Healthcare Insurance Analysis

Problem Statement:

A significant public health concern is the rising cost of healthcare. Therefore, it's crucial to be able to predict future costs and gain a solid understanding of their causes. The insurance industry must also take this analysis seriously. This analysis may be used by healthcare insurance providers to make a variety of strategic and tactical decisions

.

Objectives:

The objective of this project is to predict patients' healthcare costs and to identify factors contributing to this prediction. It will also be useful to learn the interdependencies of different factors and comprehend the significance of various tools at various stages of the healthcare cost prediction process.

Dataset Description:

Hospitalization details.xlsx
Medical Examinations.xlsx
Names.xlsx

ANALYSIS:

Data science/data analysis:

1. **Collate the files so that all the information is in one place**

1. Collate the files so that all the information is in one place

```
df = pd.merge(pd.merge(hospital,medical,on='Customer ID'),customer,on='Customer ID')
```

```
df
```

	Customer ID	year	month	date	children	charges	Hospital tier	City tier	State ID	BMI	HBA1C	Heart Issues	Any Transplants	Cancer history	NumberOfMajorSurgeries	smoker
0	Id2335	1992	Jul	9	0	563.84	tier - 2	tier - 3	R1013	17.580	4.51	No	No	No	1	No
1	Id2334	1992	Nov	30	0	570.62	tier - 2	tier - 1	R1013	17.600	4.39	No	No	No	1	No
2	Id2333	1993	Jun	30	0	600.00	tier - 2	tier - 1	R1013	16.470	6.35	No	No	Yes	1	No
3	Id2332	1992	Sep	13	0	604.54	tier - 3	tier - 3	R1013	17.700	6.28	No	No	No	1	No
4	Id2331	1998	Jul	27	0	637.26	tier - 3	tier - 3	R1013	22.340	5.57	No	No	No	1	No
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
2330	Id5	1989	Jun	19	0	55135.40	tier - 1	tier - 2	R1012	35.530	5.45	No	No	No	No major surgery	yes
2331	Id4	1991	Jun	6	1	58571.07	tier - 1	tier - 3	R1024	38.095	6.05	No	No	No	No major surgery	yes
2332	Id3	1970	?	11	3	60021.40	tier - 1	tier - 1	R1012	34.485	11.87	yes	No	No	2	yes
2333	Id2	1977	Jun	8	0	62592.87	tier - 2	tier - 3	R1013	30.360	5.77	No	No	No	No major surgery	yes
2334	Id1	1968	Oct	12	0	63770.43	tier - 1	tier - 3	R1013	47.410	7.47	No	No	No	No major surgery	yes

2335 rows × 17 columns

```
df.shape
```

```
(2335, 17)
```

```
df.describe()
```

	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

2. Check for missing values in the dataset

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```
df.isna().sum().sum()
```

```
0
```

- There are no missing values in the dataset

3. Find the percentage of rows that have trivial value (for example, ?), and delete such rows if they do not contain significant information

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```
In [101]: trivial= df[df == "?"].count(axis=1).sum()

In [102]: trivial
Out[102]: 11

In [103]: trivial.shape
Out[103]: ()

In [104]: total= df.shape[0]
          total
Out[104]: 2335

In [105]: percentage = (trivial / total_rows) * 100

In [106]: percentage
Out[106]: 0.47109207708779444
```

- 0.47109 % of rows contain the trivial values.

```
In [107]: print("Percentage of trivial rows: {:.2f}%".format(percentage))

          Percentage of trivial rows: 0.47%

In [108]: df = df[df != "?"].dropna()

In [109]: df.shape
Out[109]: (2325, 17)
```

4. Use the necessary transformation methods to deal with the nominal and ordinal categorical variables in the dataset

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```
110]: df_cat = df.select_dtypes(exclude='number')
```

```
111]: df_cat.columns
```

```
111]: Index(['Customer ID', 'year', 'month', 'Hospital tier', 'City tier',
        'State ID', 'Heart Issues', 'Any Transplants', 'Cancer history',
        'NumberOfMajorSurgeries', 'smoker', 'name'],
       dtype='object')
```

```
112]: df['Heart Issues'].value_counts()
```

```
112]: Heart Issues
      No     1405
      yes     920
      Name: count, dtype: int64
```

```
113]: df['Any Transplants'].value_counts()
```

```
113]: Any Transplants
      No     2183
      yes     142
      Name: count, dtype: int64
```

```
In [115]: df['smoker'].value_counts()
```

```
Out[115]: smoker
          No     1839
          yes     486
          Name: count, dtype: int64
```

```
In [116]: from sklearn.preprocessing import LabelEncoder
          le= LabelEncoder()
```

```
In [117]: df["Heart Issues"]=le.fit_transform(df["Heart Issues"])
          df["Any Transplants"]=le.fit_transform(df["Any Transplants"])
          df["Cancer history"]=le.fit_transform(df["Cancer history"])
          df["smoker"]=le.fit_transform(df["smoker"])
```

```
In [118]: df["Heart Issues"].value_counts()
```

```
Out[118]: Heart Issues
          0    1405
          1     920
          Name: count, dtype: int64
```

- Hospital tier and city tier are ordinal categorical variables

```
In [119]: def fun(val):
              return int(val.replace("tier", "").replace(" ", "").replace("-", ""))
```

```
In [120]: df['Hospital tier'] = df['Hospital tier'].map(fun)
```

```
In [121]: df['City tier'] = df['City tier'].map(fun)
```

```
In [122]: df
```

Out[122]:

	Customer ID	year	month	date	children	charges	Hospital tier	City tier	State ID	BMI	HBA1C	Heart Issues	Any Transplants	Cancer history	NumberOfMajorSurgeries	smoker
0	Id2335	1992	Jul	9	0	563.84	2	3	R1013	17.580	4.51	0	0	0	1	0
1	Id2334	1992	Nov	30	0	570.62	2	1	R1013	17.600	4.39	0	0	0	1	0
2	Id2333	1993	Jun	30	0	600.00	2	1	R1013	16.470	6.35	0	0	1	1	0
3	Id2332	1992	Sep	13	0	604.54	3	3	R1013	17.700	6.28	0	0	0	1	0
4	Id2331	1998	Jul	27	0	637.26	3	3	R1013	22.340	5.57	0	0	0	1	0
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
2329	Id6	1962	Aug	4	0	52590.83	1	3	R1011	32.800	6.59	0	0	0	No major surgery	1
2330	Id5	1989	Jun	19	0	55135.40	1	2	R1012	35.530	5.45	0	0	0	No major surgery	1
2331	Id4	1991	Jun	6	1	58571.07	1	3	R1024	38.095	6.05	0	0	0	No major surgery	1
2333	Id2	1977	Jun	8	0	62592.87	2	3	R1013	30.360	5.77	0	0	0	No major surgery	1
2334	Id1	1968	Oct	12	0	63770.43	1	3	R1013	47.410	7.47	0	0	0	No major surgery	1

2325 rows × 17 columns

```
In [123]: df['Hospital tier'].value_counts()
```

```
Out[123]: Hospital tier
          2    1334
          3     691
          1     300
          Name: count, dtype: int64
```

5.The dataset has State ID, which has around 16 states. All states are not represented in equal proportions in the data. Creating dummy variables for all regions may also result in too many insignificant predictors. Nevertheless, only R1011, R1012, and R1013 are worth investigating further. Create a suitable strategy to create dummy variables with these restraints.

5.The dataset has State ID, which has around 16 states. All states are not represented in equal proportions in the data. Creating dummy variables for all regions may also result in too many insignificant predictors. Nevertheless, only R1011, R1012, and R1013 are worth investigating further. Create a suitable strategy to create dummy variables with these restraints.

24]:
```
df['State ID'].value_counts()
```

24]:
```
State ID
R1013    609
R1011    574
R1012    572
R1024    159
R1026     84
R1021     70
R1016     64
R1025     40
R1023     38
R1017     36
R1019     26
R1022     14
R1014     13
R1015     11
R1018      9
R1020      6
Name: count, dtype: int64
```

```
Dummies = pd.get_dummies(df["State ID"], prefix= "State_ID")
Dummies
```

	State_ID_R1011	State_ID_R1012	State_ID_R1013	State_ID_R1014	State_ID_R1015	State_ID_R1016	State_ID_R1017	State_ID_R1018	State_ID_R1019	Stat
0	False	False	True	False	False	False	False	False	False	
1	False	False	True	False	False	False	False	False	False	
2	False	False	True	False	False	False	False	False	False	
3	False	False	True	False	False	False	False	False	False	
4	False	False	True	False	False	False	False	False	False	
...	...	...	...	...	...	...	...	...	...	
2329	True	False	False	False	False	False	False	False	False	
2330	False	True	False	False	False	False	False	False	False	
2331	False	False	False	False	False	False	False	False	False	
2333	False	False	True	False	False	False	False	False	False	
2334	False	False	True	False	False	False	False	False	False	

2325 rows × 16 columns

```python
Dummy = Dummies[['State_ID_R1011','State_ID_R1012', 'State_ID_R1013']]
Dummy
```

	State_ID_R1011	State_ID_R1012	State_ID_R1013
0	False	False	True
1	False	False	True
2	False	False	True
3	False	False	True
4	False	False	True
...	...	...	...
2329	True	False	False
2330	False	True	False
2331	False	False	False
2333	False	False	True
2334	False	False	True

2325 rows × 3 columns

