26	3	3	0	22.34	5.57	0	0	0	

In [ ]:

```
corr_mat = complete.corr()
corr_mat
```

Out[ ]:

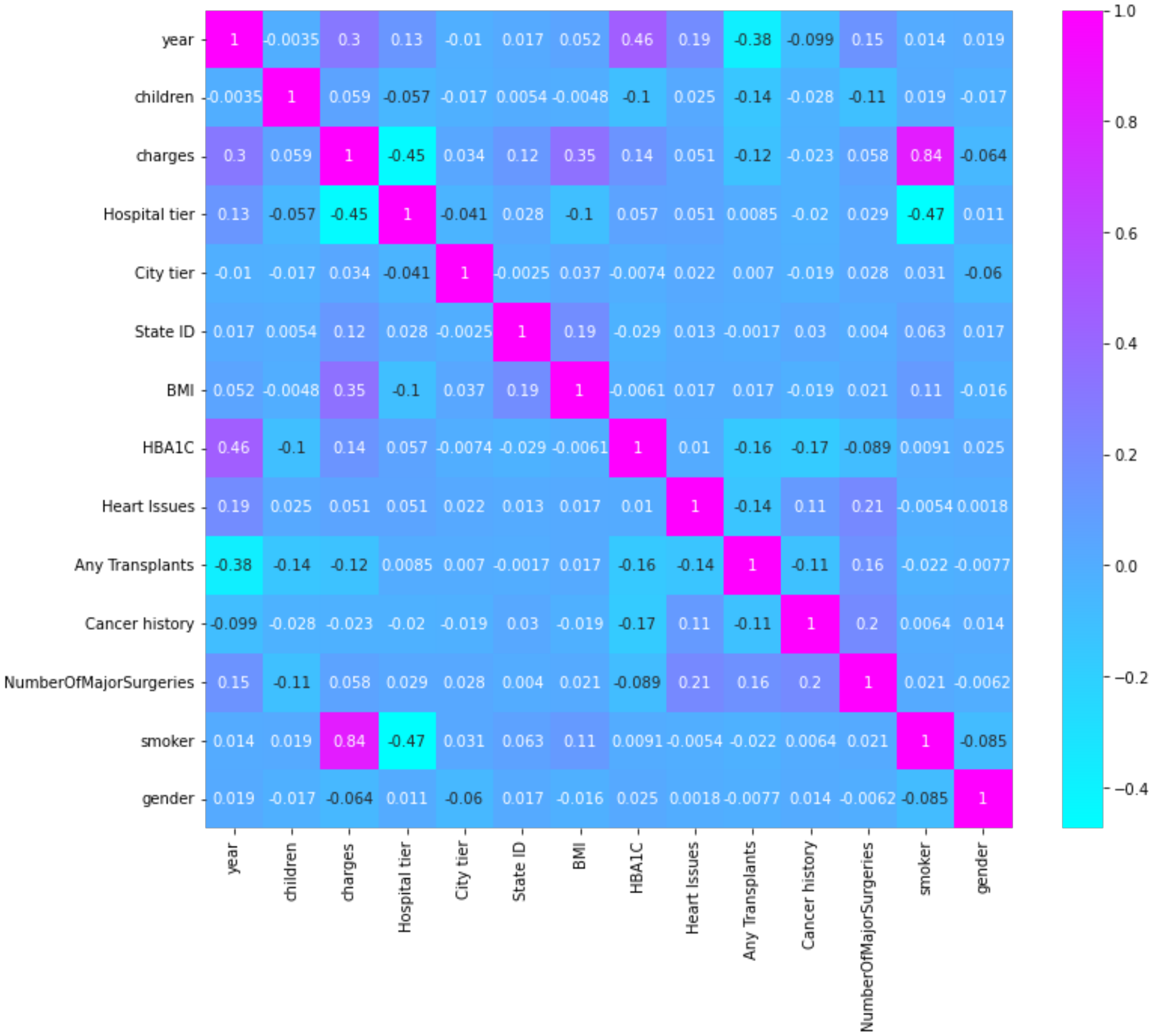
	year	children	charges	Hospital tier	City tier	State ID	BM
year	1.000000	-0.003524	0.304590	0.133767	-0.010229	0.016529	0.05245
children	-0.003524	1.000000	0.059122	-0.056550	-0.016571	0.005438	-0.00479
charges	0.304590	0.059122	1.000000	-0.448126	0.034259	0.122385	0.34769
Hospital tier	0.133767	-0.056550	-0.448126	1.000000	-0.041381	0.028370	-0.10448
City tier	-0.010229	-0.016571	0.034259	-0.041381	1.000000	-0.002504	0.03719
State ID	0.016529	0.005438	0.122385	0.028370	-0.002504	1.000000	0.18699
BMI	0.052450	-0.004793	0.347695	-0.104489	0.037198	0.186993	1.00000
HBA1C	0.457904	-0.100593	0.142246	0.056794	-0.007374	-0.028732	-0.00611
Heart Issues	0.190028	0.024967	0.051213	0.050896	0.022117	0.012596	0.01693
Any Transplants	-0.381204	-0.142340	-0.121881	0.008482	0.006999	-0.001716	0.01659
Cancer history	-0.098665	-0.027918	-0.022709	-0.020220	-0.018997	0.029709	-0.01901
NumberOfMajorSurgeries	0.151002	-0.111019	0.058482	0.029367	0.027512	0.003967	0.02085
smoker	0.013830	0.019164	0.838314	-0.473938	0.031343	0.062997	0.10928
gender	0.018750	-0.017390	-0.063895	0.010958	-0.060496	0.017376	-0.01635

In [ ]:

```
plt.figure(figsize=(12,10))
sns.heatmap(corr_mat, cmap='cool', annot= True)
```

Out[ ]:

```
<AxesSubplot:>
```



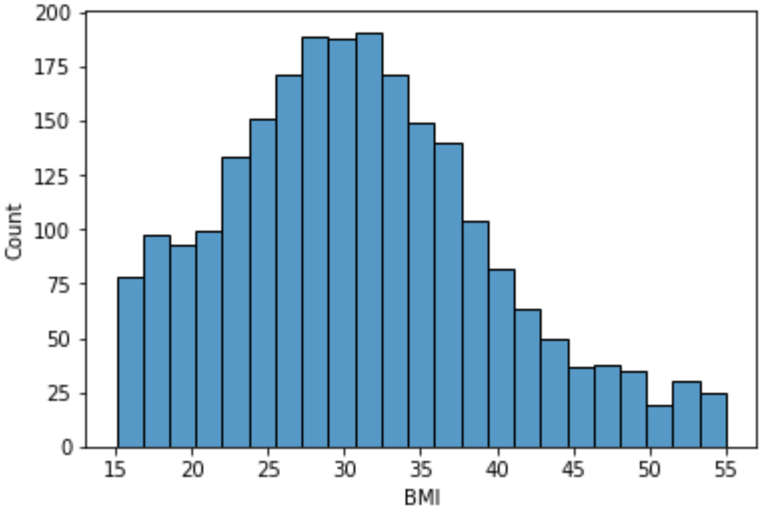
In [ ]:
```
complete.head()
```

Out[ ]:

	year	children	charges	Hospital tier	City tier	State ID	BMI	HBA1C	Heart Issues	Any Transplants	Cancer history	Num
0	31.0	0	563.84	2	3	0	17.58	4.51	0	0	0	
1	31.0	0	570.62	2	1	0	17.60	4.39	0	0	0	
2	30.0	0	600.00	2	1	0	16.47	6.35	0	0	1	
3	31.0	0	604.54	3	3	0	17.70	6.28	0	0	0	
4	25.0	0	637.26	3	3	0	22.34	5.57	0	0	0	