```python
n [128]: df
```

ut[128]:

	Customer ID	year	month	date	children	charges	Hospital tier	City tier	State ID	BMI	HBA1C	Heart Issues	Any Transplants	Cancer history	NumberOfMajorSurgeries	smc
0	Id2335	1992	Jul	9	0	563.84	2	3	R1013	17.580	4.51	0	0	0	1	
1	Id2334	1992	Nov	30	0	570.62	2	1	R1013	17.600	4.39	0	0	0	1	
2	Id2333	1993	Jun	30	0	600.00	2	1	R1013	16.470	6.35	0	0	1	1	
3	Id2332	1992	Sep	13	0	604.54	3	3	R1013	17.700	6.28	0	0	0	1	
4	Id2331	1998	Jul	27	0	637.26	3	3	R1013	22.340	5.57	0	0	0	1	
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
2329	Id6	1962	Aug	4	0	52590.83	1	3	R1011	32.800	6.59	0	0	0	No major surgery	
2330	Id5	1989	Jun	19	0	55135.40	1	2	R1012	35.530	5.45	0	0	0	No major surgery	
2331	Id4	1991	Jun	6	1	58571.07	1	3	R1024	38.095	6.05	0	0	0	No major surgery	
2333	Id2	1977	Jun	8	0	62592.87	2	3	R1013	30.360	5.77	0	0	0	No major surgery	
2334	Id1	1968	Oct	12	0	63770.43	1	3	R1013	47.410	7.47	0	0	0	No major surgery	

2325 rows × 20 columns

6. The variable NumberOfMajorSurgeries also appears to have string values. Apply a suitable method to clean up this variable

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```
]: df['NumberOfMajorSurgeries'] = df['NumberOfMajorSurgeries'].replace('No major surgery',0)

]: df['NumberOfMajorSurgeries'].value_counts()

]: NumberOfMajorSurgeries
   0    1070
   1     961
   2     272
   3      22
   Name: count, dtype: int64
```

7. Age appears to be a significant factor in this analysis. Calculate the patients' ages based on their dates of birth

7. Age appears to be a significant factor in this analysis. Calculate the patients' ages based on their dates of birth.

```
31]: df['year'] = pd.to_datetime(df['year'], format='%Y').dt.year
     df['year']

31]: 0       1992
     1       1992
     2       1993
     3       1992
     4       1998
             ...
     2329    1962
     2330    1989
     2331    1991
     2333    1977
     2334    1968
     Name: year, Length: 2325, dtype: int32

32]: df['month'] = pd.to_datetime(df['month'], format='%b').dt.month
     df['month']

32]: 0        7
     1       11
     2        6
     3        9
     4        7
             ..
     2329     8
     2330     6
     2331     6
     2333     6
     2334    10
     Name: month, Length: 2325, dtype: int32
```

```
[133]: df['DateInt'] = df['year'].astype(str) + df['month'].astype(str).str.zfill(2) + df['date'].astype(str).str.zfill(2)
```

```
[134]: df['DOB'] = pd.to_datetime(df.DateInt, format='%Y%m%d')
```

```
[135]: df.drop(['DateInt'], inplace=True, axis=1)
```

```
[136]: import datetime as dt
       current_date = dt.datetime.now()
```

```
[137]: df['Age'] = (((current_date-df.DOB).dt.days)/365).astype(int)
```

```
[138]: df.head()
```

[138]:

	Customer ID	year	month	date	children	charges	Hospital tier	City tier	State ID	BMI	...	Any Transplants	Cancer history	NumberOfMajorSurgeries	smoker	nam
0	Id2335	1992	7	9	0	563.84	2	3	R1013	17.58	...	0	0	1	0	Germa Mr. Aarc
1	Id2334	1992	11	30	0	570.62	2	1	R1013	17.60	...	0	0	1	0	Rosendah Mr. Evan
2	Id2333	1993	6	30	0	600.00	2	1	R1013	16.47	...	0	1	1	0	Alban Ms. Jul
3	Id2332	1992	9	13	0	604.54	3	3	R1013	17.70	...	0	0	1	0	River Gonzale Mr. Juan S
4	Id2331	1998	7	27	0	637.26	3	3	R1013	22.34	...	0	0	1	0	Brietzk Mr. Jorda

5 rows × 22 columns

```
In [139]: df.tail()
```

Out[139]:

	Customer ID	year	month	date	children	charges	Hospital tier	City tier	State ID	BMI	...	Any Transplants	Cancer history	NumberOfMajorSurgeries	smoker	
2329	Id6	1962	8	4	0	52590.83	1	3	R1011	32.800	...	0	0	0	1	R
2330	Id5	1989	6	19	0	55135.40	1	2	R1012	35.530	...	0	0	0	1	Ka k
2331	Id4	1991	6	6	1	58571.07	1	3	R1024	38.095	...	0	0	0	1	Ost k
2333	Id2	1977	6	8	0	62592.87	2	3	R1013	30.360	...	0	0	0	1	L Ma
2334	Id1	1968	10	12	0	63770.43	1	3	R1013	47.410	...	0	0	0	1	H

5 rows × 22 columns

```
In [140]: df
```

Out[140]:

	Customer ID	year	month	date	children	charges	Hospital tier	City tier	State ID	BMI	...	Any Transplants	Cancer history	NumberOfMajorSurgeries	smoker	
0	Id2335	1992	7	9	0	563.84	2	3	R1013	17.580	...	0	0	1	0	M
1	Id2334	1992	11	30	0	570.62	2	1	R1013	17.600	...	0	0	1	0	Ros Mr.
2	Id2333	1993	6	30	0	600.00	2	1	R1013	16.470	...	0	1	1	0	M
3	Id2332	1992	9	13	0	604.54	3	3	R1013	17.700	...	0	0	1	0	G Mr.
4	Id2331	1998	7	27	0	637.26	3	3	R1013	22.340	...	0	0	1	0	Mr
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
2329	Id6	1962	8	4	0	52590.83	1	3	R1011	32.800	...	0	0	0	1	B R
2330	Id5	1989	6	19	0	55135.40	1	2	R1012	35.530	...	0	0	0	1	Ms
2331	Id4	1991	6	6	1	58571.07	1	3	R1024	38.095	...	0	0	0	1	C Ms
2333	Id2	1977	6	8	0	62592.87	2	3	R1013	30.360	...	0	0	0	1	Lel Ma
2334	Id1	1968	10	12	0	63770.43	1	3	R1013	47.410	...	0	0	0	1	Ha

2325 rows × 22 columns

8. The gender of the patient may be an important factor in determining the cost of hospitalization. The salutations in a beneficiary's name can be used to determine their gender. Make a new field for the beneficiary's gender.

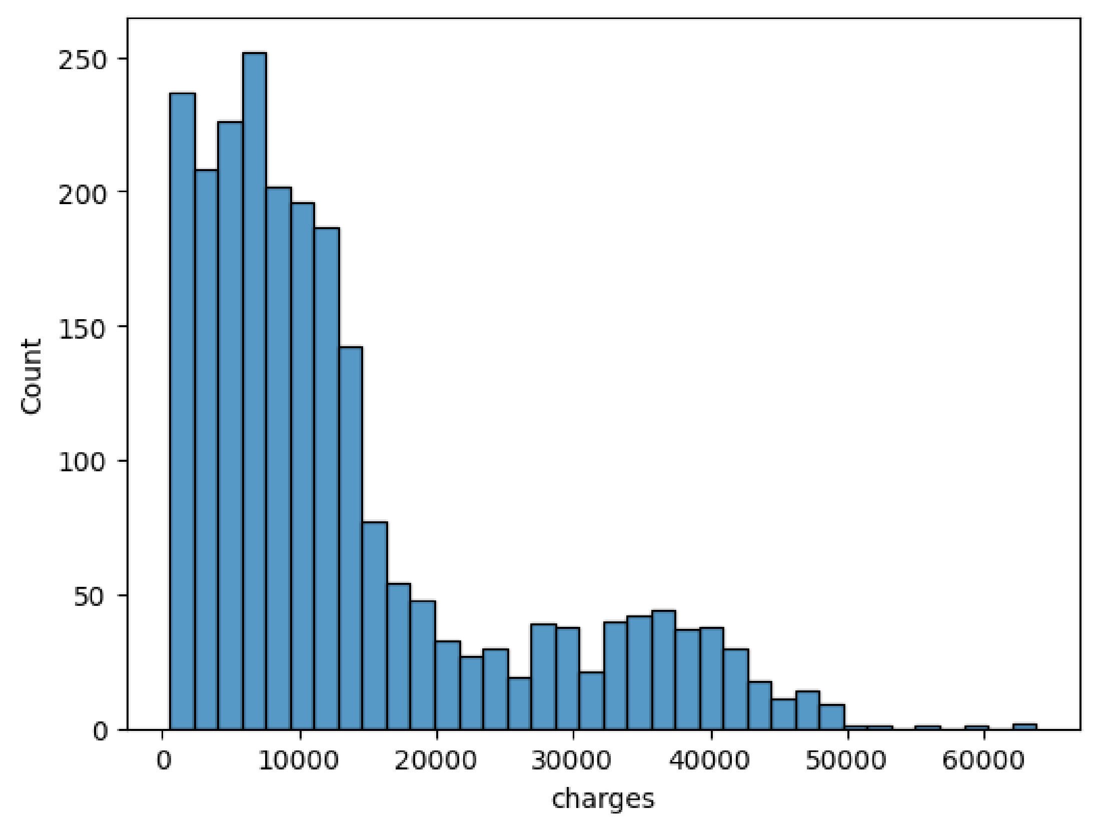
```
In [141]: def gen(x):
              if 'Ms.' in x:
                  return 0
              else:
                  return 1
```

```
In [142]: df['Gender'] = df['name'].map(gen)
```

```
In [143]: df['Gender']
```