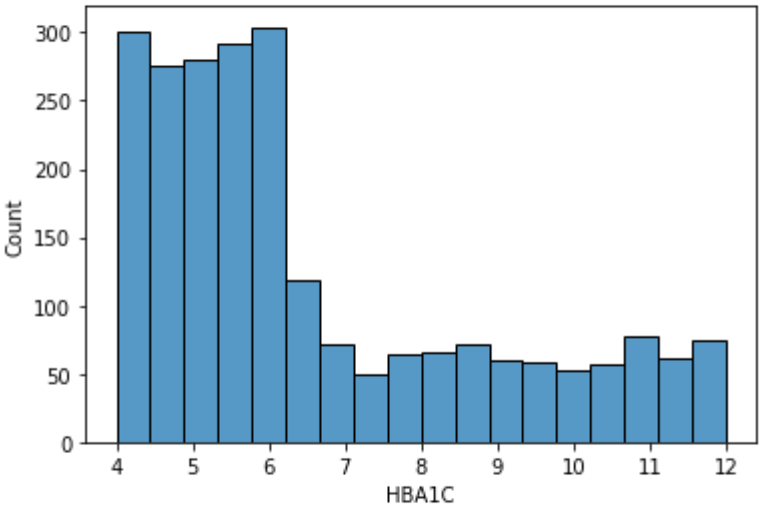
In [ ]:
```
sns.histplot(data=complete, x = "BMI")
```

Out[ ]:
```
<AxesSubplot:xlabel='BMI', ylabel='Count'>
```



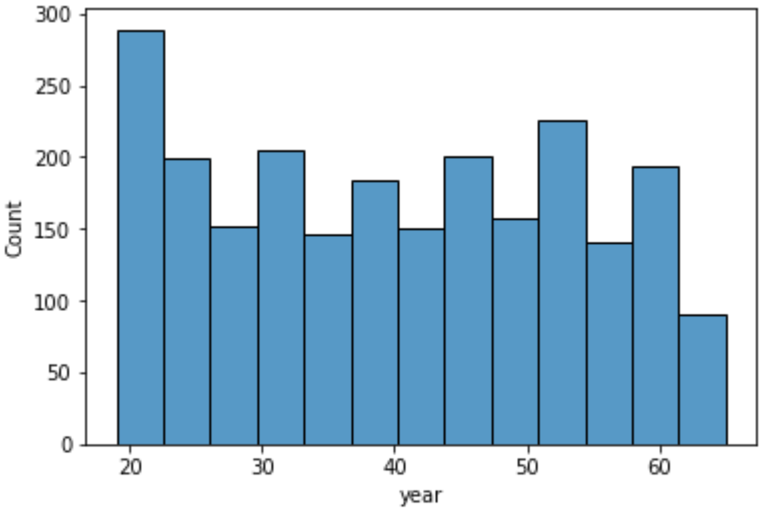
In [ ]:
```
sns.histplot(data = complete, x = "HBA1C")
```

Out[ ]:
```
<AxesSubplot:xlabel='HBA1C', ylabel='Count'>
```



In [ ]:
```
sns.histplot(data= complete, x = 'year')
```

Out[ ]:
```
<AxesSubplot:xlabel='year', ylabel='Count'>
```



In [ ]:

```
complete.drop(columns= 'age_gap', axis= 1, inplace= True)
```

In [ ]:

```
complete['BMI'].min(), complete['BMI'].max(),complete['HBA1C'].min(), complete['HBA
```

Out[ ]:

```
(15.01, 55.05, 4.0, 12.0, 563.84, 63770.43)
```

Trial # 1

In [ ]:

```
from sklearn.model_selection import train_test_split

X = complete.drop(columns='charges', axis= 1)
Y = complete['charges']



X_train, X_test, y_train, y_test = train_test_split(X, Y, test_size=.2)
```

In [ ]:

```
from sklearn.linear_model import SGDRegressor

sgd_reg = SGDRegressor( random_state=42)

#train the model
sgd_reg.fit(X_train, y_train)
```

```
c:\Users\luisl\anaconda3\envs\PythonData\lib\site-packages\sklearn\linear_model\_st
ochastic_gradient.py:1503: ConvergenceWarning: Maximum number of iteration reached
before convergence. Consider increasing max_iter to improve the fit.
  warnings.warn(
```

Out[ ]:

```
SGDRegressor(random_state=42)
```

Test the model

In [ ]:

```
y_pred = sgd_reg.predict(X_test)
```

Accuracy results

In [ ]:

```
from sklearn.metrics import mean_squared_error

mse = mean_squared_error(y_test, y_pred)
print(f"Mean Squared Error: {mse}")

rmse = np.sqrt(mse)
print(f"Root Mean Squared Error: {rmse}")
```

```
Mean Squared Error: 4145690810.1746974
Root Mean Squared Error: 64387.03914744564
```

It looks like our model is running poorly, let's try runing hyperparameter tuning and cross validate it as well

In [ ]:
```
import warnings

# Suppress FutureWarning
warnings.filterwarnings("ignore", category=FutureWarning)

# Suppress DomainWarning
from statsmodels.tools.sm_exceptions import DomainWarning
warnings.filterwarnings("ignore", category=DomainWarning)


from statsmodels.tools.sm_exceptions import ConvergenceWarning

# Suppress ConvergenceWarning
warnings.filterwarnings("ignore", category=ConvergenceWarning)




from sklearn.model_selection import GridSearchCV
from sklearn.model_selection import cross_val_score

param_grid = {
    'alpha': [0.0001, 0.001, 0.01, 0.1, 1, 10],
    'loss': ['squared_loss', 'huber'],
    'penalty': ['none', 'l2', 'l1', 'elasticnet'],
    'learning_rate': ['constant', 'optimal', 'invscaling', 'adaptive'],
    'eta0': [0.001, 0.01, 0.1]
}
grid = GridSearchCV(sgd_reg, param_grid, cv= 5, scoring='neg_root_mean_squared_erro


grid.fit(X,Y)

grid.best_params_

estimator = grid.best_estimator_

cv_results = cross_val_score(estimator, X_train, y_train, cv=5)

print(f"Cross-validation scores: {cv_results}")
print(f"Mean Cross-validation score: {np.mean(cv_results)}")

y_pred = estimator.predict(X_test)

mse = mean_squared_error(y_test, y_pred)
print(f"Mean Squared Error: {mse}")

# To get the Root Mean Squared Error (RMSE), you can take the square root of the MS
rmse = np.sqrt(mse)
print(f"Root Mean Squared Error: {rmse}")
```

```
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  warnings.warn(
Cross-validation scores: [0.7804595  0.83660537 0.82915369 0.79544271 0.79037603]
Mean Cross-validation score: 0.8064074595255301
Mean Squared Error: 23291078.68817178
Root Mean Squared Error: 4826.083162169067
```

Results

- Lets plot how accurate our model predicted the values

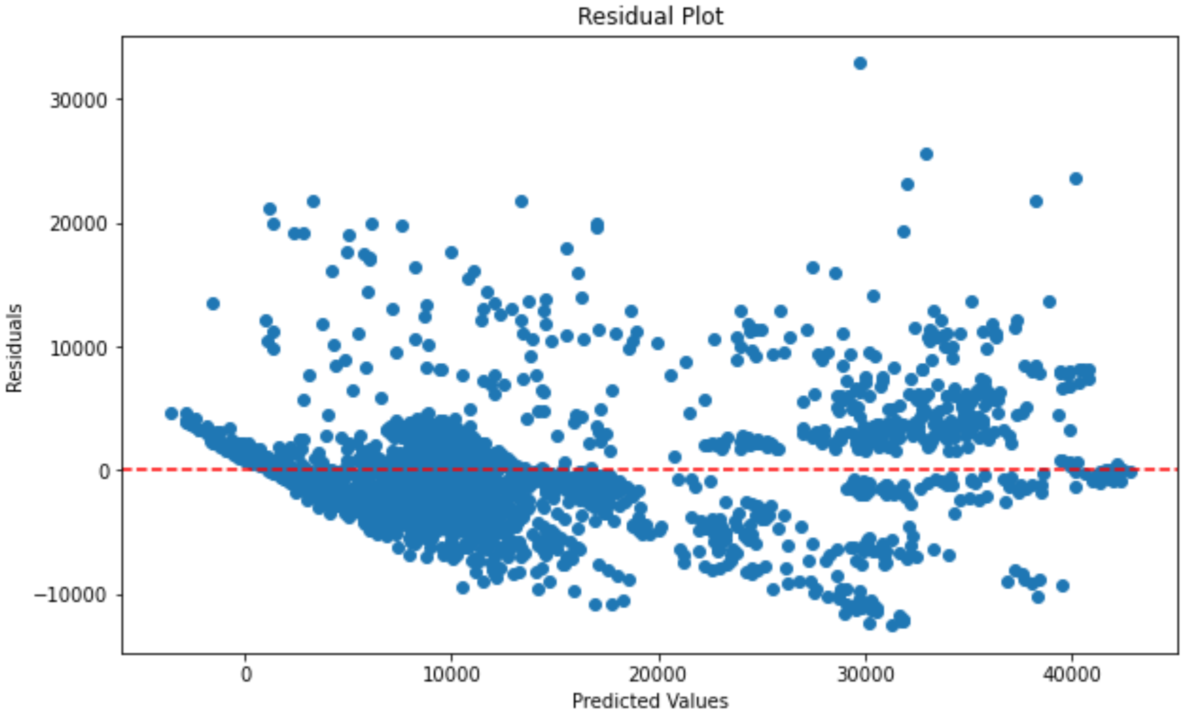
In [ ]:

```
y_pred = estimator.predict(X)
residuals = Y - y_pred
residuals
```

Out[ ]:
```
0       -2959.236994
1       -3500.168374
2       -2383.251810
3         922.024873
4        1207.508714
            ...
2330    23121.495962
2331    25605.374694
2332    21740.854442
2333    32895.545310
2334    23573.824456
Name: charges, Length: 2335, dtype: float64
```

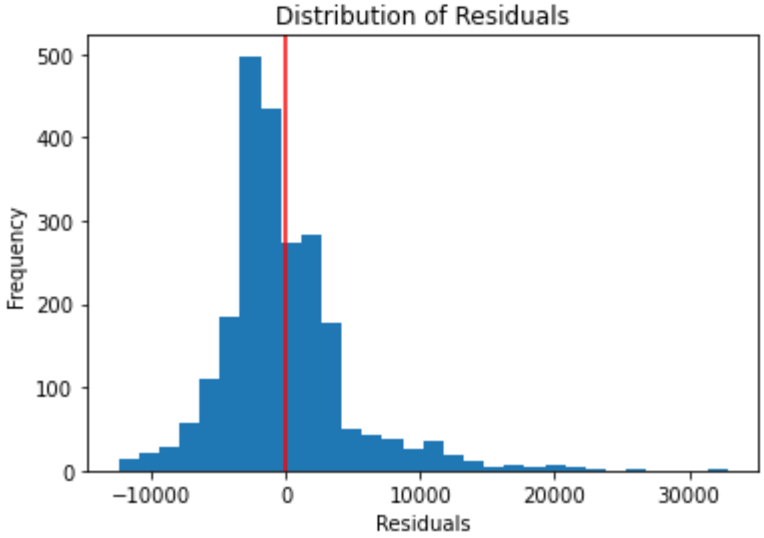
In [ ]:
```python
import matplotlib.pyplot as plt

plt.figure(figsize=(10, 6))
plt.scatter(y_pred, residuals)
plt.axhline(y=0, color='r', linestyle='--')
plt.xlabel('Predicted Values')
plt.ylabel('Residuals')
plt.title('Residual Plot')
plt.show()
```



We want to see our residuals as close to 0 as possible. We see that after the 10k predictions, our model starts to fail

In [ ]:
```python
plt.hist(residuals, bins=30)
plt.xlabel('Residuals')
plt.ylabel('Frequency')
plt.axvline(x = 0, color = 'r')
plt.title('Distribution of Residuals')
plt.show()
```



Results

In [ ]:
```
X_train.head()
```

Out[ ]:

	year	children	Hospital tier	City tier	State ID	BMI	HBA1C	Heart Issues	Any Transplants	Cancer history	NumberOf
1036	57.0	0	3	1	0	20.75	5.18	1	0	0	
2292	52.0	0	2	2	0	38.06	6.98	0	0	0	
2264	39.0	3	1	1	0	38.39	4.25	0	0	0	
1522	63.0	0	3	1	2	21.40	9.03	0	0	0	
1329	54.0	2	3	2	2	35.90	4.85	1	0	1	

Trial #2

Our Results were not favorable, let's try standardizing some of the columns

In [ ]:
```
from sklearn.preprocessing import StandardScaler

feat_to_scale = ['BMI']

prescaled_data = X[feat_to_scale]

#build the scaler
scaler = StandardScaler()
scaled_data = scaler.fit_transform(prescaled_data)

#results will be an array. I need to convert back to a DF
# use feat_to_scale list to define column names - otherwise, you'll see 0 and 1 hea
scaled_df = pd.DataFrame(scaled_data, columns=feat_to_scale)
```

In [ ]:
```
X.drop(feat_to_scale, axis=1)

X_scaled = pd.concat([X.drop(feat_to_scale, axis=1),
                      scaled_df]
                      , axis=1)

X_scaled.head()
```

Out[ ]:

	year	children	Hospital tier	City tier	State ID	HBA1C	Heart Issues	Any Transplants	Cancer history	NumberOfMajorSurg
0	31.0	0	2	3	0	4.51	0	0	0	
1	31.0	0	2	1	0	4.39	0	0	0	
2	30.0	0	2	1	0	6.35	0	0	1	
3	31.0	0	3	3	0	6.28	0	0	0	
4	25.0	0	3	3	0	5.57	0	0	0	