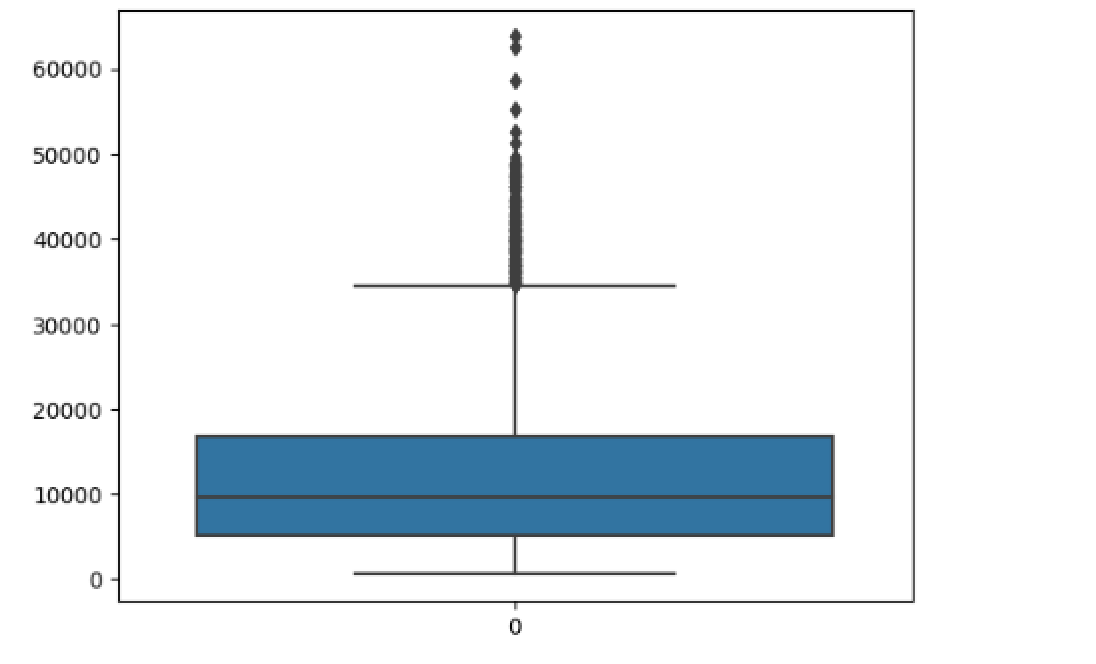
```
Out[143]: 0       1
          1       1
          2       0
          3       1
          4       1
                 ..
          2329    1
          2330    0
          2331    0
          2333    1
          2334    0
          Name: Gender, Length: 2325, dtype: int64
```

9. You should also visualize the distribution of costs using a histogram, box and whisker plot, and swarm plot.

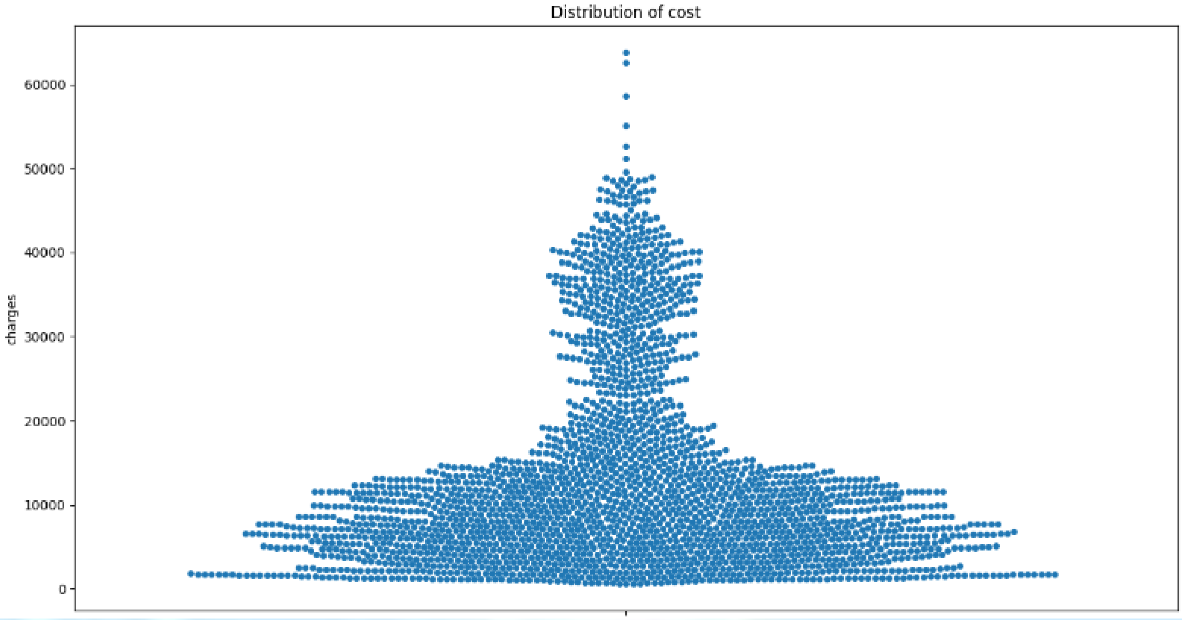



```
# box and whisker plot
sns.boxplot(df['charges'])
```

<Axes: >



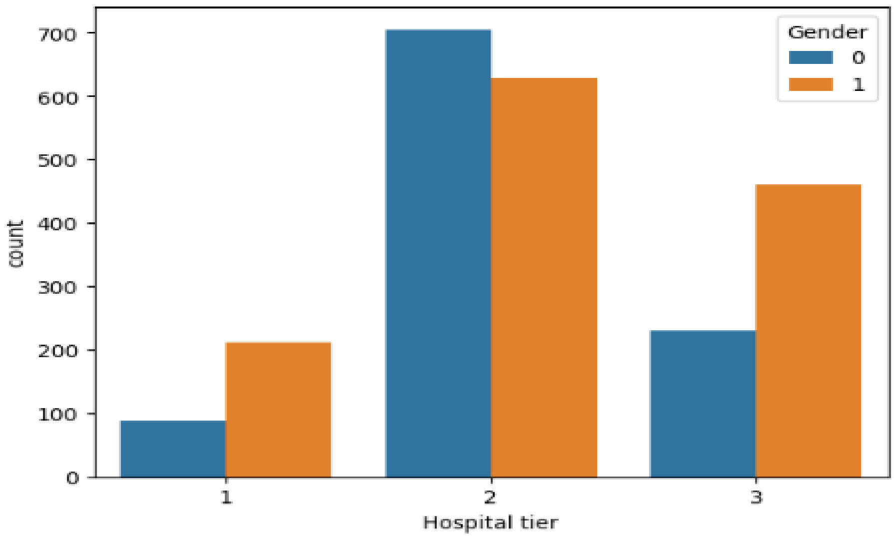
```python
# Swarm Plot
plt.figure(figsize=(15,8))
sns.swarmplot(df['charges'])
plt.title('Distribution of cost')
plt.show()
```



10. State how the distribution is different across gender and tiers of hospitals

```python
sns.countplot(data = df,x = 'Hospital tier', hue = 'Gender')
```

```
<Axes: xlabel='Hospital tier', ylabel='count'>
```



- In above plot 0 indicates female and 1 indicates male.
- In Hospital tier 1 and 3 we can see that, the count of females are less than compared to the tier 2.

11. Create a radar chart to showcase the median hospitalization cost for each tier of hospitals

11. Create a radar chart to showcase the median hospitalization cost for each tier of hospitals

```
n [149]: df[df['Hospital tier']==1].charges.median()
ut[149]: 32097.434999999998

n [150]: df[df['Hospital tier']==2].charges.median()
ut[150]: 7168.76

n [151]: df[df['Hospital tier']==3].charges.median()
ut[151]: 10676.83
```

```
import plotly.graph_objects as go
import pandas as pd

df1 = df1 = pd.DataFrame(dict(
    r=[32097.434999999998, 7168.76, 10676.83],
    theta=['Tier 1', 'Tier 2', 'Tier 3']
))

df2 = pd.concat([df1, df1.iloc[0]], ignore_index=True)

fig = go.Figure(data=go.Scatterpolar(
    r=df2['r'],
    theta=df2['theta'],
    fill='toself'
))

fig.update_layout(polar=dict(radialaxis=dict(visible=True, range=[0, 35000])))

fig.show()
```

12. Create a frequency table and a stacked bar chart to visualize the count of people in the different tiers of cities and hospitals

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```
city_freq = df["City tier"].value_counts().rename_axis('City&hospital_tier').reset_index(name='city_counts')
```