In [ ]:

```
import warnings

# Suppress FutureWarning
warnings.filterwarnings("ignore", category=FutureWarning)

# Suppress DomainWarning
from statsmodels.tools.sm_exceptions import DomainWarning
warnings.filterwarnings("ignore", category=DomainWarning)

# Your GLM model code here


# Suppress DomainWarning
warnings.filterwarnings("ignore", category=FutureWarning)

from statsmodels.tools.sm_exceptions import ConvergenceWarning

# Suppress ConvergenceWarning
warnings.filterwarnings("ignore", category=ConvergenceWarning)

X_train, X_test, y_train, y_test = train_test_split(X_scaled, Y, test_size=.2)

sgd_reg = SGDRegressor( random_state=42)

#train the model
sgd_reg.fit(X_train, y_train)


param_grid = {
    'alpha': [0.0001, 0.001, 0.01, 0.1, 1, 10],
    'loss': ['squared_loss', 'huber'],
    'penalty': ['none', 'l2', 'l1', 'elasticnet'],
    'learning_rate': ['constant', 'optimal', 'invscaling', 'adaptive'],
    'eta0': [0.001, 0.01, 0.1]
}
grid = GridSearchCV(sgd_reg, param_grid, cv= 5, scoring='neg_root_mean_squared_erro


grid.fit(X,Y)

estimator = grid.best_estimator_


cv_results = cross_val_score(estimator, X_train, y_train, cv=5)

print(f"Cross-validation scores: {cv_results}")
print(f"Mean Cross-validation score: {np.mean(cv_results)}")

y_pred = estimator.predict(X_test)

mse = mean_squared_error(y_test, y_pred)
print(f"Mean Squared Error: {mse}")

# To get the Root Mean Squared Error (RMSE), you can take the square root of the MS
rmse = np.sqrt(mse)
print(f"Root Mean Squared Error: {rmse}")
```

```
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  warnings.warn(
Cross-validation scores: [0.8499968  0.83180469 0.80543423 0.82914959 0.86894391]
Mean Cross-validation score: 0.8370658434009292
Mean Squared Error: 208415391.42197126
Root Mean Squared Error: 14436.59902546203
```
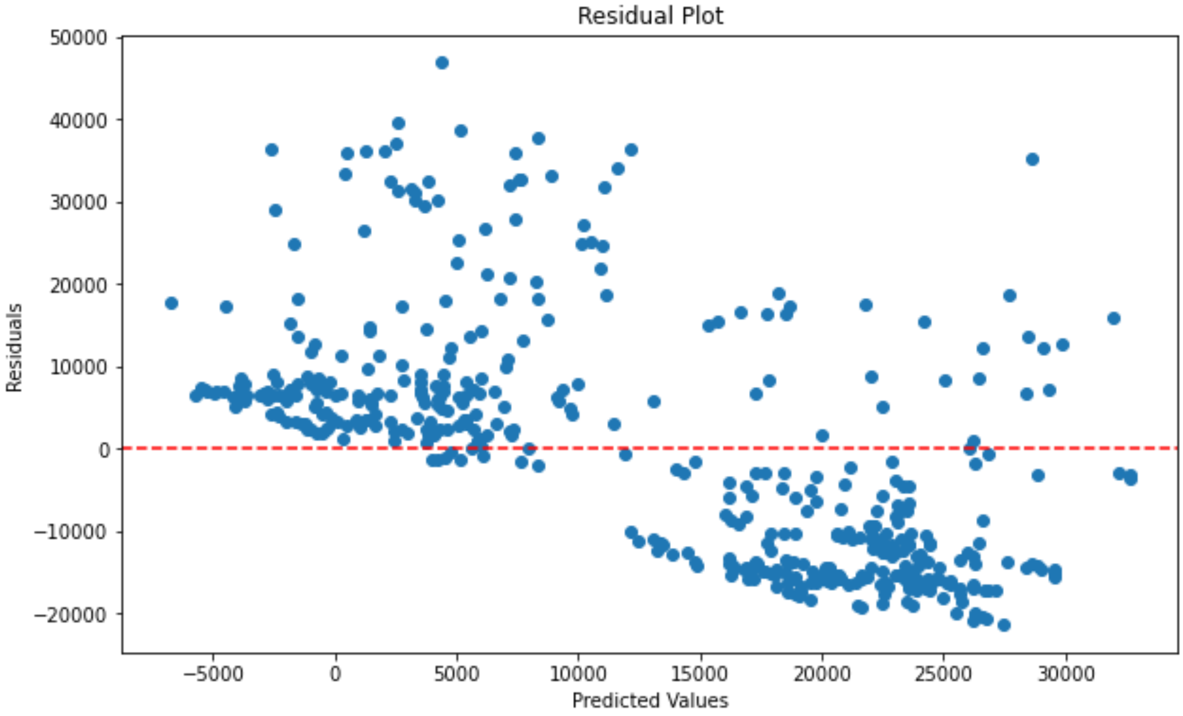

Results

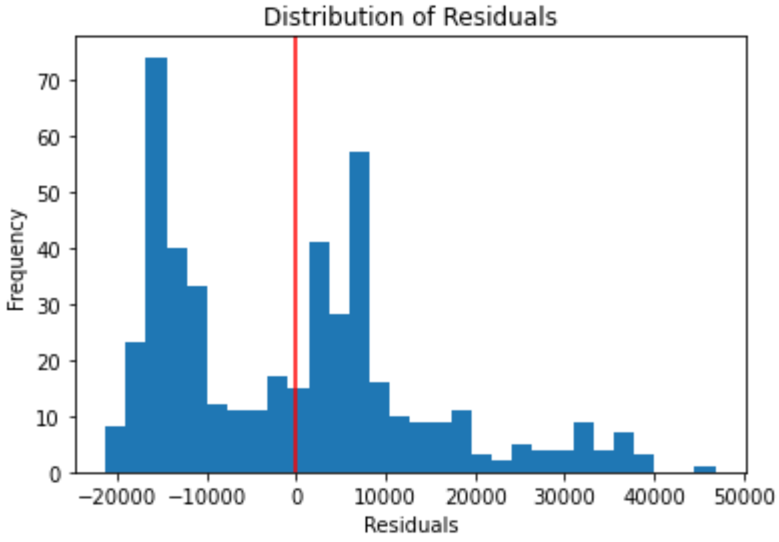
- Standardizing BMI worsen my model, let's plot and see

In [ ]:
```
residuals = y_test- y_pred
```

In [ ]:
```
import matplotlib.pyplot as plt

plt.figure(figsize=(10, 6))
plt.scatter(y_pred, residuals)
plt.axhline(y=0, color='r', linestyle='--')
plt.xlabel('Predicted Values')
plt.ylabel('Residuals')
plt.title('Residual Plot')
plt.show()
```



In [ ]:
```
plt.hist(residuals, bins=30)
plt.xlabel('Residuals')
plt.ylabel('Frequency')
plt.axvline(x = 0, color = 'r')
plt.title('Distribution of Residuals')
plt.show()
```

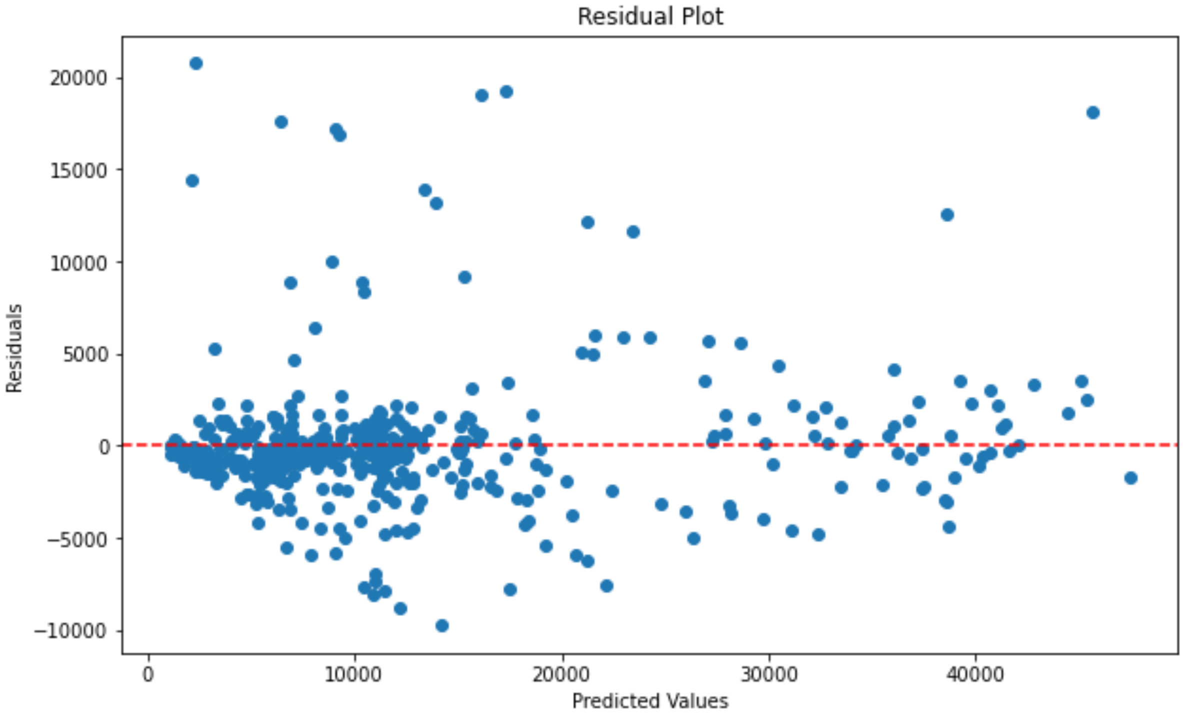


Trial # 3

In [ ]:

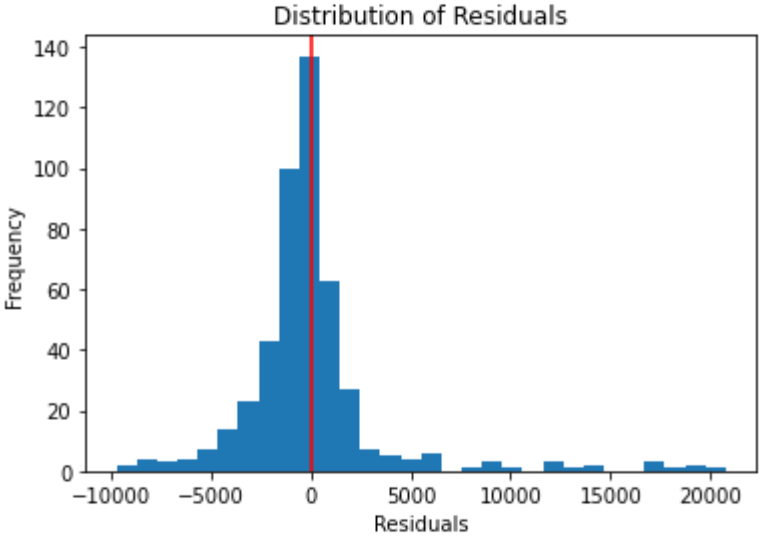
```
from sklearn.ensemble import RandomForestRegressor
rf = RandomForestRegressor(random_state=42)
# Hyperparameter grid
param_grid = {
    'n_estimators': [50, 100, 200],
    'max_depth': [None, 10, 20, 30]
}
# Grid search
grid_rf = GridSearchCV(rf, param_grid,scoring='neg_root_mean_squared_error', cv=5)
grid_rf.fit(X_train, y_train)

y_pred = grid_rf.predict(X_test)
print("Best RF Params: ", grid_rf.best_params_)
print("RF Test RMSE: ", np.sqrt(mean_squared_error(y_test,y_pred)))


residuals = y_test- y_pred

plt.figure(figsize=(10, 6))
plt.scatter(y_pred, residuals)
plt.axhline(y=0, color='r', linestyle='--')
plt.xlabel('Predicted Values')
plt.ylabel('Residuals')
plt.title('Residual Plot')
plt.show()
```

```
Best RF Params:  {'max_depth': 10, 'n_estimators': 200}
RF Test RMSE:  3605.792632543789
```



In [ ]:

```
plt.hist(residuals, bins=30)
plt.xlabel('Residuals')
plt.ylabel('Frequency')
plt.axvline(x = 0, color = 'r')
plt.title('Distribution of Residuals')
plt.show()
```

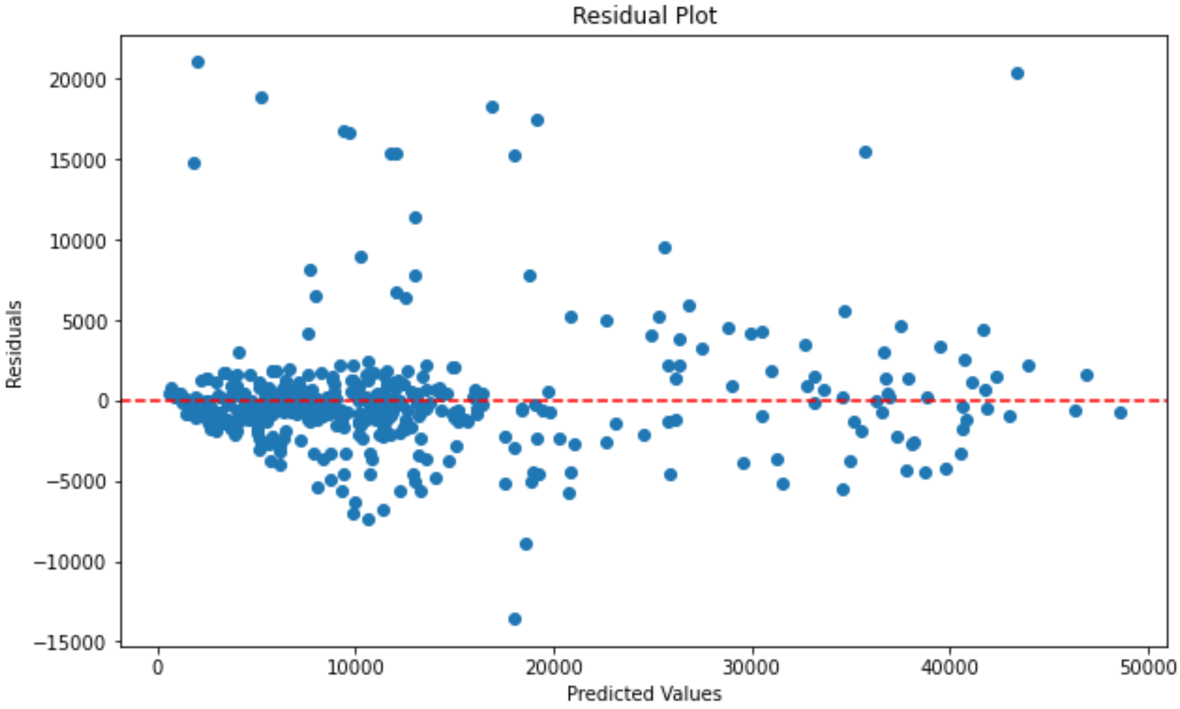


Trial # 4

In [ ]:

```
import xgboost as xgb
xg_reg = xgb.XGBRegressor(objective='reg:squarederror', random_state=42)
# Hyperparameter grid
param_grid_xgb = {
    'learning_rate': [0.01, 0.1],
    'n_estimators': [100, 200],
    'max_depth': [3, 5, 7]
}
# Grid search
grid_xgb = GridSearchCV(xg_reg, param_grid_xgb,scoring='neg_root_mean_squared_error
grid_xgb.fit(X_train, y_train)

y_pred=  grid_xgb.predict(X_test)

print("Best XGB Params: ", grid_xgb.best_params_)
print("XGB Test RMSE: ", np.sqrt(mean_squared_error(y_test,y_pred)))


residuals = y_test- y_pred

plt.figure(figsize=(10, 6))
plt.scatter(y_pred, residuals)
plt.axhline(y=0, color='r', linestyle='--')
plt.xlabel('Predicted Values')
plt.ylabel('Residuals')
plt.title('Residual Plot')
plt.show()
```

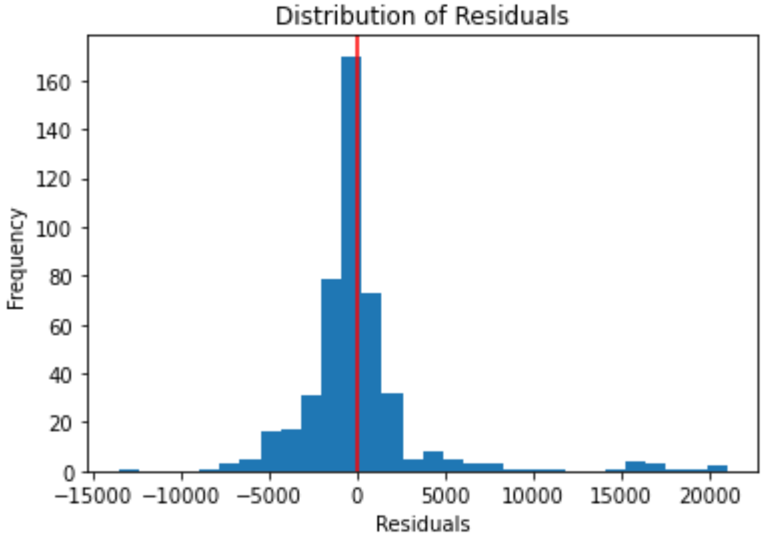
```
Best XGB Params:  {'learning_rate': 0.1, 'max_depth': 5, 'n_estimators': 100}
XGB Test RMSE:  3657.618489006806
```