```
hospital_freq = df["Hospital tier"].value_counts().rename_axis('City&hospital_tier').reset_index(name='hospital_counts')
```

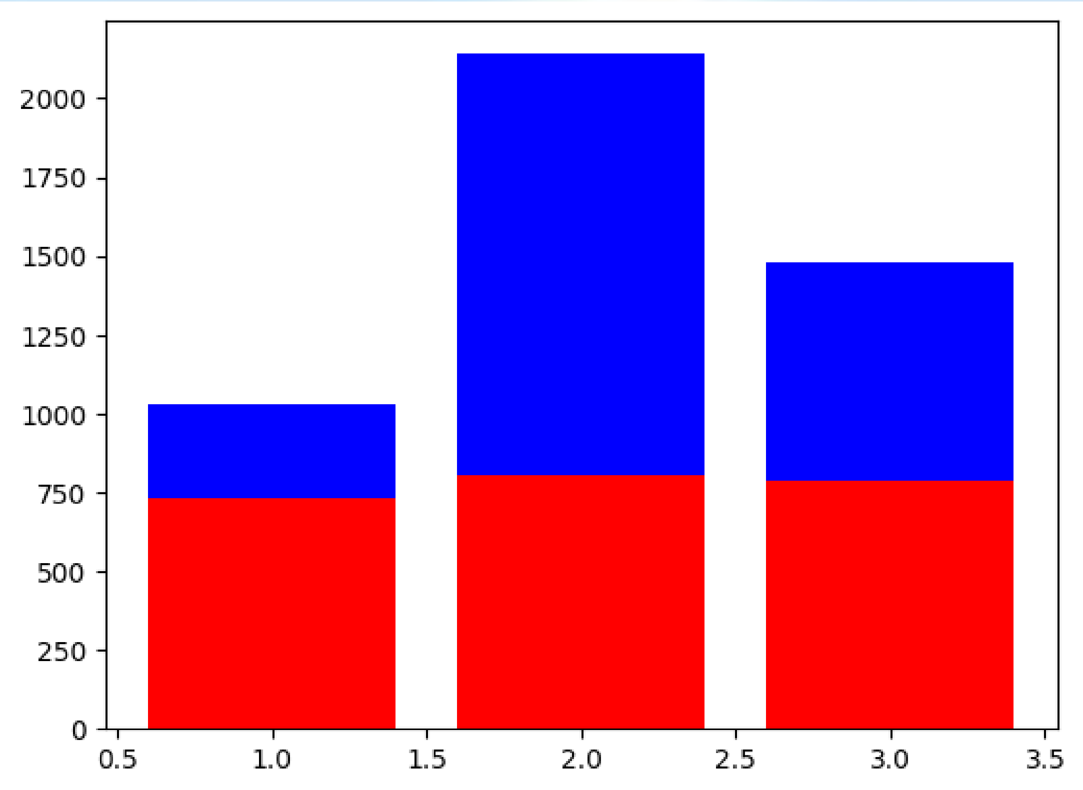
```
freq_table = pd.merge(city_freq, hospital_freq, on = 'City&hospital_tier')
```

```
freq_table
```

	City&hospital_tier	city_counts	hospital_counts
0	2	807	1334
1	3	789	691
2	1	729	300

```
x = freq_table['City&hospital_tier']
y1 = freq_table['city_counts']
y2 = freq_table['hospital_counts']

# plot bars in stack manner
plt.bar(x, y1, color='r')
plt.bar(x, y2, bottom=y1, color='b')
plt.show()
```



13. Test the following null hypotheses:
a. The average hospitalization costs for the three types of hospitals are not significantly different
b. The average hospitalization costs for the three types of cities are not significantly different c. The average hospitalization cost for smokers is not significantly different from the average cost for nonsmokers d. Smoking and heart issues are independent

```
from scipy.stats import ttest_1samp
import scipy.stats as stats
```

a. The average hospitalization costs for the three types of hospitals are not significantly different

```
print('Null Hypothesis => Average hospitalization costs for the three types of hospitals are not significantly different.')
f_val, p_val = stats.f_oneway(df[df['Hospital tier'] == 'tier,1']['charges'],
                              df[df['Hospital tier'] == 'tier,2']['charges'],
                              df[df['Hospital tier'] == 'tier,3']['charges'])
print('P-value :',p_val)
if p_val < 0.05:
    print("Reject null hypothesis")
else:
    print("Accept null hypothesis")
```

```
Null Hypothesis => Average hospitalization costs for the three types of hospitals are not significantly different.
P-value : nan
Accept null hypothesis
```

We already found the median cost of tier 1 hospitals: 32097.434999999998, median cost of tier 2 hospitals: 7168.76 and .median cost of tier 3 hospitals: 10676.83. Interpretation H0: the distributions of all samples are equal and H1: the distributions of one or more samples are not equal

```
[77]: from scipy.stats import friedmanchisquare
data1 = [32097.43]
data2 = [7168.76]
data3 = [10676.83]
stat, p = friedmanchisquare(data1, data2, data3)
print('stat=%.3f, p=%.3f' % (stat, p))
if p > 0.05:
    print('Probably the same distribution')
else:
    print('Probably different distributions')

stat=2.000, p=0.368
Probably the same distribution
```

b. The average hospitalization costs for the three types of cities are not significantly different

```
[78]: print("median cost of tier 1 city:", df[df["City tier"]==1].charges.median())
print("median cost of tier 2 city:", df[df["City tier"]==2].charges.median())
print("median cost of tier 3 city:", df[df["City tier"]==3].charges.median())

median cost of tier 1 city: 10027.15
median cost of tier 2 city: 8968.33
median cost of tier 3 city: 9880.07
```

```
[79]: data1 = [10027.15]
data2 = [8968.33]
data3 = [9880.07]
stat, p = friedmanchisquare(data1, data2, data3)
print('stat=%.3f, p=%.3f' % (stat, p))
if p > 0.05:
    print('Probably the same distribution')
else:
    print('Probably different distributions')

stat=2.000, p=0.368
Probably the same distribution
```

```
]: print('Null Hypothesis => Average hospitalization costs for the three types of cities are not significantly different.')
f_val, p_val = stats.f_oneway(df[df['City tier'] == 'tier,1']['charges'],
                              df[df['City tier'] == 'tier,2']['charges'],
                              df[df['City tier'] == 'tier,3']['charges'])
print('P-value :',p_val)
if p_val < 0.05:
    print("Reject null hypothesis")
else:
    print("Accept null hypothesis")

Null Hypothesis => Average hospitalization costs for the three types of cities are not significantly different.
P-value : nan
Accept null hypothesis
```

c. The average hospitalization cost for smokers is not significantly different from the average cost for nonsmokers

```
]: print("median cost of smoker:", df[df["smoker"]==1].charges.median())
print("median cost of non smoker:", df[df["smoker"]==0].charges.median())

median cost of smoker: 34125.475
median cost of non smoker: 7537.16
```

```
]: from scipy.stats import kruskal
data1 = [34125.475]
data2 = [7537.16]
stat, p = kruskal(data1, data2)
print('stat=%.3f, p=%.3f' % (stat, p))
if p > 0.05:
    print('Probably the same distribution')
else:
    print('Probably different distributions')

stat=1.000, p=0.317
Probably the same distribution
```

```
print('Null Hypothesis => Average hospitalization costs for smokers is not significantly different from the average cost for nonsmoke
t_val, p_val = stats.ttest_ind(df[df['smoker'] == 'yes']['charges'],
                               df[df['smoker'] == 'no']['charges'])

print('P-value :',p_val)
if p_val < 0.05:
    print("Reject null hypothesis")
else:
    print("Accept null hypothesis")
```

```
Null Hypothesis => Average hospitalization costs for smokers is not significantly different from the average cost for nonsmokers.
P-value : nan
Accept null hypothesis
```

- Interpretation H0: the two samples are independent. H1: there is a dependency between the samples.

d. Smoking and heart issues are independent

```
# d. Smoking and heart issues are independent
from scipy.stats import chi2_contingency
table = [[df["Heart Issues"].value_counts()],[df["smoker"].value_counts()]]
stat, p, dof, expected = chi2_contingency(table)
print('stat=%.3f, p=%.3f' % (stat, p))
if p > 0.05:
    print('Probably independent')
else:
    print('Probably dependent')
```

```
stat=191.145, p=0.000
Probably dependent
```

```
from scipy.stats import chi2_contingency
contingency_table = pd.crosstab(df['smoker'], df['Heart Issues'])
chi2, p, dof, expected = chi2_contingency(contingency_table)
print(f'P-value = {p}')
if p < 0.05:
    print("Reject the null hypothesis, Smoking and heart issues are independent.")
else:
    print("Accept null hypothesis, Smoking and heart issues are independent.")
```

```
P-value = 0.7694797581780767
Accept null hypothesis, Smoking and heart issues are independent.
```

Machine Learning

1.Examine the correlation between predictors to identify highly correlated predictors. Use a heatmap to visualize this.

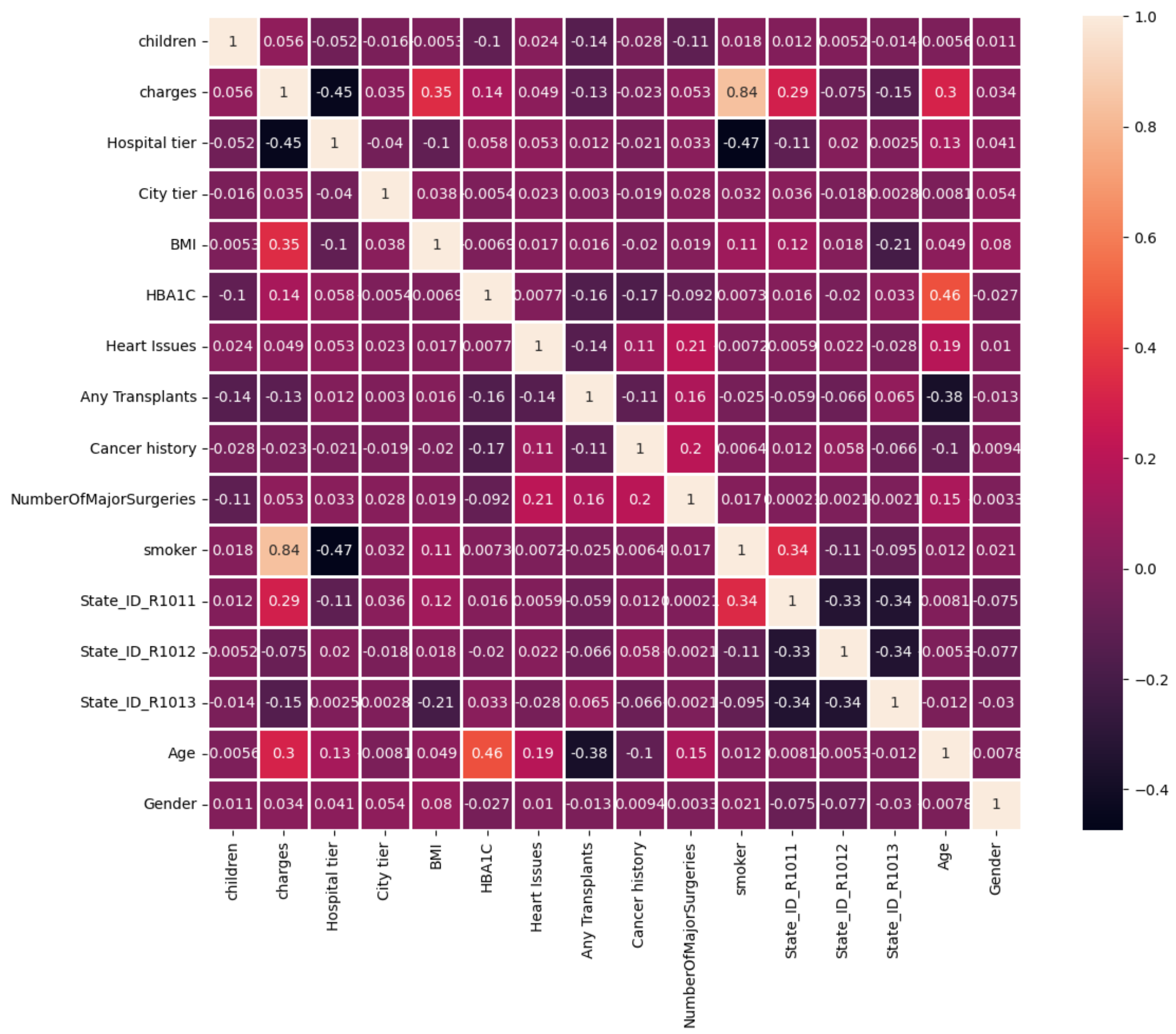
1.Examine the correlation between predictors to identify highly correlated predictors. Use a heatmap to visualize this.