In [ ]:
```
X_test.shape
```

Out[ ]:
```
(467, 13)
```

In [ ]:
```
plt.hist(residuals, bins=30)
plt.xlabel('Residuals')
plt.ylabel('Frequency')
plt.axvline(x = 0, color = 'r')
plt.title('Distribution of Residuals')
plt.show()
```



Observations

- The first run of my models with my initial data clean up and data engineering prove unseccesful in all models cases.
- Standardizing some of the deatures did not help as well
- The target variable has not bee modified, I will use log scale to maintain outlier integrity

Target log adjustment

In [ ]:
```
complete['log_charges'] = np.log1p(complete['charges'])
```

SGDR Trial # 5

In [ ]:
```
from sklearn.model_selection import train_test_split, cross_val_score, GridSearchCV
from sklearn.linear_model import SGDRegressor
import warnings


# Suppress DomainWarning
warnings.filterwarnings("ignore", category=FutureWarning)

from statsmodels.tools.sm_exceptions import ConvergenceWarning

# Suppress ConvergenceWarning
warnings.filterwarnings("ignore", category=ConvergenceWarning)


X = complete.drop(columns = ['charges', 'log_charges'])
Y = complete['log_charges']

X_train, X_test, y_train, y_test = train_test_split(X,Y, random_state = 50)
```

In [ ]:
```
sdg = SGDRegressor(random_state = 42)
```

In [ ]:

```
import warnings

# Suppress FutureWarning
warnings.filterwarnings("ignore", category=FutureWarning)

# Suppress DomainWarning
from statsmodels.tools.sm_exceptions import DomainWarning
warnings.filterwarnings("ignore", category=DomainWarning)

from statsmodels.tools.sm_exceptions import ConvergenceWarning

# Suppress ConvergenceWarning
warnings.filterwarnings("ignore", category=ConvergenceWarning)

param_grid = {
    'alpha': [0.0001, 0.001, 0.01, 0.1, 1, 10],
    'loss': ['squared_loss', 'huber'],
    'penalty': ['none', 'l2', 'l1', 'elasticnet'],
    'learning_rate': ['constant', 'optimal', 'invscaling', 'adaptive'],
    'eta0': [0.001, 0.01, 0.1]}

grid = GridSearchCV(sdg, param_grid, cv= 5,  scoring='neg_root_mean_squared_error')

grid.fit(X_train, y_train)

estimator = grid.best_estimator_

cv_results = cross_val_score(estimator, X_train, y_train, cv = 5)
```

```
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```

In [ ]:

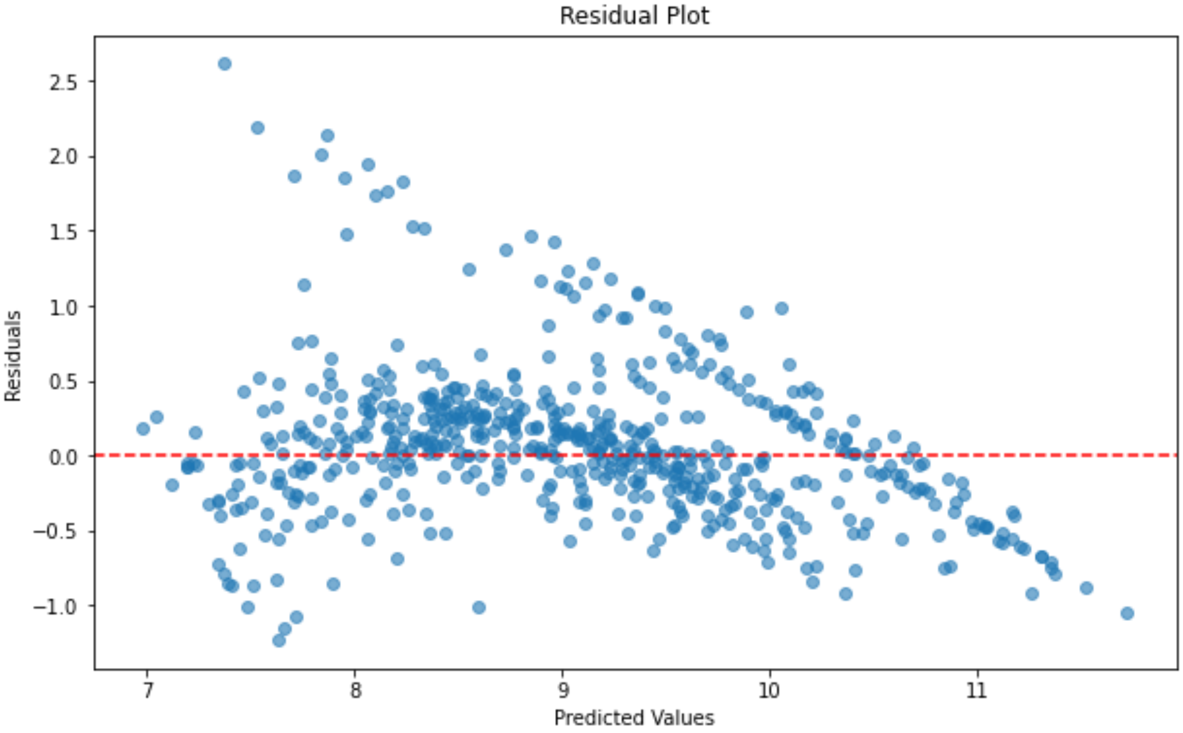
```python
print(f"Cross-validation scores: {cv_results}")
print(f"Mean Cross-validation score: {np.mean(cv_results)}")

y_pred = estimator.predict(X_test)

mse = mean_squared_error(y_test, y_pred)
print(f"Mean Squared Error: {mse}")

# To get the Root Mean Squared Error (RMSE), you can take the square root of the MS
rmse = np.sqrt(mse)
print(f"Root Mean Squared Error: {rmse}")
```

```
Cross-validation scores: [0.69058975 0.61751005 0.68974829 0.73647069 0.70310803]
Mean Cross-validation score: 0.6874853621420922
Mean Squared Error: 0.2593246540753813
Root Mean Squared Error: 0.509239289603013
```

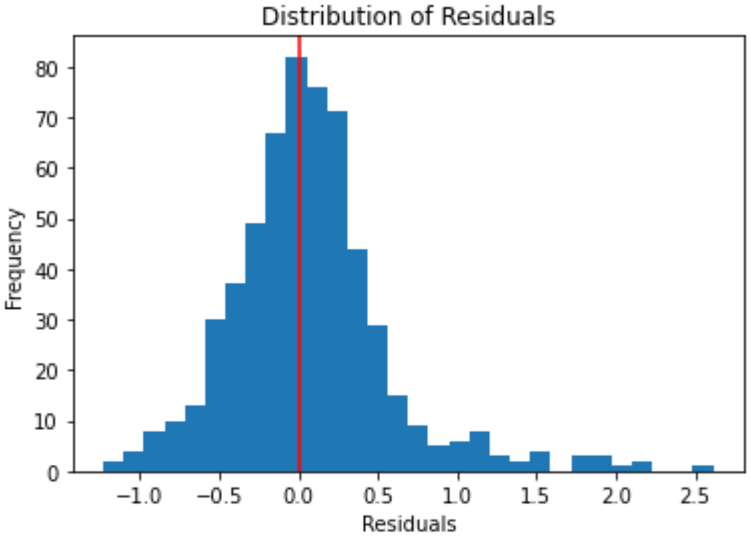
In [ ]:

```python
residuals = y_test- y_pred

plt.figure(figsize=(10, 6))
plt.scatter(y_pred, residuals, alpha = .6)
plt.axhline(y=0, color='r', linestyle='--')
plt.xlabel('Predicted Values')
plt.ylabel('Residuals')
plt.title('Residual Plot')
plt.show()
```



In [ ]:
```
plt.hist(residuals, bins=30)
plt.xlabel('Residuals')
plt.ylabel('Frequency')
plt.axvline(x = 0, color = 'r')
plt.title('Distribution of Residuals')
plt.show()
```



Trial # 6 Forest Regressor, target adjustment

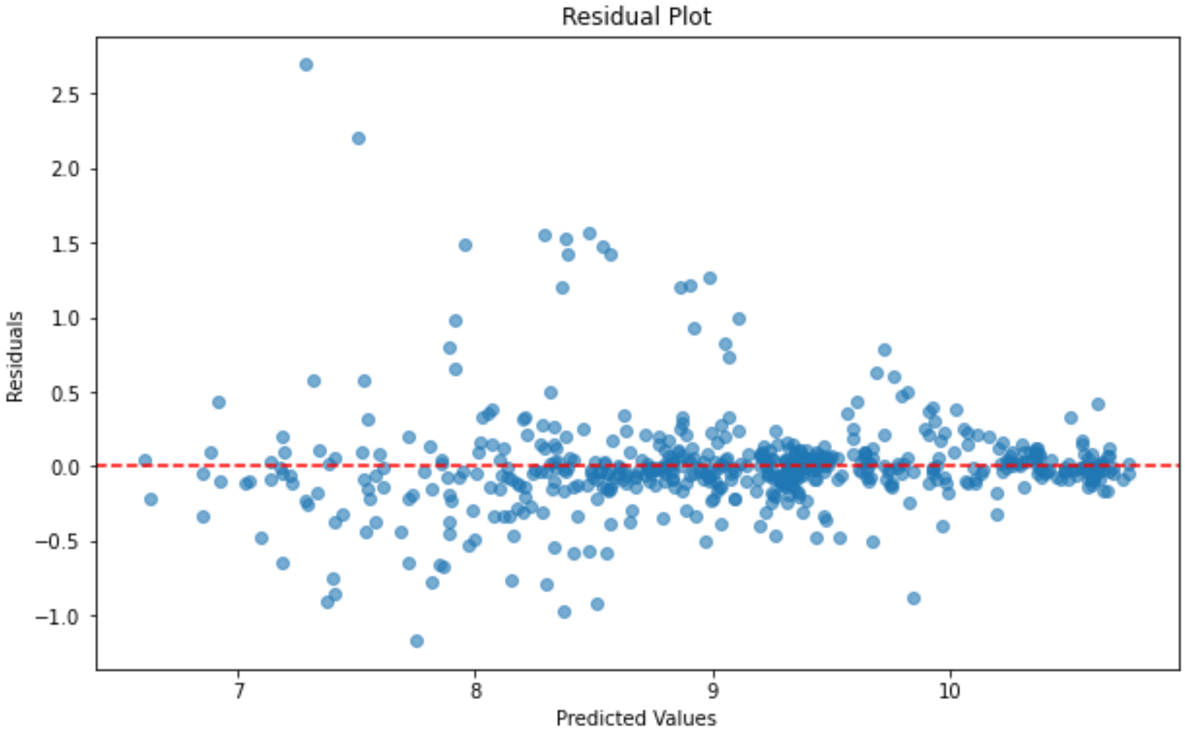
In [ ]:
```
from sklearn.ensemble import RandomForestRegressor
rf = RandomForestRegressor(random_state=42)
# Hyperparameter grid
param_grid = {
    'n_estimators': [50, 100, 200],
    'max_depth': [None, 10, 20, 30]
}
# Grid search
grid_rf = GridSearchCV(rf, param_grid,scoring='neg_root_mean_squared_error', cv=5)
grid_rf.fit(X_train, y_train)

y_pred = grid_rf.predict(X_test)
print("Best RF Params: ", grid_rf.best_params_)
print("RF Test RMSE: ", np.sqrt(mean_squared_error(y_test,y_pred)))


residuals = y_test- y_pred

plt.figure(figsize=(10, 6))
plt.scatter(y_pred, residuals, alpha = .6)
plt.axhline(y=0, color='r', linestyle='--')
plt.xlabel('Predicted Values')
plt.ylabel('Residuals')
plt.title('Residual Plot')
plt.show()
```

```
Best RF Params:  {'max_depth': 10, 'n_estimators': 100}
RF Test RMSE:  0.33668390466859094
```



In [ ]:
```
plt.hist(residuals, bins=30)
plt.xlabel('Residuals')
plt.ylabel('Frequency')
plt.axvline(x = 0, color = 'r')
plt.title('Distribution of Residuals')
plt.show()
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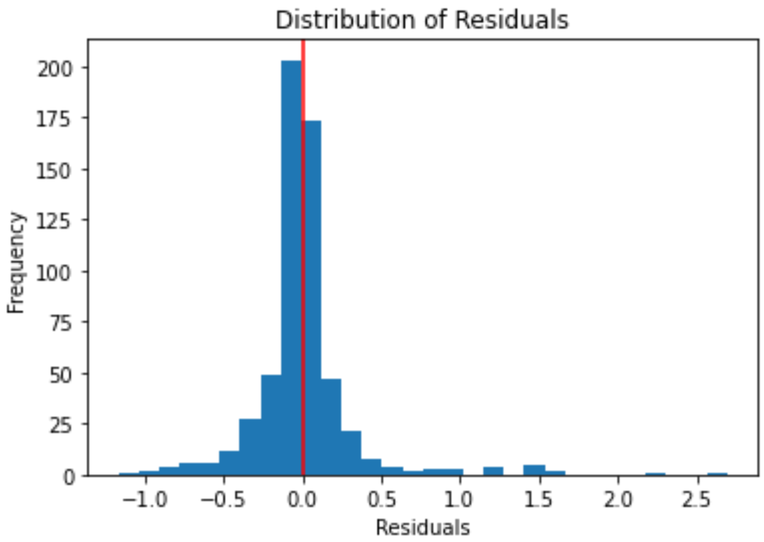