```
df.drop(["Customer ID","State ID",'name', 'year', 'month', 'date', 'DOB'], inplace=True, axis=1)
```

```
df.head()
```

	children	charges	Hospital tier	City tier	BMI	HBA1C	Heart Issues	Any Transplants	Cancer history	NumberOfMajorSurgeries	smoker	State_ID_R1011	State_ID_R1012
0	0	563.84	2	3	17.58	4.51	0	0	0	1	0	False	False
1	0	570.62	2	1	17.60	4.39	0	0	0	1	0	False	False
2	0	600.00	2	1	16.47	6.35	0	0	1	1	0	False	False
3	0	604.54	3	3	17.70	6.28	0	0	0	1	0	False	False
4	0	637.26	3	3	22.34	5.57	0	0	0	1	0	False	False

```
plt.figure(figsize=(15,10))
sns.heatmap(df.corr(),square=True,annot=True,linewidths=1)
```



3. **Develop and evaluate the final model using regression with a stochastic gradient descent optimizer. Also, ensure that you apply all the following suggestions**

   a. Create five folds in the data, and introduce a variable to identify the folds
   b. For each fold, run a for loop and ensure that 80 percent of the data is used to train the model and the remaining 20 percent is used to validate it in each iteration
   c. Develop five distinct models and five distinct validation scores (root mean squared error values)
   d. Determine the variable importance scores, and identify the redundant variables

```
from sklearn.model_selection import train_test_split
```

```
x = df.drop(["charges"], axis=1)
y = df['charges']
x_train, x_test, y_train, y_test = train_test_split(x,y, test_size=.20,random_state=10)
from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
x_train = sc.fit_transform(x_train)
x_test = sc.fit_transform(x_test)
from sklearn.linear_model import SGDRegressor
```

```
from sklearn.model_selection import GridSearchCV
params = {'alpha': [0.0001, 0.001, 0.01, 0.05, 0.1, 0.2,0.3,0.4,0.5,
0.6,0.7,0.8,0.9,1.0,2.0,3.0,4.0,5.0,6.0,7.0,8.0,
9.0,10.0,20,50,100,500,1000],
'penalty': ['l2', 'l1', 'elasticnet']}
sgd = SGDRegressor()
# Cross Validation
folds = 5
model_cv = GridSearchCV(estimator = sgd,
param_grid = params,
scoring = 'neg_mean_absolute_error',
cv = folds,
return_train_score = True,
verbose = 1)
model_cv.fit(x_train,y_train)
```

```
Fitting 5 folds for each of 84 candidates, totalling 420 fits

GridSearchCV(cv=5, estimator=SGDRegressor(),
             param_grid={'alpha': [0.0001, 0.001, 0.01, 0.05, 0.1, 0.2, 0.3,
                                   0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 2.0, 3.0,
                                   4.0, 5.0, 6.0, 7.0, 8.0, 9.0, 10.0, 20, 50,
                                   100, 500, 1000],
                         'penalty': ['l2', 'l1', 'elasticnet']},
             return_train_score=True, scoring='neg_mean_absolute_error',
```

```
model_cv.best_params_
```

```
{'alpha': 4.0, 'penalty': 'l1'}
```

```
sgd = SGDRegressor(alpha= 100, penalty= 'l1')
```

```
sgd.fit(x_train, y_train)
```

```
SGDRegressor(alpha=100, penalty='l1')
```

```
sgd.score(x_test, y_test)
```

```
0.8711282239533751
```

```
 y_pred = sgd.predict(x_test)
```

```
from sklearn.metrics import mean_squared_error, mean_absolute_error
sgd_mae = mean_absolute_error(y_test, y_pred)
sgd_mse = mean_squared_error(y_test, y_pred)
sgd_rmse = sgd_mse*(1/2.0)
```

```
print("MAE:", sgd_mae)
print("MSE:", sgd_mse)
print("RMSE:", sgd_rmse)
```

```
MAE: 2681.183902514782
MSE: 18756962.940102503
RMSE: 9378481.470051251
```

```
importance = sgd.coef_
pd.DataFrame(importance, index = x.columns, columns=['Feature_imp'])
```

	Feature_imp
children	324.625902
Hospital tier	-1135.536560
City tier	0.000000
BMI	2697.227677
HBA1C	138.011477
Heart Issues	0.000000
Any Transplants	0.000000
Cancer history	0.000000
NumberOfMajorSurgeries	0.000000
smoker	8998.720349
State_ID_R1011	0.000000
State_ID_R1012	0.000000
State_ID_R1013	-218.159993
Age	3401.726864
Gender	0.000000

4. **Use random forest and extreme gradient boosting for cost prediction, share your cross-validation results, and calculate the variable importance scores**

3. Use random forest and extreme gradient boosting for cost prediction, share your cross validation results, and calculate the variable importance scores

```
from sklearn.ensemble import RandomForestRegressor
```

```
rf = RandomForestRegressor(n_estimators = 1000, random_state = 42)
```

```
rf.fit(x_train, y_train)
```

```
RandomForestRegressor(n_estimators=1000, random_state=42)
```

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.

```
score = rf.score(x_test,y_test)
score
```

```
0.901740825808739
```

```
y_pred = rf.predict(x_test)
```

```
rf_mae = mean_absolute_error(y_test, y_pred)
```

```
rf_mae
```

```
1940.0160889462331
```

Extreme gradient boosting

```
from sklearn.ensemble import GradientBoostingRegressor
```

```
gbr = GradientBoostingRegressor(n_estimators = 1000, random_state = 42)
```

```
gbr.fit(x_train, y_train)
```

```
GradientBoostingRegressor(n_estimators=1000, random_state=42)
```

n 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.

```
score = gbr.score(x_test,y_test)
score
```

```
0.8650084426981199
```

```
y_pred = gbr.predict(x_test)
```

```
gbr_mae = mean_absolute_error(y_test, y_pred)
gbr_mae
```

```
2424.08578378777
```

- Since Mean Absolute Eroor of Random Forest is less than extreme gradient boosting, Random Forest algorithm works well.

4.Case scenario: 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.

4.Case scenario: 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.

22]:
```
df.columns
```

22]:
```
Index(['children', 'charges', 'Hospital tier', 'City tier', 'BMI', 'HBA1C',
       'Heart Issues', 'Any Transplants', 'Cancer history',
       'NumberOfMajorSurgeries', 'smoker', 'State_ID_R1011', 'State_ID_R1012',
       'State_ID_R1013', 'Age', 'Gender'],
      dtype='object')
```

23]:
```
date = str(19881228)
date1 = pd.to_datetime(date, format = "%Y%m%d")
```

26]:
```
current_date = dt.datetime.now()
current_date
```

26]:
```
datetime.datetime(2023, 5, 25, 18, 55, 19, 779951)
```

27]:
```
age = (current_date - date1)
age
```

27]:
```
Timedelta('12566 days 18:55:19.779951')
```

28]:
```
age = int(12566/365)
age
```

28]:
```
34
```

- So the age of Christopher, Ms. Jayna is 34

```
height_m = 170/100
height_sq = height_m*height_m
BMI = 85/height_sq
np.round(BMI,2)
```

```
29.41
```

- BMI is 29.41

```
df.columns
```

```
Index(['children', 'Hospital tier', 'City tier', 'BMI', 'HBA1C',
       'Heart Issues', 'Any Transplants', 'Cancer history',
       'NumberOfMajorSurgeries', 'smoker', 'State_ID_R1011', 'State_ID_R1012',
       'State_ID_R1013', 'age', 'gender'],
      dtype='object')
```

```
list = [[2,1,1,29.41,5.8,0,0,0,0,1,1,0,0,34,0]]
```

```
df = pd.DataFrame(list, columns = ['children','Hospital tier', 'City tier', 'BMI', 'HBA1C','Heart Issues', 'Any Transplants'
                                   'Cancer history','NumberOfMajorSurgeries', 'smoker', 'State_ID_R1011', 'State_ID_R1012',
                                   'State_ID_R1013', 'age', 'gender'] )
df
```

	children	Hospital tier	City tier	BMI	HBA1C	Heart Issues	Any Transplants	Cancer history	NumberOfMajorSurgeries	smoker	State_ID_R1011	State_ID_R1012	State_ID_R1013
0	2	1	1	29.41	5.8	0	0	0	0	1	1	0	0

5. Find the predicted hospitalization cost using all models. The predicted value should be the mean of the five models' predicted values.

5. Find the predicted hospitalization cost using all models. The predicted value should be the mean of the five models' predicted values.

```
[274]: Hospital_cost = []
```

```
[275]: Cost1 = sgd.predict(df)
Hospital_cost.append(Cost1)
Cost2 = rf.predict(df)
Hospital_cost.append(Cost2)
Cost3 = gbr.predict(df)
Hospital_cost.append(Cost3)
avg_cost = np.mean(Hospital_cost)
avg_cost
```

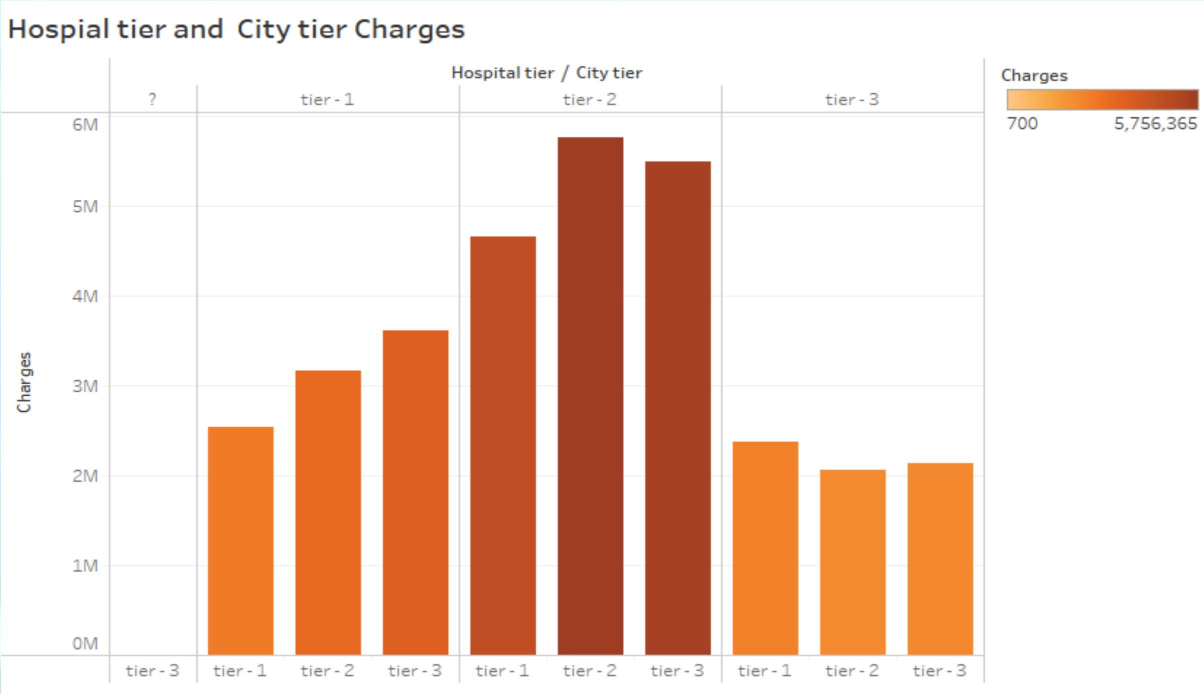
```
[275]: 104554.8763667323
```

- The mean of the five models' predicted avaerage value is 104554.8763667323

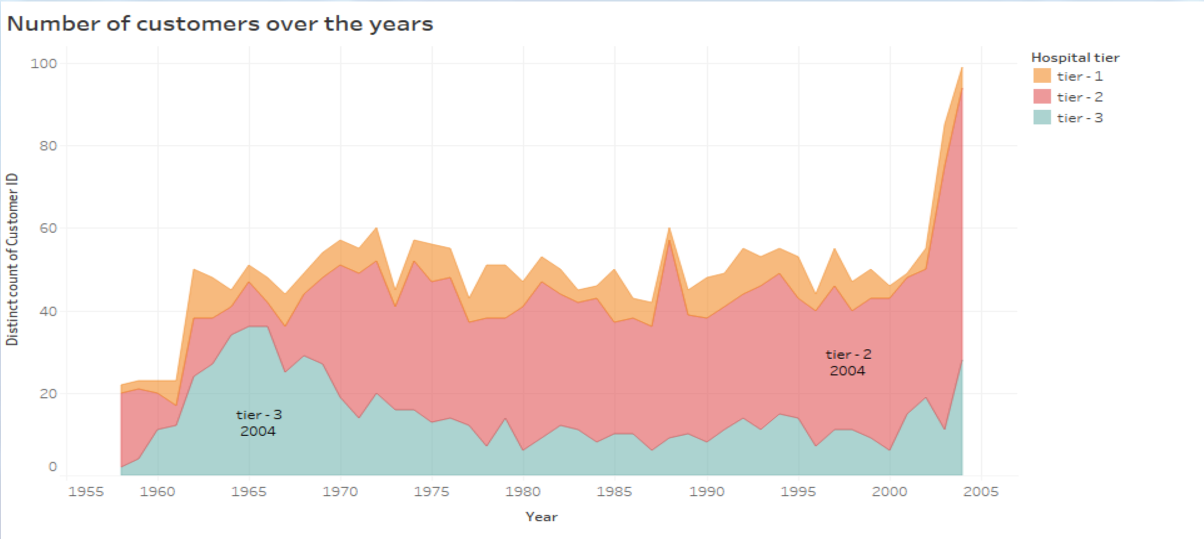
Tableau

1. **Create a dashboard in Tableau by selecting the appropriate chart types and business metrics**

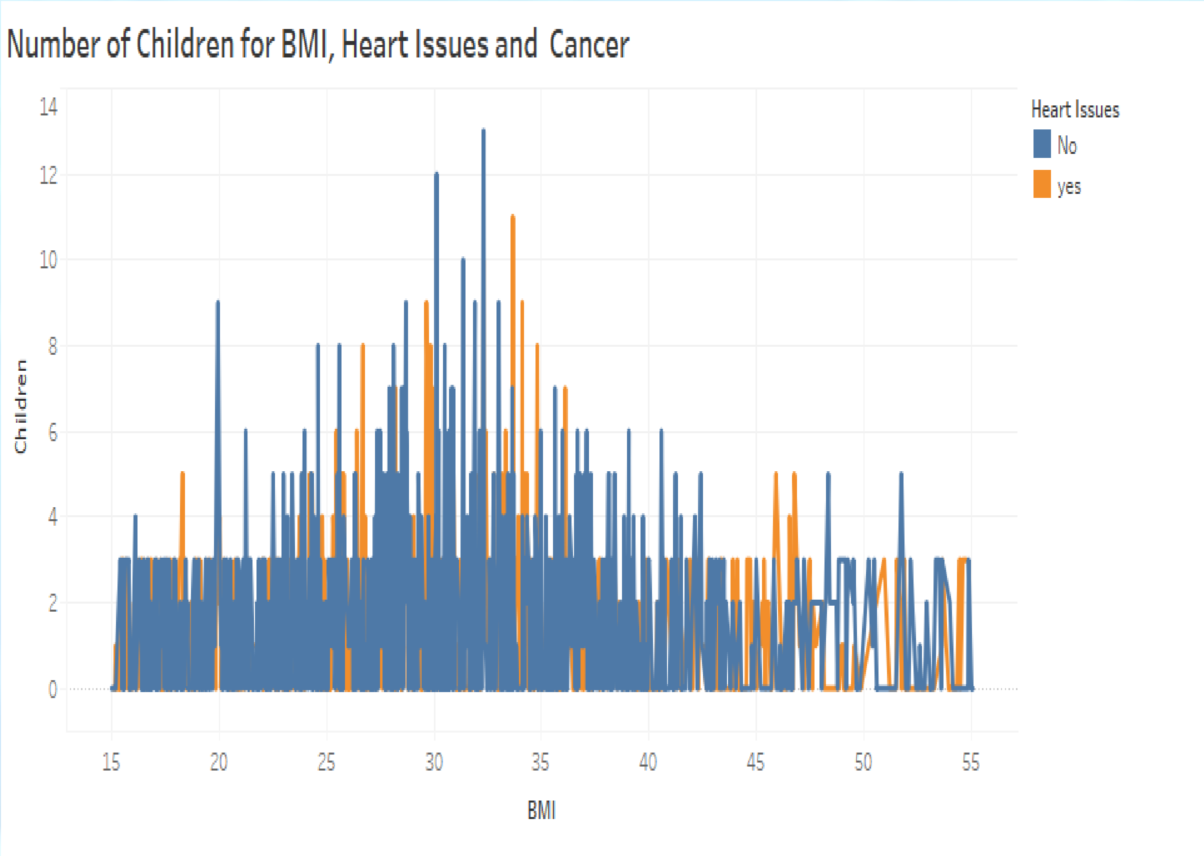
Hospital tier and city tier charges:



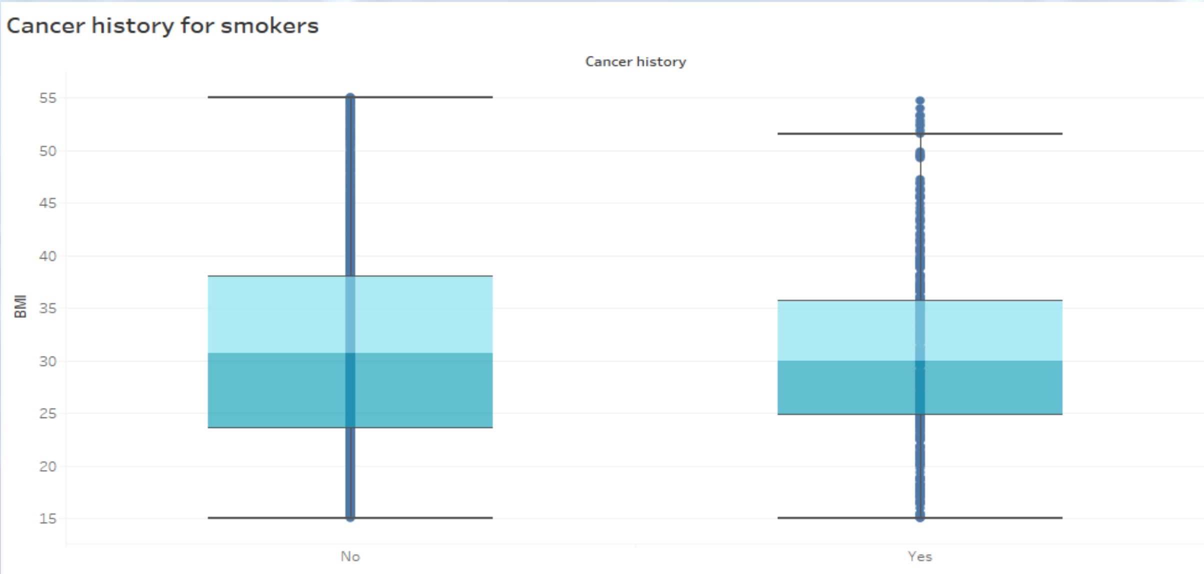
Number of customers over the years:



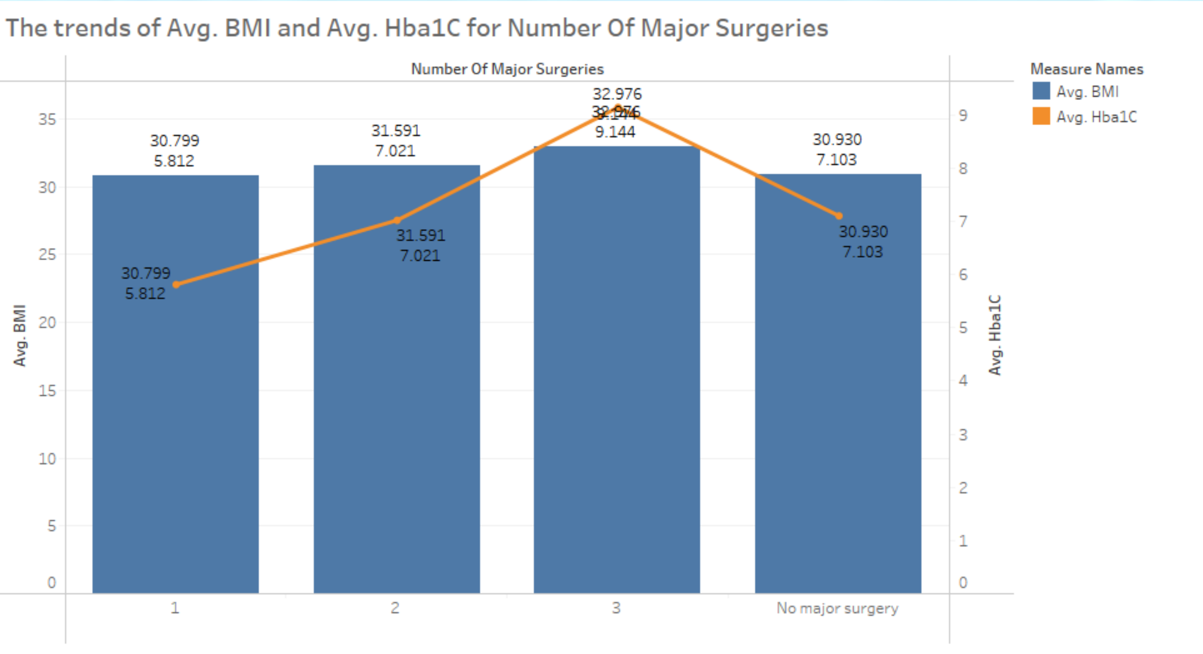
Number of children for BMI, heart issues and Cancer:



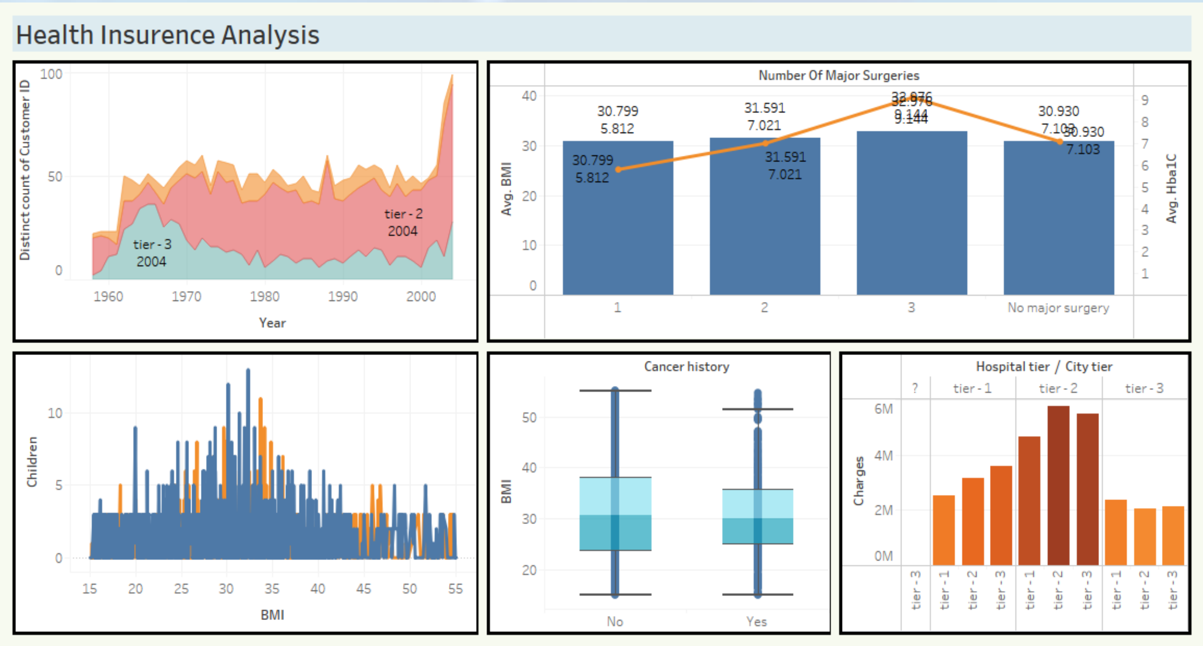
Cancer history for smokers:



The trends of AVG.Hba1c for number of major Surgeries:



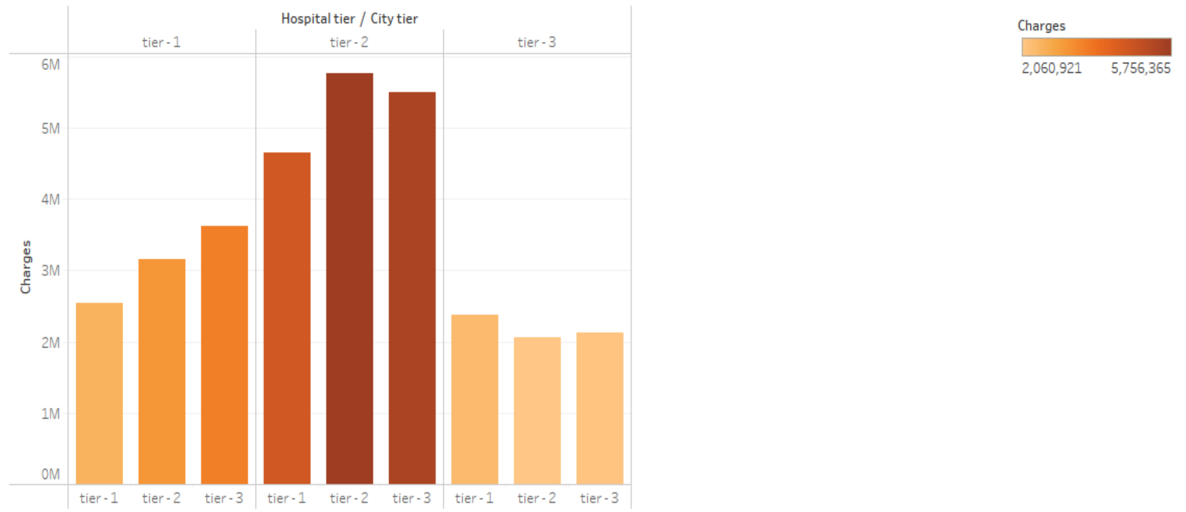
Dashboard:



Story :

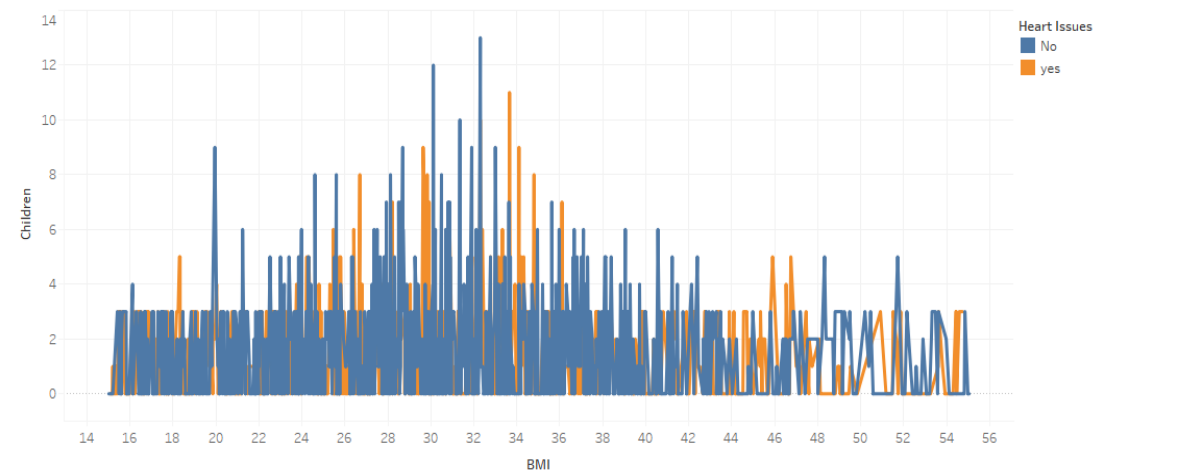
Story 1

Sum of Charges for each City tier broken down by Hospital tier. Color shows sum of Charges. The data is filtered on Action (Hospital tier,Year), which keeps 143 members. The view is filtered on Hospital tier and City tier. The Hospital tier filter keeps ?, tier - 1, tier - 2 and tier - 3. The City tier filter keeps tier - 1, tier - 2 and tier - 3.



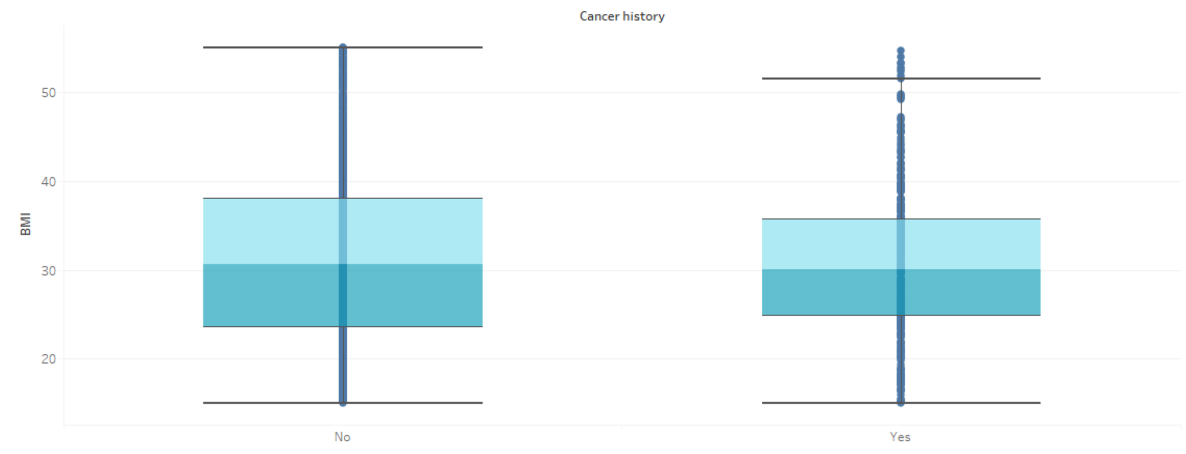
Story 1

The trend of sum of Children for BMI. Color shows details about Heart Issues. The data is filtered on Cancer history and Action (Hospital tier,Year). The Cancer history filter keeps No and Yes. The Action (Hospital tier,Year) filter keeps 143 members.



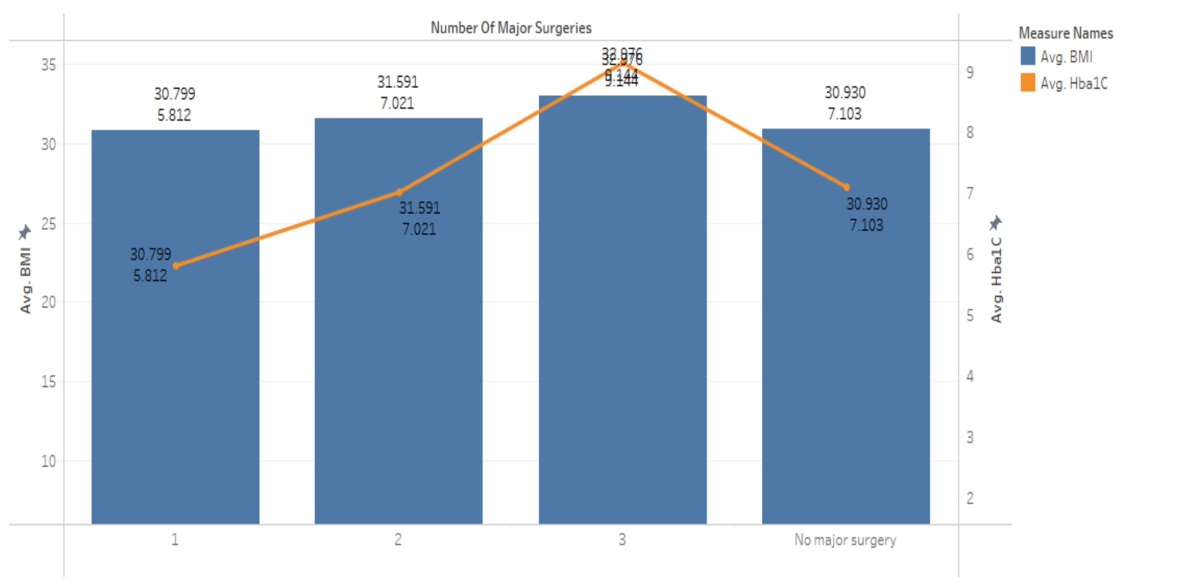
Story 1

BMI for each Cancer history. Details are shown for Smoker. The data is filtered on Action (Hospital tier,Year), which keeps 143 members. The view is filtered on Smoker, which keeps No and yes.



Story 1

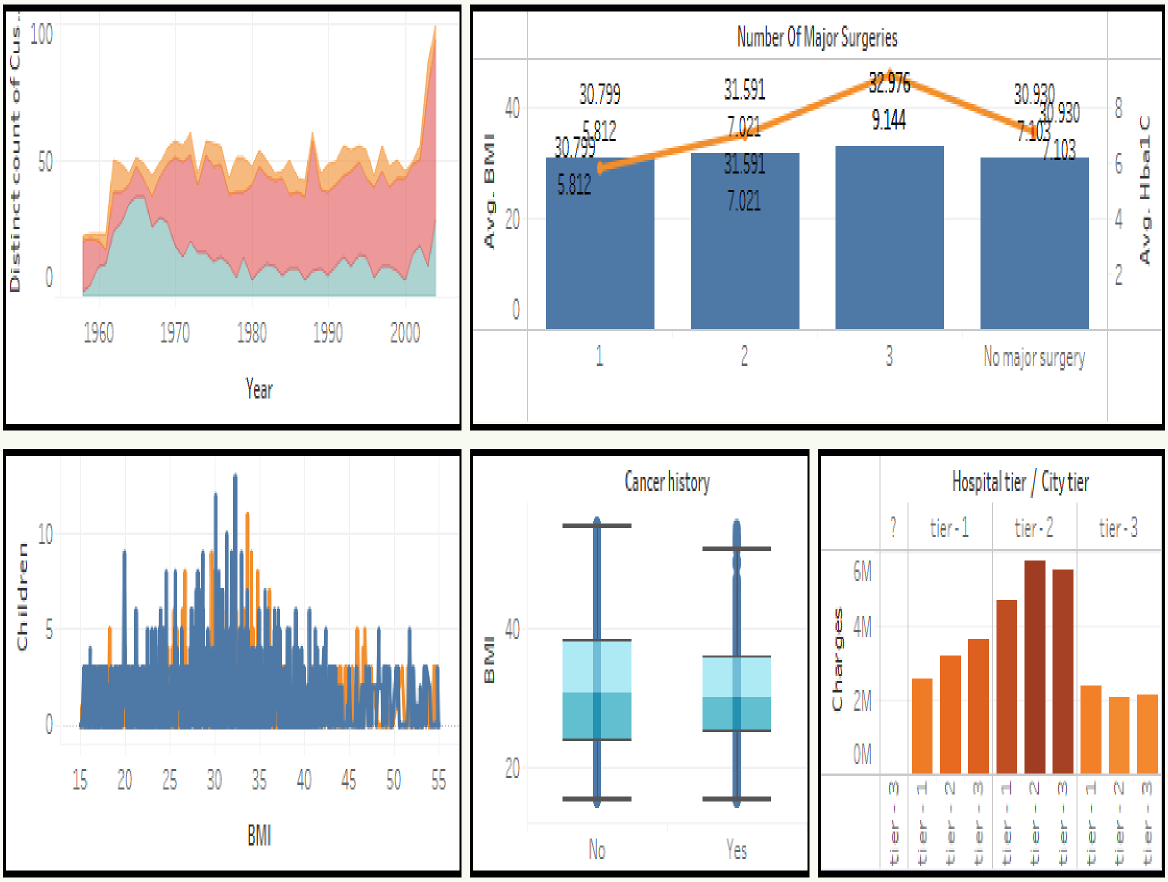
The trends of Avg. BMI and Avg. Hba1C for Number Of Major Surgeries. Color shows details about Avg. BMI and Avg. Hba1C. The marks are labeled by Avg. BMI and Avg. Hba1C. The data is filtered on Action (Hospital tier,Year), which keeps 143 members.



Story 1

This is the Final Dashboard to coclude all the graph.

Health Insurence Analysis



THANK YOU