Trial # 7 XGB Target Adjustment

In [ ]:

```
import xgboost as xgb
xg_reg = xgb.XGBRegressor(objective='reg:squarederror', random_state=42)
# Hyperparameter grid
param_grid_xgb = {
    'learning_rate': [0.01, 0.1],
    'n_estimators': [100, 200],
    'max_depth': [3, 5, 7]
}
# Grid search
grid_xgb = GridSearchCV(xg_reg, param_grid_xgb,scoring='neg_root_mean_squared_error
grid_xgb.fit(X_train, y_train)

y_pred=  grid_xgb.predict(X_test)

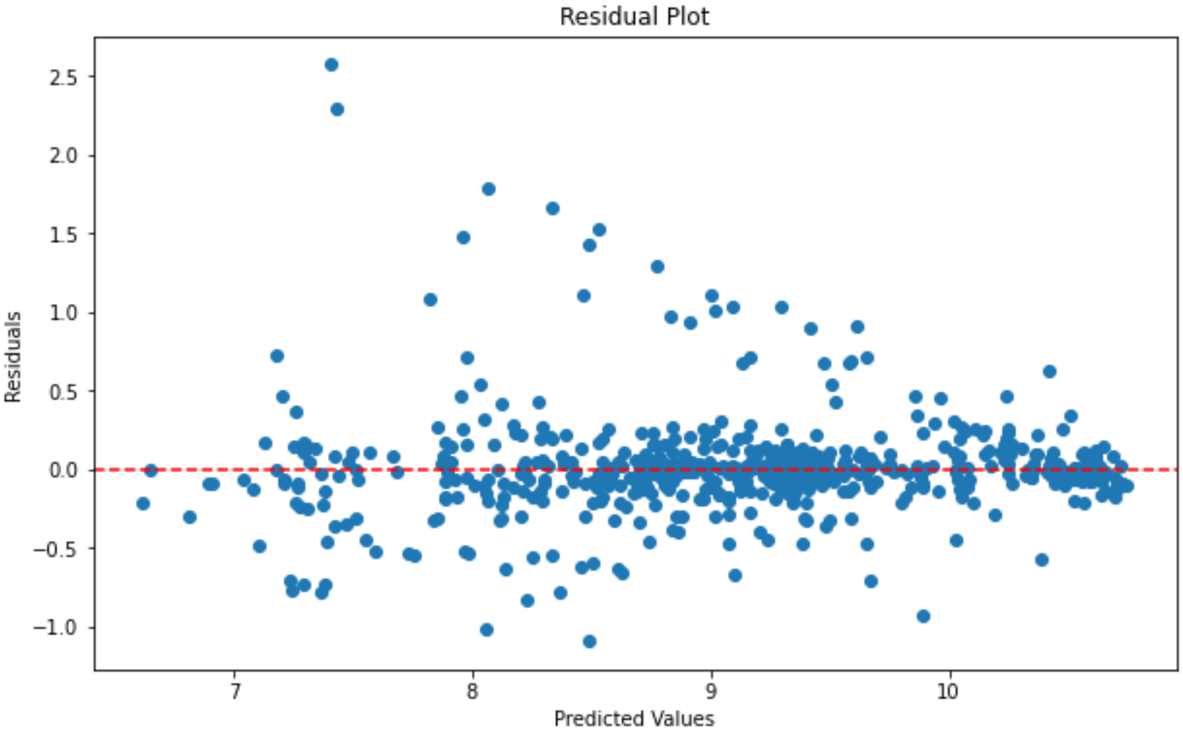
print("Best XGB Params: ", grid_xgb.best_params_)
print("XGB Test RMSE: ", np.sqrt(mean_squared_error(y_test,y_pred)))

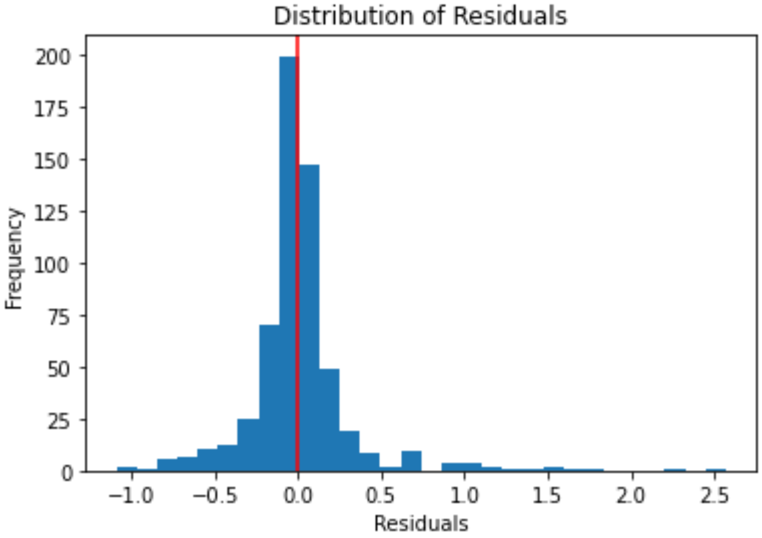

residuals = y_test- y_pred

plt.figure(figsize=(10, 6))
plt.scatter(y_pred, residuals)
plt.axhline(y=0, color='r', linestyle='--')
plt.xlabel('Predicted Values')
plt.ylabel('Residuals')
plt.title('Residual Plot')
plt.show()


plt.hist(residuals, bins=30)
plt.xlabel('Residuals')
plt.ylabel('Frequency')
plt.axvline(x = 0, color = 'r')
plt.title('Distribution of Residuals')
plt.show()
```

```
Best XGB Params:  {'learning_rate': 0.1, 'max_depth': 7, 'n_estimators': 100}
XGB Test RMSE:  0.33796427992413947
```





From Trials 5 to 7 you see much more promising predictions for our Model, changing the target value to a Log, greatly improved our results

Real Test Case Example:

Estimate the cost of hospitalization for Christopher, Ms. Jayna (her date of birth is 12/28/1988, height is 170 cm, and weight is 85 kgs). She lives in a tier 1 city and her state's State ID is R1011. She lives with her partner and two children. She was found to be nondiabetic (HbA1c = 5.8). She smokes but is otherwise healthy. She has had no transplants or major surgeries. Her father died of lung cancer. Hospitalization costs will be estimated using tier 1 hospitals.

- BMI needed to be caluculate

In [ ]:

```python
data ={
    'year':35,
    'children':2,
    'Hospital tier': 1,
    'City tier': 1,
    'State ID' : 2,
    'BMI': 29.41,
    'HBA1C': 5.8,
    'Heart Issues': 0,
    'Any Transplants': 0,
    'Cancer history': 1,
    'NumberOfMajorSurgeries':0,
    'smoker':1,
    'gender':1

}
```

In [ ]:

```python
lady_Test = pd.DataFrame(data, index = [0])
```

In [ ]:

```python
lady_Test
```

Out[ ]:

	year	children	Hospital tier	City tier	State ID	BMI	HBA1C	Heart Issues	Any Transplants	Cancer history	NumberOfMaj
0	35	2	1	1	2	29.41	5.8	0	0	1	

XGB Prediction

In [ ]:

```python
y_pred_XBG =  grid_xgb.predict(lady_Test)
```

In [ ]:

```python
xgb_ = np.exp(y_pred_XBG)
xgb_
```

Out[ ]:

```
array([20353.576], dtype=float32)
```

Random Forest Regressor Prediction

In [ ]:

```python
y_pred_RF = grid_rf.predict(lady_Test)
rf_ = np.exp(y_pred_RF)
rf_
```

Out[ ]:
```
array([22257.76501075])
```

SGDR Prediction

In [ ]:
```
y_pred_SGDR = estimator.predict(lady_Test)
sgdr_ = np.exp(y_pred_SGDR)
sgdr_
```

Out[ ]:
```
array([21889.49748076])
```

Predicted Cost

In [ ]:
```
predicted_value_total = (xgb_ + rf_ + sgdr_) / 3
predicted_value_total
```

Out[ ]:
```
array([21500.27955446])
```

In [ ]:
```
complete.to_csv('complete.csv', index = False)
```

In [ ]:
```
complete
```

Out[ ]:

	year	children	charges	Hospital tier	City tier	State ID	BMI	HBA1C	Heart Issues	Any Transplants	Cancer history
0	31.0	0	563.84	2	3	0	17.580	4.51	0	0	0
1	31.0	0	570.62	2	1	0	17.600	4.39	0	0	0
2	30.0	0	600.00	2	1	0	16.470	6.35	0	0	1
3	31.0	0	604.54	3	3	0	17.700	6.28	0	0	0
4	25.0	0	637.26	3	3	0	22.340	5.57	0	0	0
...	...	...	...	...	...	...	...	...	...	...	...
2330	34.0	0	55135.40	1	2	1	35.530	5.45	0	0	0
2331	32.0	1	58571.07	1	3	3	38.095	6.05	0	0	0
2332	53.0	3	60021.40	1	1	1	34.485	11.87	1	0	0
2333	46.0	0	62592.87	2	3	0	30.360	5.77	0	0	0
2334	55.0	0	63770.43	1	3	0	47.410	7.47	0	0	0

2335 rows × 15 columns

In [ ]: