Data Science Capstone

Course-end Project 2- Healthcare

By - Arka Prava Panda

Importing Libraries

In [18]:
```
%matplotlib inline
import numpy as np
import pandas as pd
import warnings
warnings.filterwarnings("ignore")

import matplotlib.pyplot as plt
from matplotlib import style
import seaborn as sns
```

Loading Dataset

In [36]:
```
data = pd.read_csv('health_care_diabetes_raw.csv')
```

In [20]:
```
data.head()
```

Out[20]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

In [21]:
```
data.shape
```

Out[21]:
```
(768, 9)
```

Project Task: Week 1 -- Data Exploration and Missing Values Treatment

In [22]:
```
#Checking for null values in Dataset
data.isnull().any()
```

Out[22]:
```
Pregnancies                 False
Glucose                     False
BloodPressure               False
SkinThickness               False
Insulin                     False
BMI                         False
DiabetesPedigreeFunction    False
Age                         False
Outcome                     False
dtype: bool
```

Since the 0 value in Glucose,BloodPressure,SkinThickness,Insulin and BMI variables represent missing values.Lets find now many instances are there in each of the above variables

In [23]:
```
data[data['Glucose']==0]
```

Out[23]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
75	1	0	48	20	0	24.7	0.140	22	0
182	1	0	74	20	23	27.7	0.299	21	0
342	1	0	68	35	0	32.0	0.389	22	0
349	5	0	80	32	0	41.0	0.346	37	1
502	6	0	68	41	0	39.0	0.727	41	1

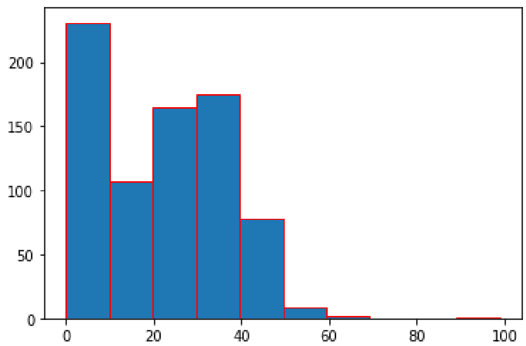
In [168]:
```
(5/765)*100
#only 0.6% of data is having missing values in Glucose column. No need to worry we can ignore them
```

Out[168]:
```
0.6535947712418301
```

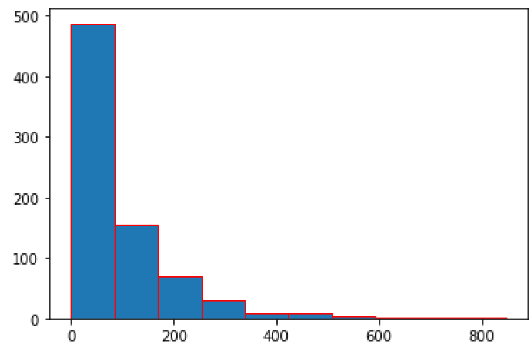
In [24]:
```
(data[data['BloodPressure']==0]).shape
```

Out[24]:
```
(35, 9)
```

In [170]:
```
(35/765)*100
#4.5% of data is having missing values in BloodPressure column
```
Out[170]:
```
4.57516339869281
```
In [25]:
```
(data[data['SkinThickness']==0]).shape
```
Out[25]:
```
(227, 9)
```
In [30]:
```
(227/765)*100
#29.6% of data is having missing values in SkinThickness column
```
Out[30]:
```
29.673202614379086
```
In [26]:
```
(data[data['Insulin']==0]).shape
```
Out[26]:
```
(374, 9)
```
In [33]:
```
(374/765)*100
#~49% of data is having missing values in Insulin column
```
Out[33]:
```
48.888888888888886
```
In [27]:
```
(data[data['BMI']==0]).shape
```
Out[27]:
```
(11, 9)
```
In [36]:
```
(11/765)*100
#1.4% of data is having missing values in BMI column
```
Out[36]:
```
1.4379084967320261
```
Since Insulin and SkinThickness are having higher percentages of missing values lets try to fill up the missing values

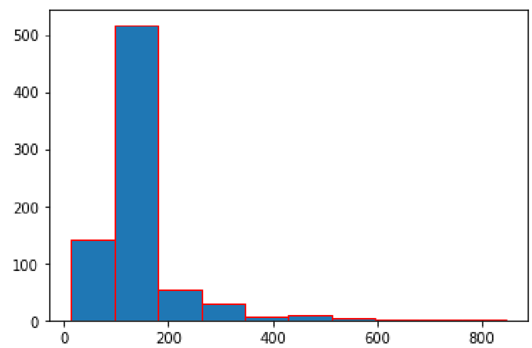
In [28]:
```
plt.hist(data['SkinThickness'],edgecolor='red')
```
Out[28]:
```
(array([231., 107., 165., 175.,  78.,   9.,   2.,   0.,   0.,   1.]),
 array([ 0. ,  9.9, 19.8, 29.7, 39.6, 49.5, 59.4, 69.3, 79.2, 89.1, 99. ]),
 <a list of 10 Patch objects>)
```


In [175]:
```
data[data['SkinThickness']!=0]['SkinThickness'].describe()
```
Out[175]:
```
count    541.000000
mean      29.153420
std       10.476982
min        7.000000
25%       22.000000
50%       29.000000
75%       36.000000
max       99.000000
Name: SkinThickness, dtype: float64
```

In [29]:
```
plt.hist(data['Insulin'],edgecolor='red')
```
Out[29]:
```
(array([487., 155.,  70.,  30.,   8.,   9.,   5.,   1.,   2.,   1.]),
 array([  0. ,  84.6, 169.2, 253.8, 338.4, 423. , 507.6, 592.2, 676.8,
        761.4, 846. ]),
 <a list of 10 Patch objects>)
```


In [30]:
```
data[data['Insulin']!=0]['Insulin'].describe()
```
Out[30]:
```
count    394.000000
mean     155.548223
std      118.775855
min       14.000000
25%       76.250000
50%      125.000000
75%      190.000000
max      846.000000
Name: Insulin, dtype: float64
```

Mean value of Skinthickness is ~29 and the mean value of Insulin is ~155 let impute the missing values with means

In [31]:
```
from numpy import nan
dataset_imputed = data
dataset_imputed[['SkinThickness','Insulin']] = dataset_imputed[['SkinThickness','Insulin']].replace(0, nan)
```
In [32]:
```
dataset_imputed.fillna(dataset_imputed.mean(), inplace=True)
```
In [33]:
```
plt.hist(dataset_imputed['Insulin'],edgecolor='red')
```
Out[33]:
```
(array([142., 517.,  55.,  29.,   7.,  10.,   4.,   1.,   2.,   1.]),
 array([ 14. ,  97.2, 180.4, 263.6, 346.8, 430. , 513.2, 596.4, 679.6,
        762.8, 846. ]),
 <a list of 10 Patch objects>)
```


In [37]:
```
data.describe()
```
Out[37]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876	33.240885	0.348958
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.000000	0.000000
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.000000	0.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41.000000	1.000000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	1.000000

In [38]:
```
dataset_imputed.describe()
```

Out[38]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	120.894531	69.105469	29.153420	155.548223	31.992578	0.471876	33.240885	0.348958
std	3.369578	31.972618	19.355807	8.790942	85.021108	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.000000	0.000000	7.000000	14.000000	0.000000	0.078000	21.000000	0.000000
25%	1.000000	99.000000	62.000000	25.000000	121.500000	27.300000	0.243750	24.000000	0.000000
50%	3.000000	117.000000	72.000000	29.153420	155.548223	32.000000	0.372500	29.000000	0.000000
75%	6.000000	140.250000	80.000000	32.000000	155.548223	36.600000	0.626250	41.000000	1.000000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	1.000000

In [181]:
```
dataset_imputed.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
Pregnancies                 768 non-null int64
Glucose                     768 non-null int64
BloodPressure               768 non-null int64
SkinThickness               768 non-null float64
Insulin                     768 non-null float64
BMI                         768 non-null float64
DiabetesPedigreeFunction    768 non-null float64
Age                         768 non-null int64
Outcome                     768 non-null int64
dtypes: float64(4), int64(5)
memory usage: 54.1 KB
```

In [39]:
```
Positive = dataset_imputed[dataset_imputed['Outcome']==1]
Positive.head(5)
```

Out[39]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35.00000	155.548223	33.6	0.627	50	1
2	8	183	64	29.15342	155.548223	23.3	0.672	32	1
4	0	137	40	35.00000	168.000000	43.1	2.288	33	1
6	3	78	50	32.00000	88.000000	31.0	0.248	26	1
8	2	197	70	45.00000	543.000000	30.5	0.158	53	1

In [40]:
```
Negative = dataset_imputed[dataset_imputed['Outcome']==0]
Negative.head(5)
```

Out[40]:

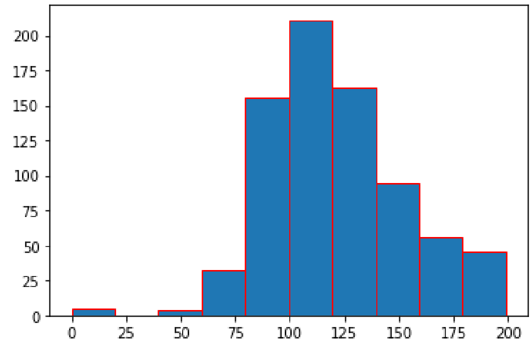
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
1	1	85	66	29.00000	155.548223	26.6	0.351	31	0
3	1	89	66	23.00000	94.000000	28.1	0.167	21	0
5	5	116	74	29.15342	155.548223	25.6	0.201	30	0
7	10	115	0	29.15342	155.548223	35.3	0.134	29	0
10	4	110	92	29.15342	155.548223	37.6	0.191	30	0

In [41]:
```
dataset_imputed['Glucose'].value_counts().head(5)
```

Out[41]:
```
100    17
99     17
129    14
125    14
111    14
Name: Glucose, dtype: int64
```

In [42]:
```
plt.hist(dataset_imputed['Glucose'],edgecolor='red')
```

Out[42]:
```
(array([  5.,   0.,   4.,  32., 156., 211., 163.,  95.,  56.,  46.]),
 array([  0. ,  19.9,  39.8,  59.7,  79.6,  99.5, 119.4, 139.3, 159.2,
        179.1, 199. ]),
 <a list of 10 Patch objects>)
```

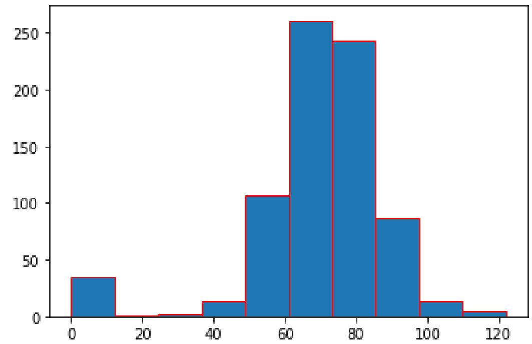


In [43]:
```
dataset_imputed['BloodPressure'].value_counts().head(7)
```

Out[43]:
```
70    57
74    52
68    45
78    45
72    44
64    43
80    40
Name: BloodPressure, dtype: int64
```

In [44]:
```
plt.hist(dataset_imputed['BloodPressure'],edgecolor='red')
```

Out[44]:
```
(array([ 35.,   1.,   2.,  13., 107., 261., 243.,  87.,  14.,   5.]),
 array([  0. ,  12.2,  24.4,  36.6,  48.8,  61. ,  73.2,  85.4,  97.6,
        109.8, 122. ]),
 <a list of 10 Patch objects>)
```

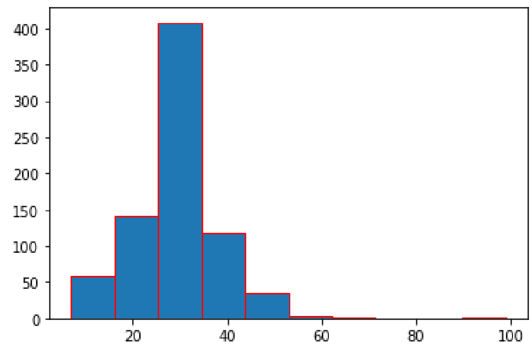


In [45]:
```
dataset_imputed['SkinThickness'].value_counts().head(7)
```

Out[45]:
```
29.15342    227
32.00000     31
30.00000     27
27.00000     23
23.00000     22
33.00000     20
18.00000     20
Name: SkinThickness, dtype: int64
```

In [46]:
```
plt.hist(dataset_imputed['SkinThickness'],edgecolor='red')
```

Out[46]:
```
(array([ 59., 141., 408., 118.,  36.,   4.,   1.,   0.,   0.,   1.]),
 array([ 7. , 16.2, 25.4, 34.6, 43.8, 53. , 62.2, 71.4, 80.6, 89.8, 99. ]),
 <a list of 10 Patch objects>)
```

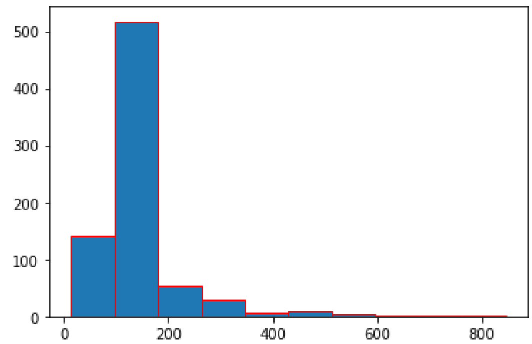


In [47]:
```
dataset_imputed['Insulin'].value_counts().head(7)
```

Out[47]:
```
155.548223    374
105.000000     11
140.000000      9
130.000000      9
120.000000      8
180.000000      7
94.000000       7
Name: Insulin, dtype: int64
```

In [48]:
```
plt.hist(dataset_imputed['Insulin'],edgecolor='red')
```

Out[48]:
```
(array([142., 517.,  55.,  29.,   7.,  10.,   4.,   1.,   2.,   1.]),
 array([ 14. ,  97.2, 180.4, 263.6, 346.8, 430. , 513.2, 596.4, 679.6,
        762.8, 846. ]),
 <a list of 10 Patch objects>)
```

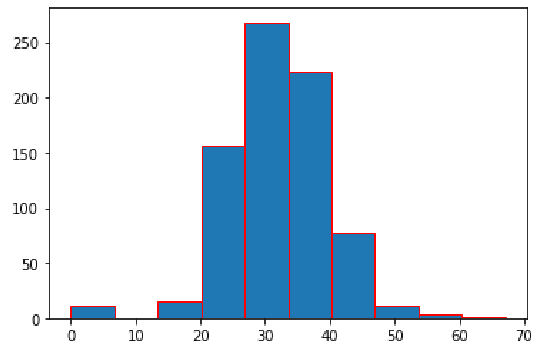


In [49]:
```
dataset_imputed['BMI'].value_counts().head(7)
```

Out[49]:
```
32.0    13
31.6    12
31.2    12
0.0     11
33.3    10
32.4    10
32.8     9
Name: BMI, dtype: int64
```

In [50]:
```
plt.hist(dataset_imputed['BMI'],edgecolor='red')
```

Out[50]:
```
(array([ 11.,   0.,  15., 156., 268., 224.,  78.,  12.,   3.,   1.]),
 array([ 0.  ,  6.71, 13.42, 20.13, 26.84, 33.55, 40.26, 46.97, 53.68,
        60.39, 67.1 ]),
 <a list of 10 Patch objects>)
```



In [51]:
```
dataset_imputed.describe().transpose()
```

Out[51]:

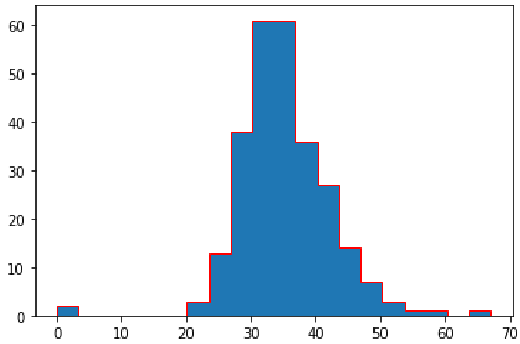
	count	mean	std	min	25%	50%	75%	max
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.000000	6.000000	17.00
Glucose	768.0	120.894531	31.972618	0.000	99.00000	117.000000	140.250000	199.00
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	72.000000	80.000000	122.00
SkinThickness	768.0	29.153420	8.790942	7.000	25.00000	29.153420	32.000000	99.00
Insulin	768.0	155.548223	85.021108	14.000	121.50000	155.548223	155.548223	846.00
BMI	768.0	31.992578	7.884160	0.000	27.30000	32.000000	36.600000	67.10
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.372500	0.626250	2.42
Age	768.0	33.240885	11.760232	21.000	24.00000	29.000000	41.000000	81.00
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.000000	1.000000	1.00

Project Task: Week 2 -- Correlation Analysis and Scatter Plots

In [52]:
```
Positive.shape
```
Out[52]:
```
(268, 9)
```

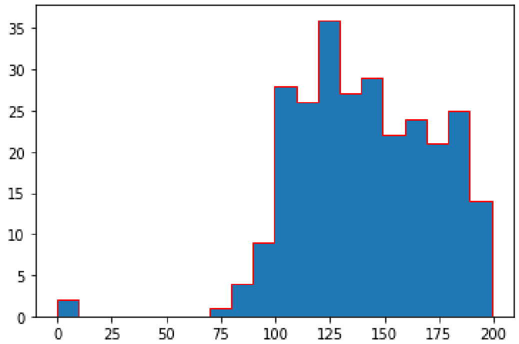
In [53]:
```
Negative.shape
```
Out[53]:
```
(500, 9)
```

In [54]:
```
plt.hist(Positive['BMI'],histtype='stepfilled',bins=20,edgecolor='red')
```
Out[54]:
```
(array([ 2.,  0.,  0.,  0.,  0.,  0.,  3., 13., 38., 61., 61., 36., 27.,
        14.,  7.,  3.,  1.,  1.,  0.,  1.]),
 array([ 0.   ,  3.355,  6.71 , 10.065, 13.42 , 16.775, 20.13 , 23.485,
        26.84 , 30.195, 33.55 , 36.905, 40.26 , 43.615, 46.97 , 50.325,
        53.68 , 57.035, 60.39 , 63.745, 67.1  ]),
 <a list of 1 Patch objects>)
```



In [55]:
```
Positive['BMI'].value_counts().head(7)
```
Out[55]:
```
32.9    8
31.6    7
33.3    6
30.5    5
32.0    5
31.2    5
32.4    4
Name: BMI, dtype: int64
```

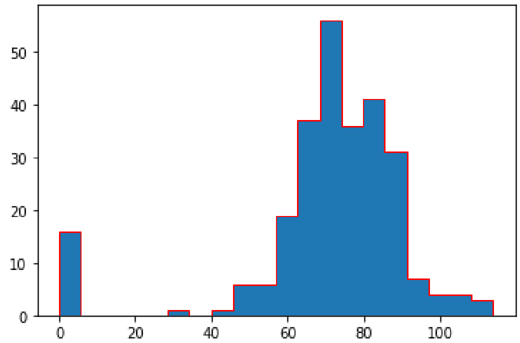
In [56]:
```
plt.hist(Positive['Glucose'],histtype='stepfilled',bins=20,edgecolor='red')
```
Out[56]:
```
(array([ 2.,  0.,  0.,  0.,  0.,  0.,  0.,  1.,  4.,  9., 28., 26., 36.,
        27., 29., 22., 24., 21., 25., 14.]),
 array([  0.  ,   9.95,  19.9 ,  29.85,  39.8 ,  49.75,  59.7 ,  69.65,
         79.6 ,  89.55,  99.5 , 109.45, 119.4 , 129.35, 139.3 , 149.25,
        159.2 , 169.15, 179.1 , 189.05, 199.  ]),
 <a list of 1 Patch objects>)
```



In [57]:
```
Positive['Glucose'].value_counts().head(7)
```
Out[57]:
```
125    7
158    6
128    6
115    6
129    6
146    5
162    5
Name: Glucose, dtype: int64
```

In [58]:
```
plt.hist(Positive['BloodPressure'],histtype='stepfilled',bins=20,edgecolor='red')
```

Out[58]:
```
(array([16.,  0.,  0.,  0.,  0.,  1.,  0.,  1.,  6.,  6., 19., 37., 56.,
        36., 41., 31.,  7.,  4.,  4.,  3.]),
 array([  0. ,   5.7,  11.4,  17.1,  22.8,  28.5,  34.2,  39.9,  45.6,
         51.3,  57. ,  62.7,  68.4,  74.1,  79.8,  85.5,  91.2,  96.9,
        102.6, 108.3, 114. ]),
 <a list of 1 Patch objects>)
```

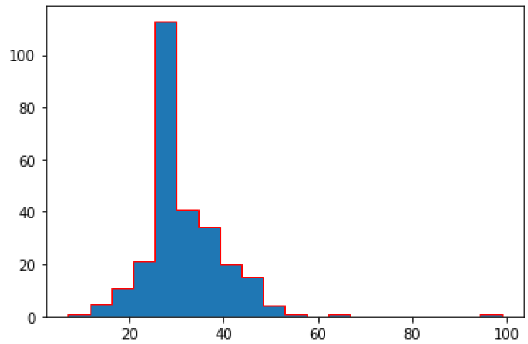


In [59]:
```
Positive['BloodPressure'].value_counts().head(7)
```

Out[59]:
```
70    23
76    18
78    17
74    17
72    16
0     16
82    13
Name: BloodPressure, dtype: int64
```

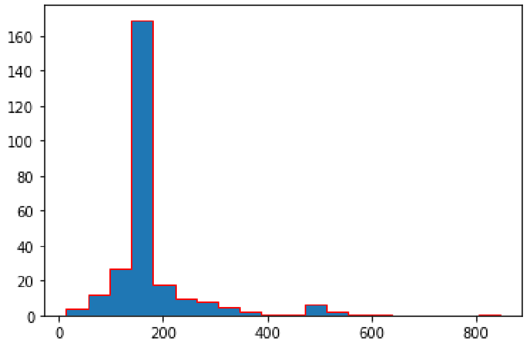
In [60]:
```
plt.hist(Positive['SkinThickness'],histtype='stepfilled',bins=20,edgecolor='red')
```

Out[60]:
```
(array([  1.,   5.,  11.,  21., 113.,  41.,  34.,  20.,  15.,   4.,   1.,
          0.,   1.,   0.,   0.,   0.,   0.,   0.,   0.,   1.]),
 array([ 7. , 11.6, 16.2, 20.8, 25.4, 30. , 34.6, 39.2, 43.8, 48.4, 53. ,
        57.6, 62.2, 66.8, 71.4, 76. , 80.6, 85.2, 89.8, 94.4, 99. ]),
 <a list of 1 Patch objects>)
```



In [61]:
```
Positive['SkinThickness'].value_counts().head(7)
```

Out[61]:
```
29.15342    88
32.00000    14
30.00000     9
33.00000     9
39.00000     8
36.00000     8
37.00000     8
Name: SkinThickness, dtype: int64
```

In [62]:
```
plt.hist(Positive['Insulin'],histtype='stepfilled',bins=20,edgecolor='red')
```
Out[62]:
```
(array([  4.,  12.,  27., 169.,  18.,  10.,   8.,   5.,   2.,   1.,   1.,
          6.,   2.,   1.,   1.,   0.,   0.,   0.,   0.,   1.]),
 array([ 14. ,  55.6,  97.2, 138.8, 180.4, 222. , 263.6, 305.2, 346.8,
        388.4, 430. , 471.6, 513.2, 554.8, 596.4, 638. , 679.6, 721.2,
        762.8, 804.4, 846. ]),
 <a list of 1 Patch objects>)
```


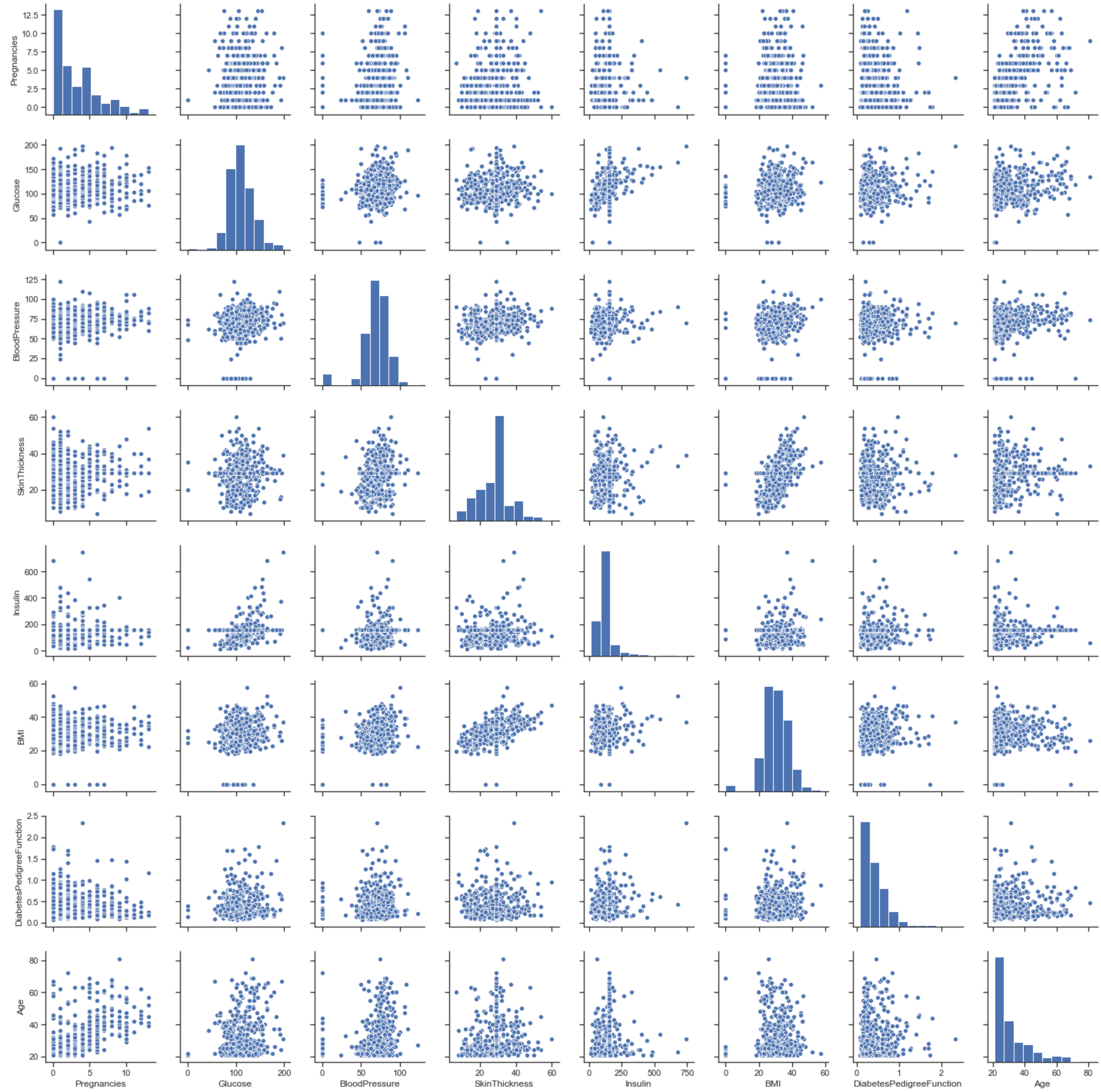
In [63]:
```
Positive['Insulin'].value_counts().head(7)
```
Out[63]:
```
155.548223    138
130.000000      6
180.000000      4
156.000000      3
175.000000      3
144.000000      2
194.000000      2
Name: Insulin, dtype: int64
```

Scatter plots

In [ ]:
```
#Pair plots for all dataset
sns.set(style="ticks", color_codes=True)
g = sns.pairplot(dataset_imputed,hue="Outcome")
```

In [65]:
```
#Pair plots for all Positive cases
sns.set(style="ticks", color_codes=True)
g = sns.pairplot(Positive[['Pregnancies','Glucose','BloodPressure','SkinThickness','Insulin','BMI','DiabetesPedigreeFu
```

In [66]:
```python
#Pair plots for all Negative cases
sns.set(style="ticks", color_codes=True)
g = sns.pairplot(Negative[['Pregnancies','Glucose','BloodPressure','SkinThickness','Insulin','BMI','DiabetesPedigreeFu
```



Correlation Analysis and Heat map

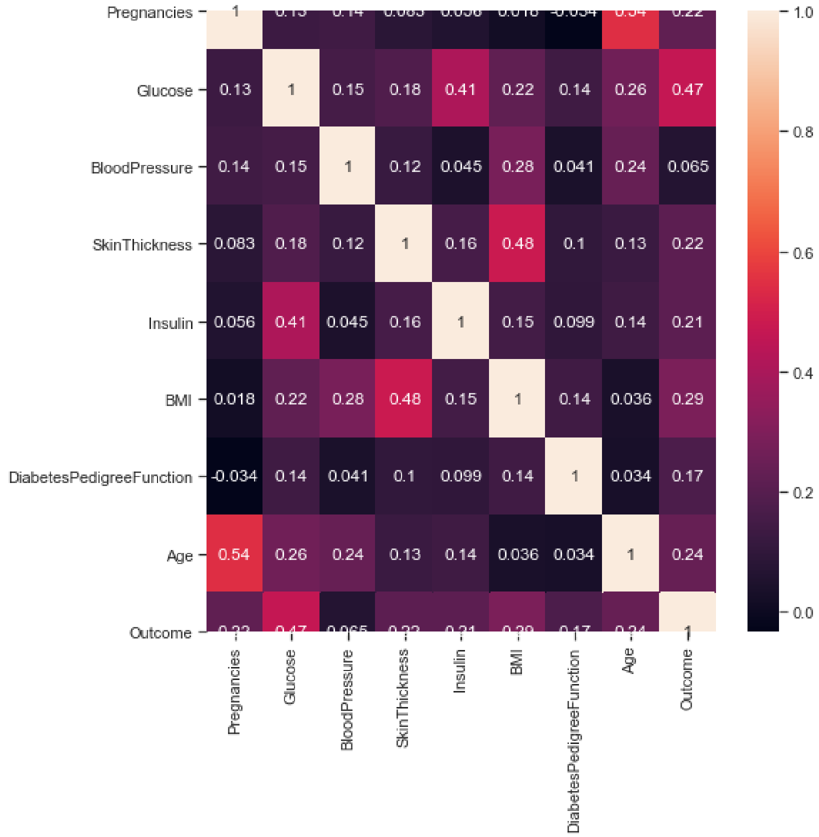
In [67]:
```python
### correlation matrix
dataset_imputed.corr()
```

Out[67]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
Pregnancies	1.000000	0.129459	0.141282	0.082989	0.056027	0.017683	-0.033523	0.544341	0.221898
Glucose	0.129459	1.000000	0.152590	0.182455	0.407699	0.221071	0.137337	0.263514	0.466581
BloodPressure	0.141282	0.152590	1.000000	0.123444	0.045319	0.281805	0.041265	0.239528	0.065068
SkinThickness	0.082989	0.182455	0.123444	1.000000	0.158139	0.480496	0.100966	0.127872	0.215299
Insulin	0.056027	0.407699	0.045319	0.158139	1.000000	0.149468	0.098634	0.136734	0.214411
BMI	0.017683	0.221071	0.281805	0.480496	0.149468	1.000000	0.140647	0.036242	0.292695
DiabetesPedigreeFunction	-0.033523	0.137337	0.041265	0.100966	0.098634	0.140647	1.000000	0.033561	0.173844
Age	0.544341	0.263514	0.239528	0.127872	0.136734	0.036242	0.033561	1.000000	0.238356
Outcome	0.221898	0.466581	0.065068	0.215299	0.214411	0.292695	0.173844	0.238356	1.000000

In [68]:
```python
plt.subplots(figsize=(8,8))
sns.heatmap(dataset_imputed.corr(),annot=True)
```

Out[68]: <matplotlib.axes._subplots.AxesSubplot at 0x1a4a1aaa848>



Correlation Results :

1 There are not much multicolinearity
2 Pregnancies and Age have some positive corelation
3 Glucose has some postive corelation with the outcome variable
4 Skin thickness and BMI has some positive corelation
5 Insulin and Glucose has some positive corelation

Project Task: Week 3 and Week 4 -- Data Modelling and Model Performance Evaluation

Model 1 : Logistic Regression

In [69]:
```python
dataset_imputed.head(5)
```

Out[69]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35.00000	155.548223	33.6	0.627	50	1
1	1	85	66	29.00000	155.548223	26.6	0.351	31	0
2	8	183	64	29.15342	155.548223	23.3	0.672	32	1
3	1	89	66	23.00000	94.000000	28.1	0.167	21	0
4	0	137	40	35.00000	168.000000	43.1	2.288	33	1

In [70]:
```python
features = dataset_imputed.iloc[:,[0,1,2,3,4,5,6,7]].values
label = dataset_imputed.iloc[:,8].values
```

In [71]:
```python
#Train test split
from sklearn.model_selection import train_test_split
X_train,X_test,y_train,y_test = train_test_split(features,
                                                label,
                                                test_size=0.2,
                                                random_state =10)
```

In [ ]:
```python
#Create model
from sklearn.linear_model import LogisticRegression
logRegModel = LogisticRegression()
logRegModel.fit(X_train,y_train)
```

In [73]:
```python
print(logRegModel.score(X_train,y_train))
print(logRegModel.score(X_test,y_test))
```

```
0.7817589576547231
0.7402597402597403
```

In [74]:
```python
y_pred = logRegModel.predict(X_test)
print('Accuracy of logistic regression classifier on test set: {:.2f}'.format(logRegModel.score(X_test, y_test)))
```

```
Accuracy of logistic regression classifier on test set: 0.74
```

In [75]:
```python
from sklearn.metrics import confusion_matrix
confusion_matrix = confusion_matrix(y_test, y_pred)
print(confusion_matrix)
```

```
[[87  8]
 [32 27]]
```

In [76]:
```python
from sklearn.metrics import classification_report
print(classification_report(y_test, y_pred))
```

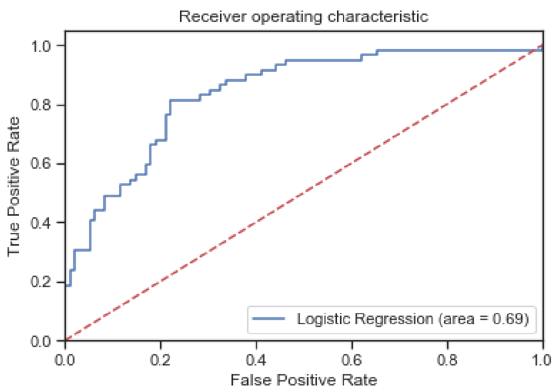
```
              precision    recall  f1-score   support

           0       0.73      0.92      0.81        95
           1       0.77      0.46      0.57        59

    accuracy                           0.74       154
   macro avg       0.75      0.69      0.69       154
weighted avg       0.75      0.74      0.72       154
```

In [77]:
```python
from sklearn.metrics import roc_auc_score
from sklearn.metrics import roc_curve
logit_roc_auc = roc_auc_score(y_test, logRegModel.predict(X_test))
fpr, tpr, thresholds = roc_curve(y_test, logRegModel.predict_proba(X_test)[:,1])
plt.figure()
plt.plot(fpr, tpr, label='Logistic Regression (area = %0.2f)' % logit_roc_auc)
plt.plot([0, 1], [0, 1],'r--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver operating characteristic')
plt.legend(loc="lower right")
plt.savefig('Log_ROC')
print('AUC: %.3f' % logit_roc_auc)
plt.show()
```

```
AUC: 0.687
```



Model 2 : Decision Tree Classifier

In [78]:
```
#Hyper Parameter tuning of max_dept
from sklearn.tree import DecisionTreeClassifier
from sklearn import metrics
for i in range(3,20):
    print("For max_depth = ",i)
    DTModel = DecisionTreeClassifier(max_depth=i)
    DTModel.fit(X_train,y_train)
    y_pred = DTModel.predict(X_test)
    print("Accuracy:",metrics.accuracy_score(y_test, y_pred))
```

```
For max_depth =  3
Accuracy: 0.6883116883116883
For max_depth =  4
Accuracy: 0.7402597402597403
For max_depth =  5
Accuracy: 0.7597402597402597
For max_depth =  6
Accuracy: 0.7597402597402597
For max_depth =  7
Accuracy: 0.7597402597402597
For max_depth =  8
Accuracy: 0.7467532467532467
For max_depth =  9
Accuracy: 0.7597402597402597
For max_depth =  10
Accuracy: 0.7727272727272727
For max_depth =  11
Accuracy: 0.7142857142857143
For max_depth =  12
Accuracy: 0.6818181818181818
For max_depth =  13
Accuracy: 0.7272727272727273
For max_depth =  14
Accuracy: 0.7337662337662337
For max_depth =  15
Accuracy: 0.7012987012987013
For max_depth =  16
Accuracy: 0.7142857142857143
For max_depth =  17
Accuracy: 0.6948051948051948
For max_depth =  18
Accuracy: 0.7142857142857143
For max_depth =  19
Accuracy: 0.6883116883116883
```

Highest Accuracy of Decision Tree Model can be obtained on Max_Depth = 10

In [79]:
```
DTModel = DecisionTreeClassifier(max_depth=10)
DTModel.fit(X_train,y_train)
y_pred = DTModel.predict(X_test)
```

In [80]:
```
DTModel.score(X_train,y_train)
```

Out[80]:
```
0.9267100977198697
```

In [81]:
```
DTModel.score(X_test,y_test)
```

Out[81]:
```
0.7532467532467533
```

In [82]:
```
print('Accuracy of Decision Tree regression classifier on test set: {:.2f}'.format(DTModel.score(X_test, y_test)))
```

```
Accuracy of Decision Tree regression classifier on test set: 0.75
```

In [83]:
```
from sklearn.metrics import confusion_matrix
confusion_matrix = confusion_matrix(y_test, y_pred)
print(confusion_matrix)
```

```
[[77 18]
 [20 39]]
```

In [132]:
```
from sklearn.metrics import classification_report
print(classification_report(y_test, y_pred))
```

```
              precision    recall  f1-score   support

           0       0.75      0.87      0.81        95
           1       0.72      0.53      0.61        59

    accuracy                           0.74       154
   macro avg       0.73      0.70      0.71       154
weighted avg       0.74      0.74      0.73       154
```

In [133]:
```
from sklearn.metrics import precision_score
print("Precision score: {}".format(precision_score(y_test,y_pred)))
```

```
Precision score: 0.7209302325581395
```

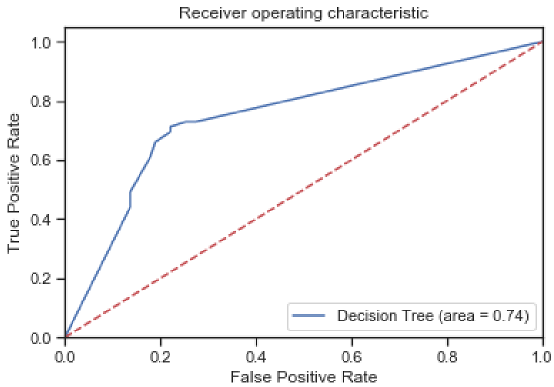
In [134]:
```
from sklearn.metrics import recall_score

print("Recall score: {}".format(recall_score(y_test,y_pred)))
```

```
Recall score: 0.5254237288135594
```

In [104]:
```
from sklearn.metrics import roc_auc_score
from sklearn.metrics import roc_curve
dt_roc_auc = roc_auc_score(y_test, DTModel.predict(X_test))
fpr, tpr, thresholds = roc_curve(y_test, DTModel.predict_proba(X_test)[:,1])
plt.figure()
plt.plot(fpr, tpr, label='Decision Tree (area = %0.2f)' % dt_roc_auc)
plt.plot([0, 1], [0, 1],'r--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver operating characteristic')
plt.legend(loc="lower right")
plt.savefig('DT_ROC')
print('AUC: %.3f' % dt_roc_auc)
plt.show()
```

```
AUC: 0.736
```



Model 3 : Random Forest Classifier

In [ ]:
```
from sklearn.ensemble import RandomForestClassifier
rf = RandomForestClassifier()
rf.fit(X_train, y_train)
y_pred = rf.predict(X_test)
```

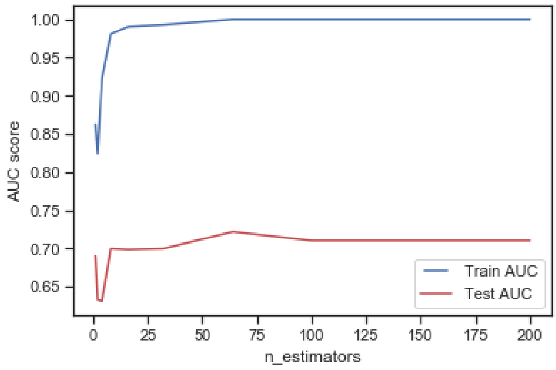
In [136]:
```
from sklearn.metrics import roc_curve, auc
false_positive_rate, true_positive_rate, thresholds = roc_curve(y_test, y_pred)
roc_auc = auc(false_positive_rate, true_positive_rate)
roc_auc
```

Out[136]:
```
0.7302408563782337
```

In [137]:
```
#Hyper Parameter tuning of n_estimators

n_estimators = [1, 2, 4, 8, 16, 32, 64, 100, 200]
train_results = []
test_results = []
for estimator in n_estimators:
    rf = RandomForestClassifier(n_estimators=estimator, n_jobs=-1)
    rf.fit(X_train, y_train)
    train_pred = rf.predict(X_train)
    false_positive_rate, true_positive_rate, thresholds = roc_curve(y_train, train_pred)
    roc_auc = auc(false_positive_rate, true_positive_rate)
    train_results.append(roc_auc)
    y_pred = rf.predict(X_test)
    false_positive_rate, true_positive_rate, thresholds = roc_curve(y_test, y_pred)
    roc_auc = auc(false_positive_rate, true_positive_rate)
    test_results.append(roc_auc)
```

In [138]:
```
from matplotlib.legend_handler import HandlerLine2D
line1, = plt.plot(n_estimators, train_results, 'b', label="Train AUC")
line2, = plt.plot(n_estimators, test_results, 'r', label="Test AUC")
plt.legend(handler_map={line1: HandlerLine2D(numpoints=2)})
plt.ylabel('AUC score')
plt.xlabel('n_estimators')
plt.show()
```



In [139]:
```
rfModel = RandomForestClassifier(n_estimators=60)
rfModel.fit(X_train, y_train)
y_pred = rfModel.predict(X_test)
```

In [140]:
```
false_positive_rate, true_positive_rate, thresholds = roc_curve(y_test, y_pred)
roc_auc = auc(false_positive_rate, true_positive_rate)
roc_auc
```

Out[140]: 0.7238180196253345

In [141]:
```
rfModel.score(X_train,y_train)
```

Out[141]: 1.0

In [142]:
```
rfModel.score(X_test,y_test)
```

Out[142]: 0.7662337662337663

In [143]:
```
print('Accuracy of Random Forest regression classifier on test set: {:.2f}'.format(rfModel.score(X_test, y_test)))
```

```
Accuracy of Random Forest regression classifier on test set: 0.77
```

In [144]:
```
from sklearn.metrics import confusion_matrix
confusion_matrix = confusion_matrix(y_test, y_pred)
print(confusion_matrix)
```

```
[[86  9]
 [27 32]]
```

In [145]:
```
from sklearn.metrics import classification_report
print(classification_report(y_test, y_pred))
```

```
              precision    recall  f1-score   support

           0       0.76      0.91      0.83        95
           1       0.78      0.54      0.64        59

    accuracy                           0.77       154
   macro avg       0.77      0.72      0.73       154
weighted avg       0.77      0.77      0.76       154
```

In [146]:
```
from sklearn.metrics import precision_score
print("Precision score: {}".format(precision_score(y_test,y_pred)))
```

```
Precision score: 0.7804878048780488
```

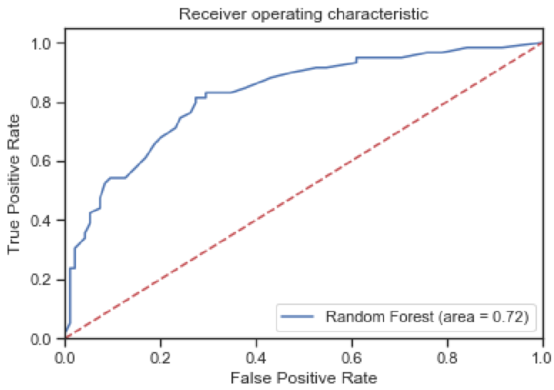
In [147]:
```
from sklearn.metrics import recall_score

print("Recall score: {}".format(recall_score(y_test,y_pred)))
```

```
Recall score: 0.5423728813559322
```

In [148]:
```
from sklearn.metrics import roc_auc_score
from sklearn.metrics import roc_curve
rf_roc_auc = roc_auc_score(y_test, rfModel.predict(X_test))
fpr, tpr, thresholds = roc_curve(y_test, rfModel.predict_proba(X_test)[:,1])
plt.figure()
plt.plot(fpr, tpr, label='Random Forest (area = %0.2f)' % rf_roc_auc)
plt.plot([0, 1], [0, 1],'r--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver operating characteristic')
plt.legend(loc="lower right")
plt.savefig('RF_ROC')
print('AUC: %.3f' % rf_roc_auc)
plt.show()
```

```
AUC: 0.724
```



Model 4 : Support Vector Machine

In [119]:
```
#Support Vector Classifier

from sklearn.svm import SVC
SVMmodel = SVC(kernel='rbf',
           gamma='auto')
SVMmodel.fit(X_train,y_train)
```

Out[119]:
```
SVC(C=1.0, cache_size=200, class_weight=None, coef0=0.0,
    decision_function_shape='ovr', degree=3, gamma='auto', kernel='rbf',
    max_iter=-1, probability=False, random_state=None, shrinking=True,
    tol=0.001, verbose=False)
```

In [120]:
```
SVMmodel.score(X_train,y_train)
```

Out[120]:
```
1.0
```

In [121]:
```
SVMmodel.score(X_test,y_test)
```

Out[121]:
```
0.6168831168831169
```

Model 5 : KNN Classifier

In [122]:
```
#Applying K-NN
from sklearn.neighbors import KNeighborsClassifier
knnClassifier = KNeighborsClassifier(n_neighbors=7,
                             metric='minkowski',
                             p = 2)
knnClassifier.fit(X_train,y_train)
```

Out[122]:
```
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                     metric_params=None, n_jobs=None, n_neighbors=7, p=2,
                     weights='uniform')
```

In [123]:
```
knnClassifier.score(X_train,y_train)
```

Out[123]:
```
0.8045602605863192
```

In [124]:
```
knnClassifier.score(X_test,y_test)
```

Out[124]:
```
0.7272727272727273
```

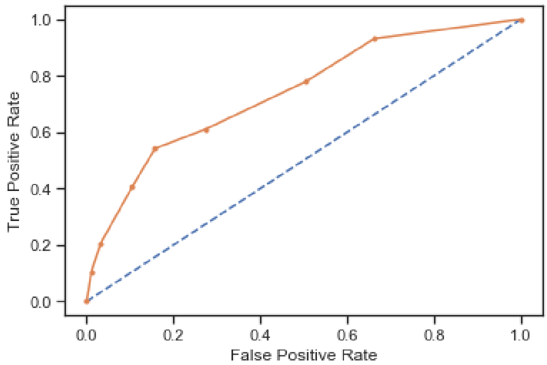
In [125]:
```python
#Preparing ROC Curve (Receiver Operating Characteristics Curve)
from sklearn.metrics import roc_curve
from sklearn.metrics import roc_auc_score

# predict probabilities

probs = knnClassifier.predict_proba(X_test)
# keep probabilities for the positive outcome only
probs = probs[:, 1]
# calculate AUC
auc = roc_auc_score(y_test, probs)
print('AUC: %.3f' % auc)
# calculate roc curve
fpr, tpr, thresholds = roc_curve(y_test, probs)
print("True Positive Rate - {}, False Positive Rate - {} Thresholds - {}".format(tpr,fpr,thresholds))
# plot no skill
plt.plot([0, 1], [0, 1], linestyle='--')
# plot the roc curve for the model
plt.plot(fpr, tpr, marker='.')
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
```

```
AUC: 0.739
True Positive Rate - [0.         0.10169492 0.20338983 0.40677966 0.54237288 0.61016949
 0.77966102 0.93220339 1.        ], False Positive Rate - [0.         0.01052632 0.03157895 0.10526316 0.15789474 0.2
7368421
 0.50526316 0.66315789 1.        ] Thresholds - [2.         1.         0.85714286 0.71428571 0.57142857 0.42857143
 0.28571429 0.14285714 0.        ]
```

Out[125]:
```
Text(0, 0.5, 'True Positive Rate')
```



In [126]:
```python
print('Accuracy of KNN classifier on test set: {:.2f}'.format(knnClassifier.score(X_test, y_test)))
```

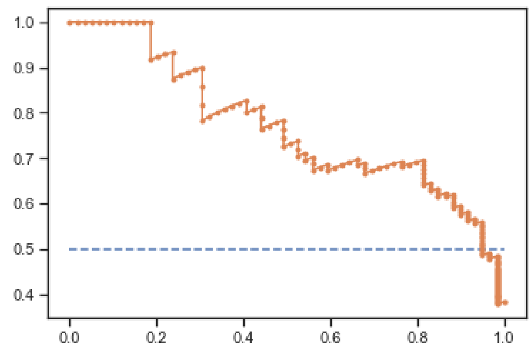
```
Accuracy of KNN classifier on test set: 0.73
```

In [127]:
```
#Precision Recall Curve for Logistic Regression

from sklearn.metrics import precision_recall_curve
from sklearn.metrics import f1_score
from sklearn.metrics import auc
from sklearn.metrics import average_precision_score
# predict probabilities
probs = logRegModel.predict_proba(X_test)
# keep probabilities for the positive outcome only
probs = probs[:, 1]
# predict class values
yhat = logRegModel.predict(X_test)
# calculate precision-recall curve
precision, recall, thresholds = precision_recall_curve(y_test, probs)
# calculate F1 score
f1 = f1_score(y_test, yhat)
# calculate precision-recall AUC
auc = auc(recall, precision)
# calculate average precision score
ap = average_precision_score(y_test, probs)
print('f1=%.3f auc=%.3f ap=%.3f' % (f1, auc, ap))
# plot no skill
plt.plot([0, 1], [0.5, 0.5], linestyle='--')
# plot the precision-recall curve for the model
plt.plot(recall, precision, marker='.')
```

```
f1=0.574 auc=0.769 ap=0.772
```

Out[127]: [<matplotlib.lines.Line2D at 0x1a4a25d4608>]

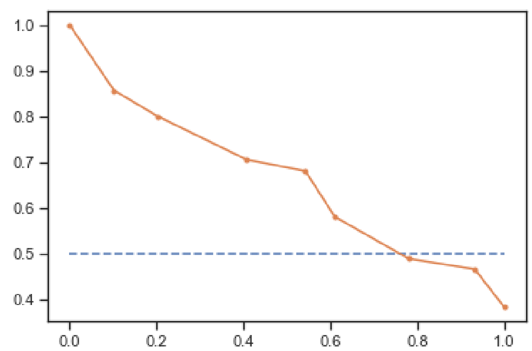


In [128]:
```
#Precision Recall Curve for KNN

from sklearn.metrics import precision_recall_curve
from sklearn.metrics import f1_score
from sklearn.metrics import auc
from sklearn.metrics import average_precision_score
# predict probabilities
probs = knnClassifier.predict_proba(X_test)
# keep probabilities for the positive outcome only
probs = probs[:, 1]
# predict class values
yhat = knnClassifier.predict(X_test)
# calculate precision-recall curve
precision, recall, thresholds = precision_recall_curve(y_test, probs)
# calculate F1 score
f1 = f1_score(y_test, yhat)
# calculate precision-recall AUC
auc = auc(recall, precision)
# calculate average precision score
ap = average_precision_score(y_test, probs)
print('f1=%.3f auc=%.3f ap=%.3f' % (f1, auc, ap))
# plot no skill
plt.plot([0, 1], [0.5, 0.5], linestyle='--')
# plot the precision-recall curve for the model
plt.plot(recall, precision, marker='.')
```

```
f1=0.604 auc=0.661 ap=0.624
```

Out[128]: [<matplotlib.lines.Line2D at 0x1a49e72d788>]

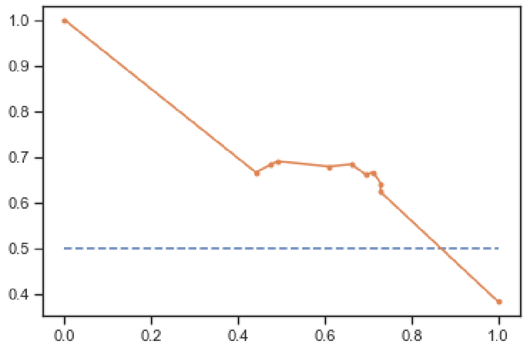


In [129]:
```python
#Precision Recall Curve for Decission Tree Classifier

from sklearn.metrics import precision_recall_curve
from sklearn.metrics import f1_score
from sklearn.metrics import auc
from sklearn.metrics import average_precision_score
# predict probabilities
probs = DTModel.predict_proba(X_test)
# keep probabilities for the positive outcome only
probs = probs[:, 1]
# predict class values
yhat = DTModel.predict(X_test)
# calculate precision-recall curve
precision, recall, thresholds = precision_recall_curve(y_test, probs)
# calculate F1 score
f1 = f1_score(y_test, yhat)
# calculate precision-recall AUC
auc = auc(recall, precision)
# calculate average precision score
ap = average_precision_score(y_test, probs)
print('f1=%.3f auc=%.3f ap=%.3f' % (f1, auc, ap))
# plot no skill
plt.plot([0, 1], [0.5, 0.5], linestyle='--')
# plot the precision-recall curve for the model
plt.plot(recall, precision, marker='.')
```

```
f1=0.672 auc=0.699 ap=0.593
```

Out[129]: [<matplotlib.lines.Line2D at 0x1a4a50eb108>]

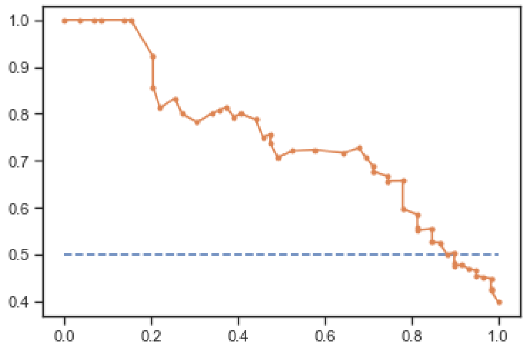


In [130]:
```python
#Precision Recall Curve for Random Forest

from sklearn.metrics import precision_recall_curve
from sklearn.metrics import f1_score
from sklearn.metrics import auc
from sklearn.metrics import average_precision_score
# predict probabilities
probs = rfModel.predict_proba(X_test)
# keep probabilities for the positive outcome only
probs = probs[:, 1]
# predict class values
yhat = rfModel.predict(X_test)
# calculate precision-recall curve
precision, recall, thresholds = precision_recall_curve(y_test, probs)
# calculate F1 score
f1 = f1_score(y_test, yhat)
# calculate precision-recall AUC
auc = auc(recall, precision)
# calculate average precision score
ap = average_precision_score(y_test, probs)
print('f1=%.3f auc=%.3f ap=%.3f' % (f1, auc, ap))
# plot no skill
plt.plot([0, 1], [0.5, 0.5], linestyle='--')
# plot the precision-recall curve for the model
plt.plot(recall, precision, marker='.')
```

```
f1=0.608 auc=0.745 ap=0.741
```

Out[130]: [<matplotlib.lines.Line2D at 0x1a4a24134c8>]



We observed that Random Forest is best performing model for this dataset

Accuracy of 77%

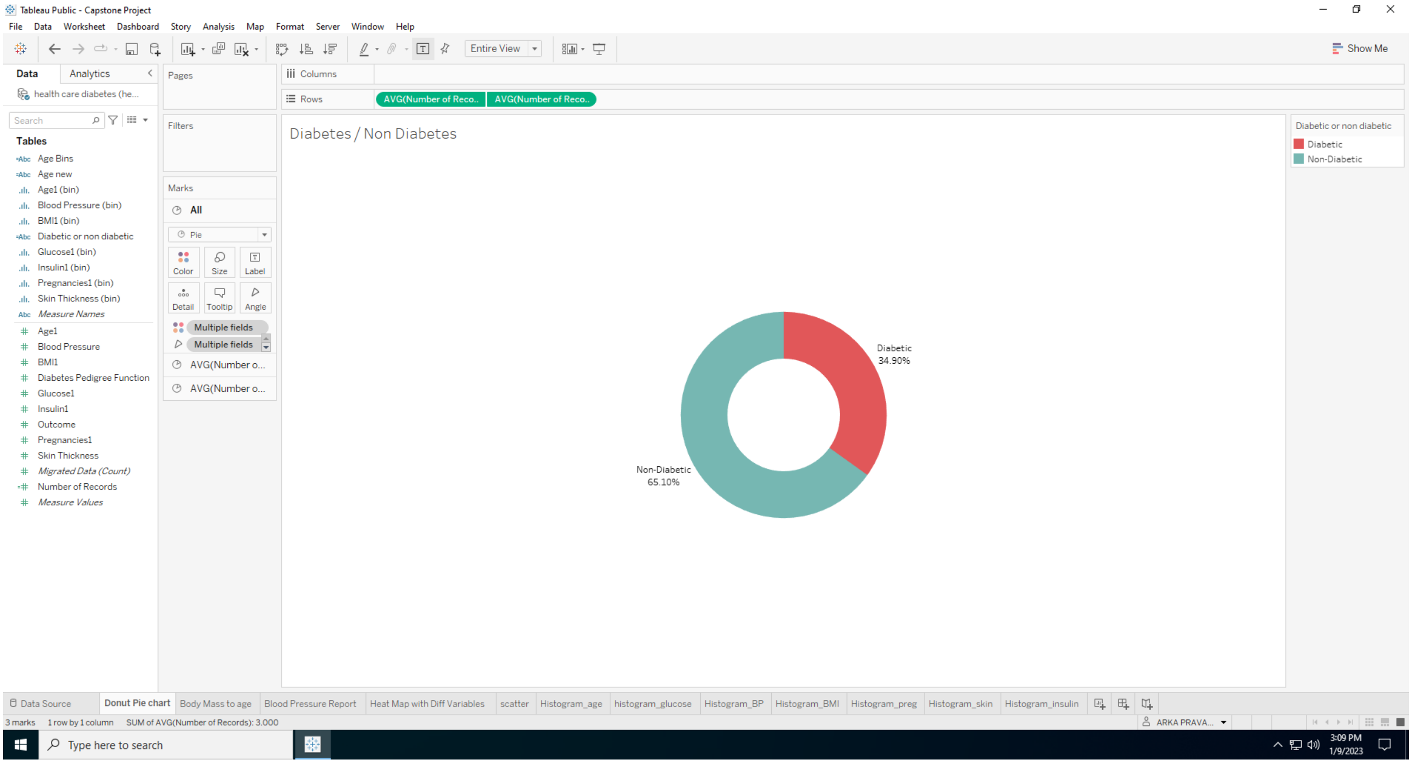
Precision = 0.78

Recall = 0.54

AUC = 0.72

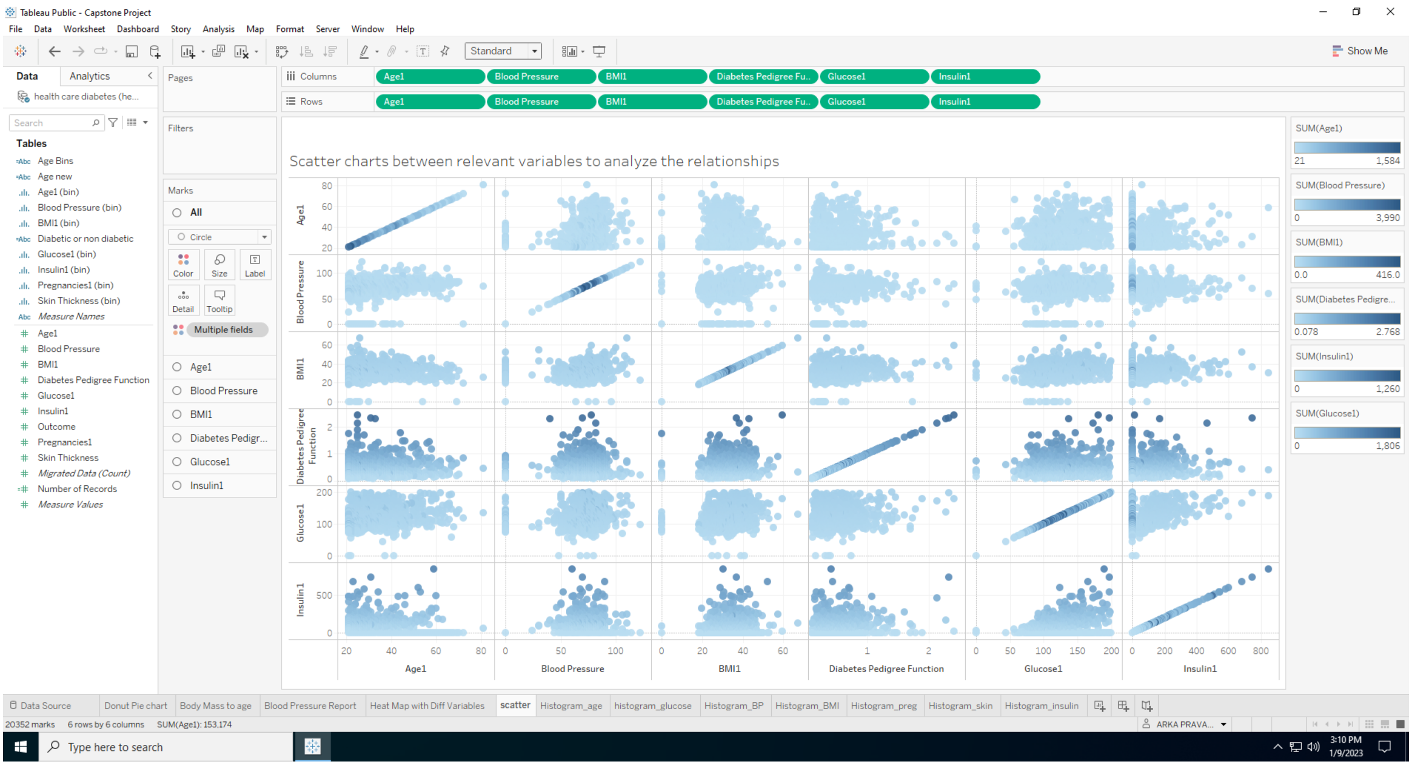
Data Reporting

1) First we have created a pie chart to designate between diabetic and non diabetic patients

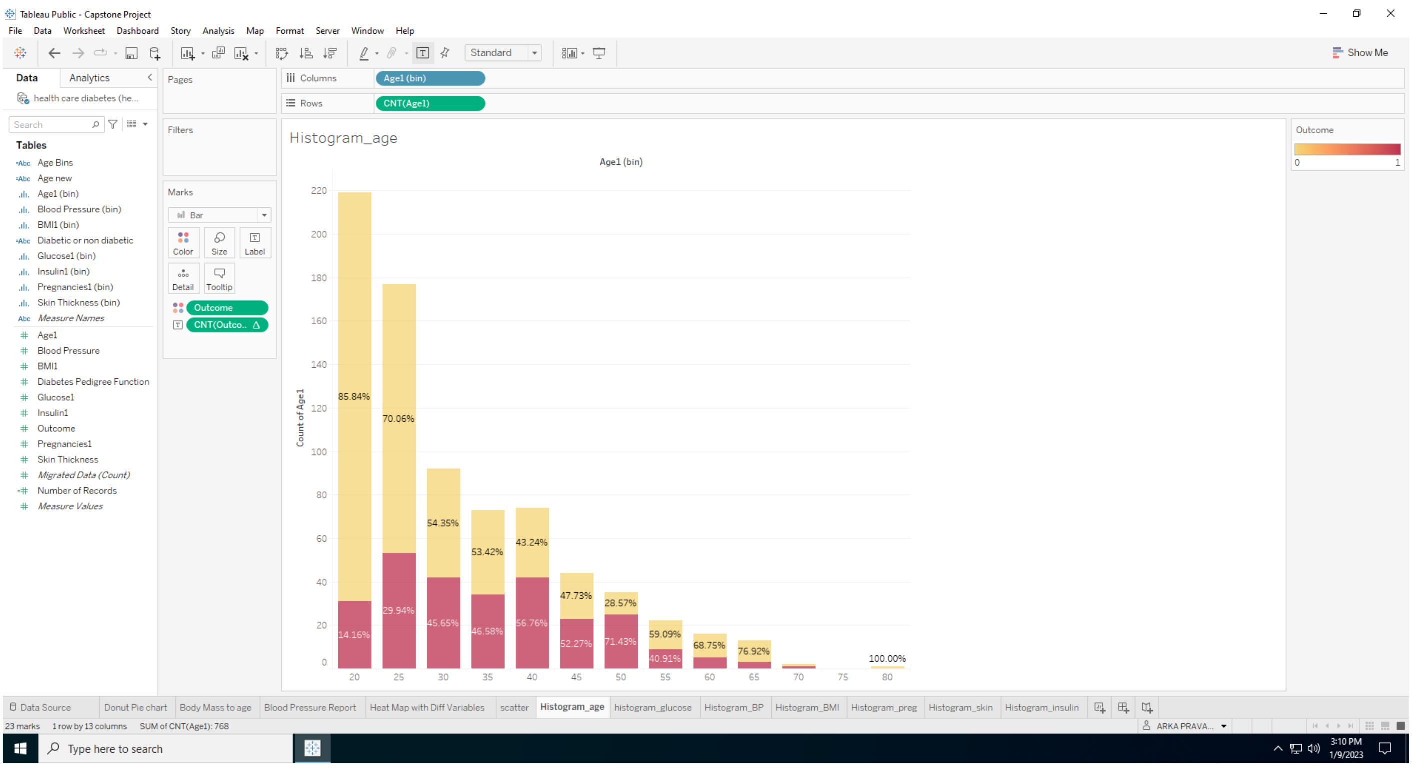


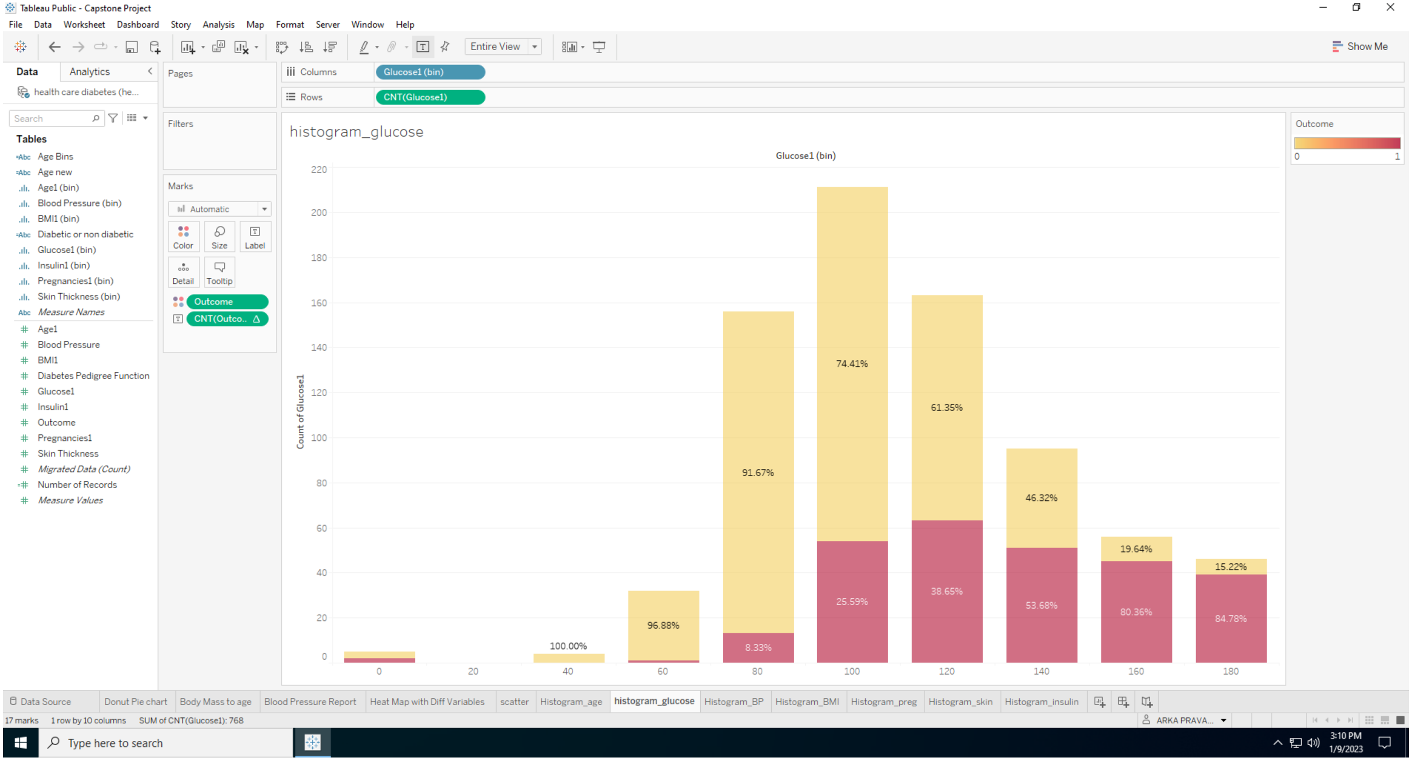
We can observe that 65.10% of the patients are non-diabetic whereas 34.90% of the patients are diabetic

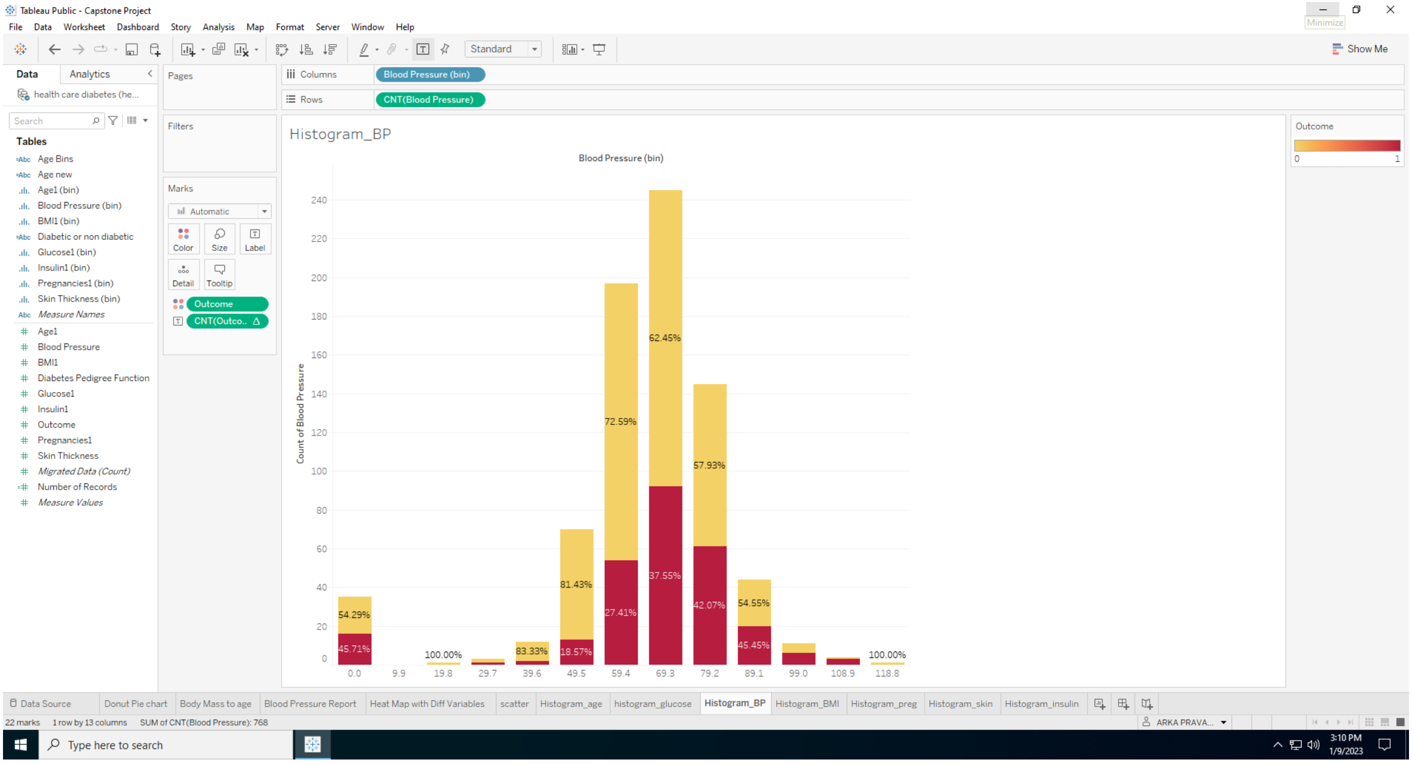
2) Next we have created scatter charts between relevant variables to analyze the relationships



3) Plotted histogram or frequency charts to analyze the distribution of the data




histogram_glucose
Glucose1 (bin)
Count of Glucose1
100.00%
96.88%
91.67%
8.33%
74.41%
25.59%
61.35%
38.65%
46.32%
53.68%
19.64%
80.36%
15.22%
84.78%
Outcome


Histogram_BP
Blood Pressure (bin)
Count of Blood Pressure
54.29%
45.71%
100.00%
83.33%
81.43%
18.57%
72.59%
27.41%
62.45%
37.55%
57.93%
42.07%
54.55%
45.45%
100.00%
Outcome

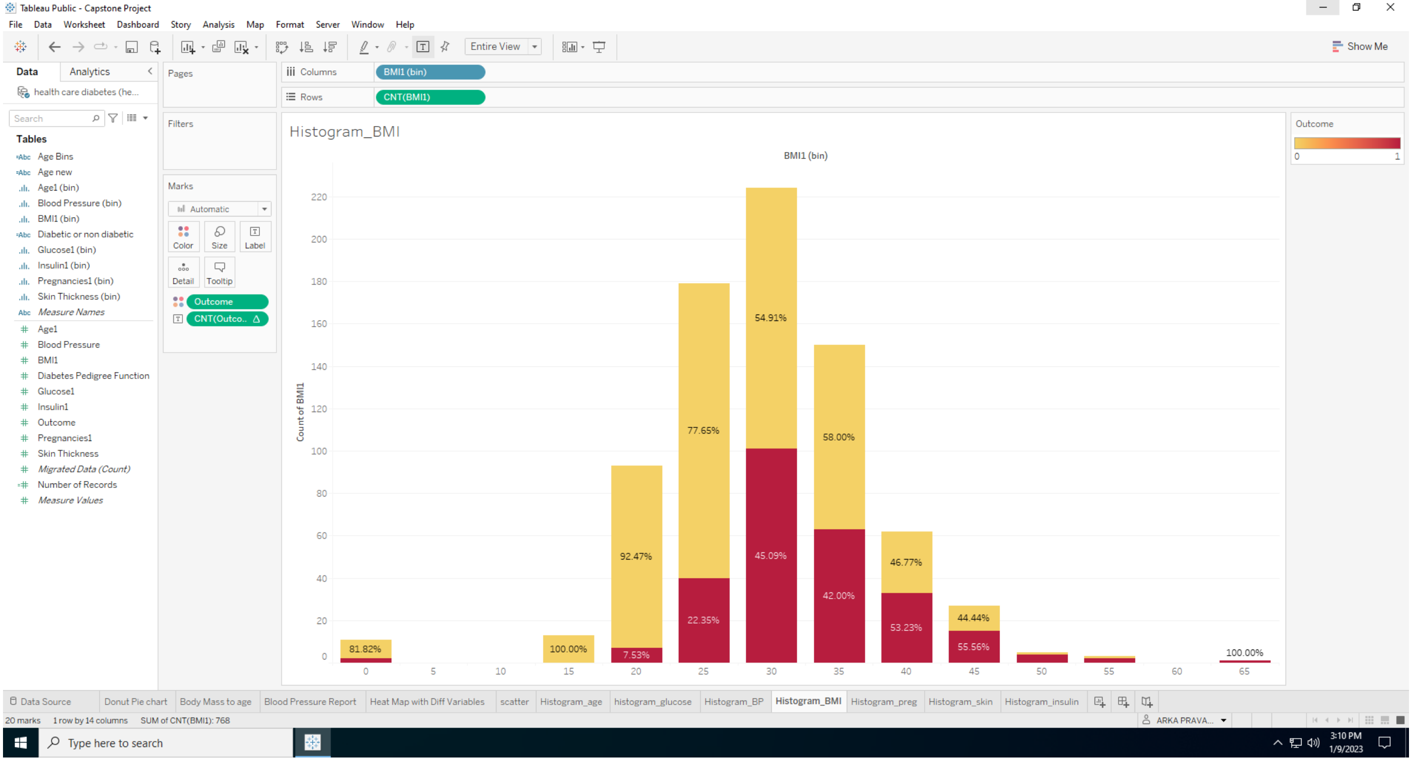


Tableau Public - Capstone Project
Histogram_BMI
BMI1 (bin)
Count of BMI1
81.82%
100.00%
92.47%
7.53%
77.65%
22.35%
54.91%
45.09%
58.00%
42.00%
46.77%
53.23%
44.44%
55.56%
100.00%
Outcome
20 marks 1 row by 14 columns SUM of CNT(BMI1): 768

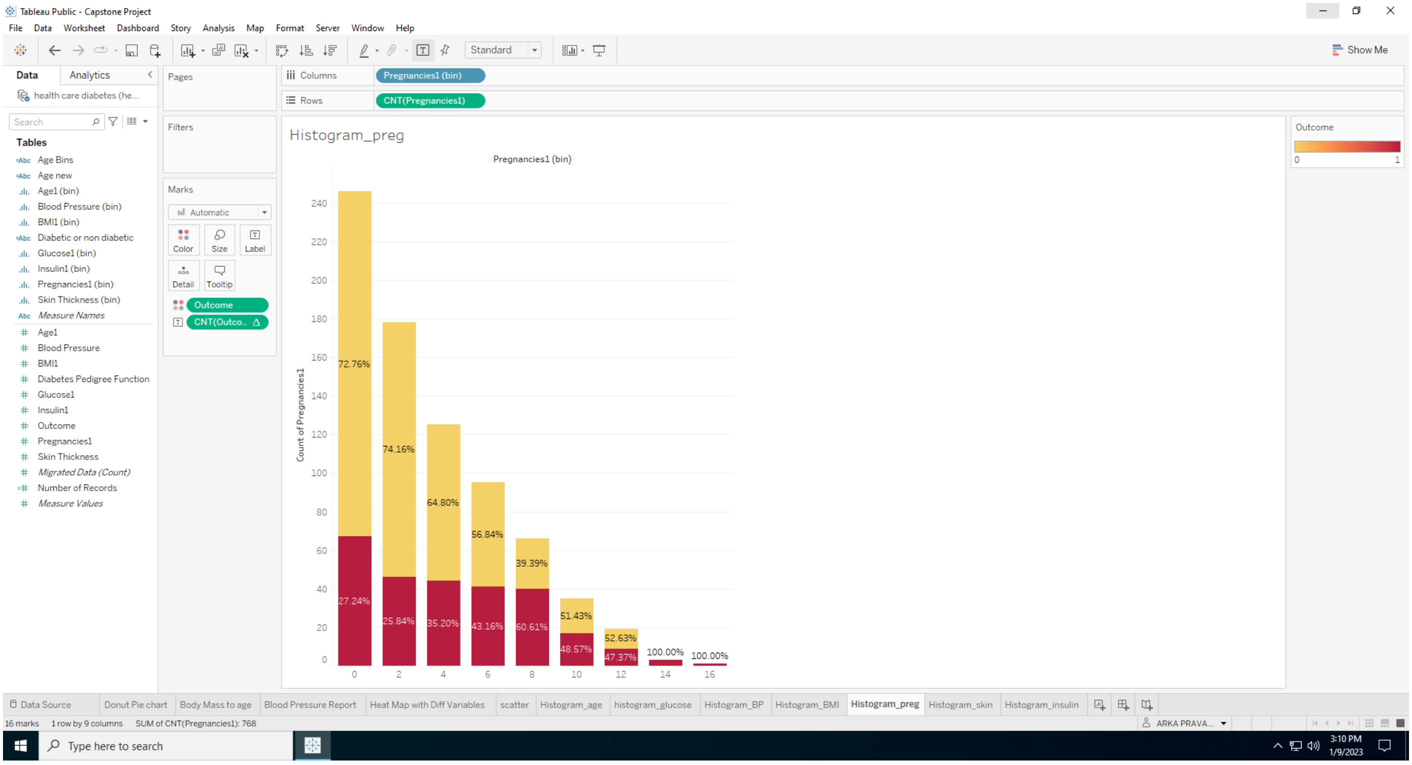
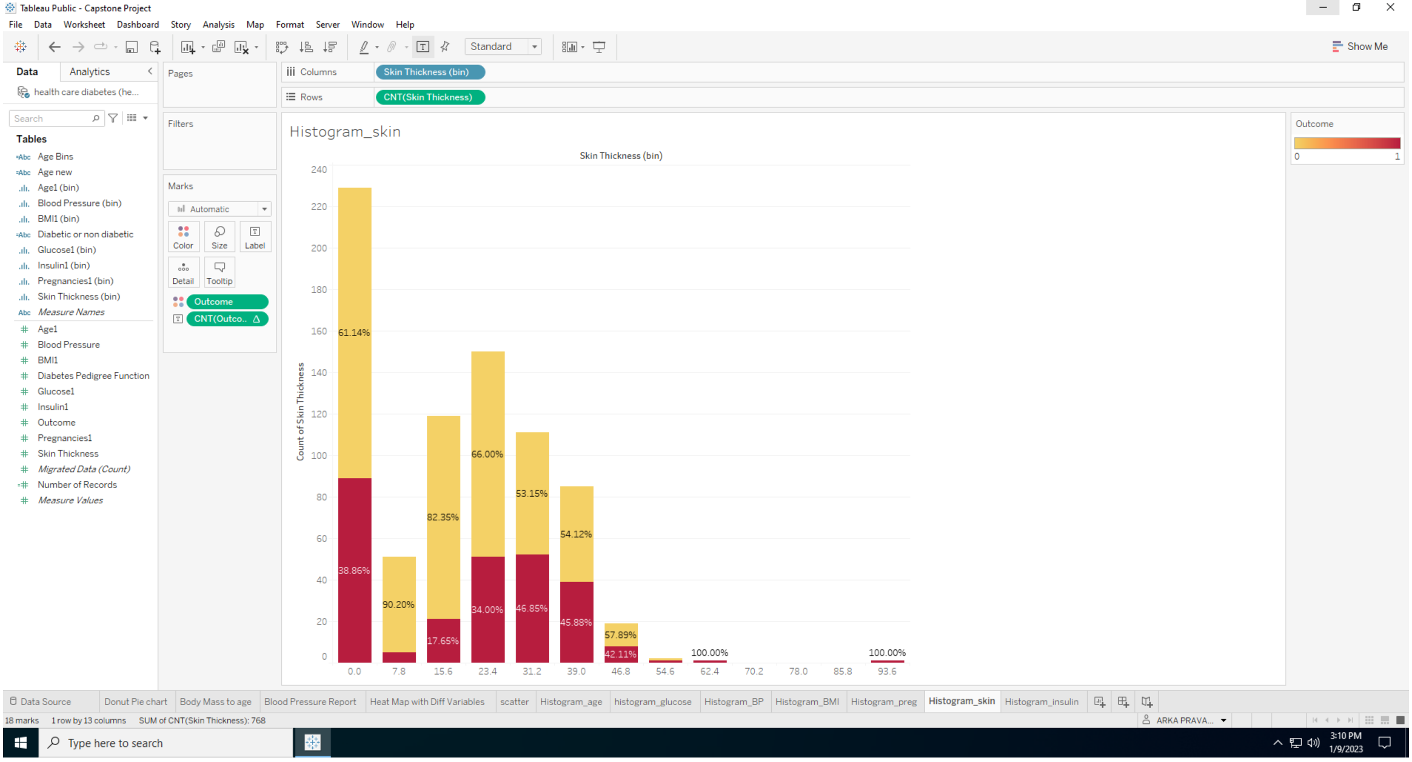
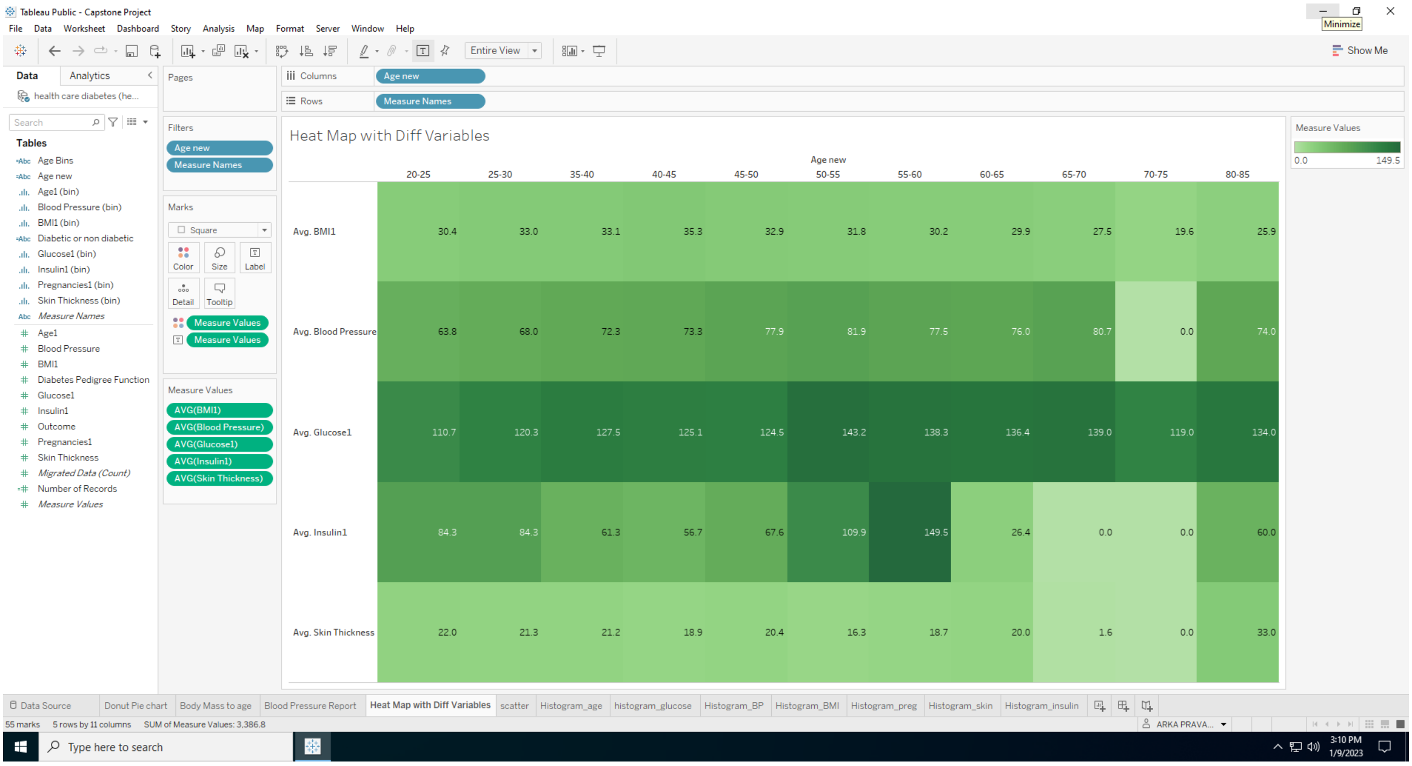


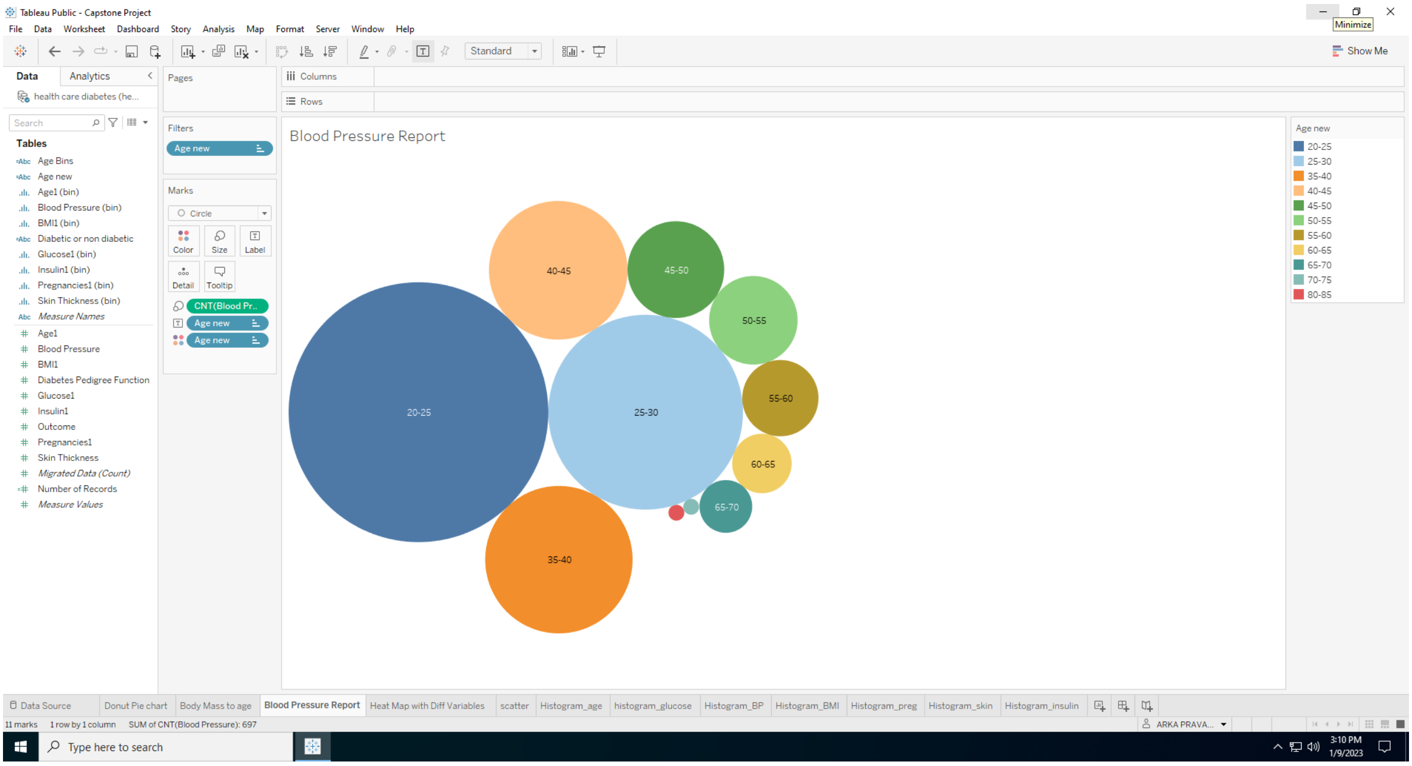
Tableau Public - Capstone Project
Histogram_preg
Pregnancies1 (bin)
Count of Pregnancies1
72.76%
27.24%
74.16%
25.84%
64.80%
35.20%
56.84%
43.16%
39.39%
60.61%
51.43%
48.57%
52.63%
47.37%
100.00%
100.00%
Outcome
16 marks 1 row by 9 columns SUM of CNT(Pregnancies1): 768



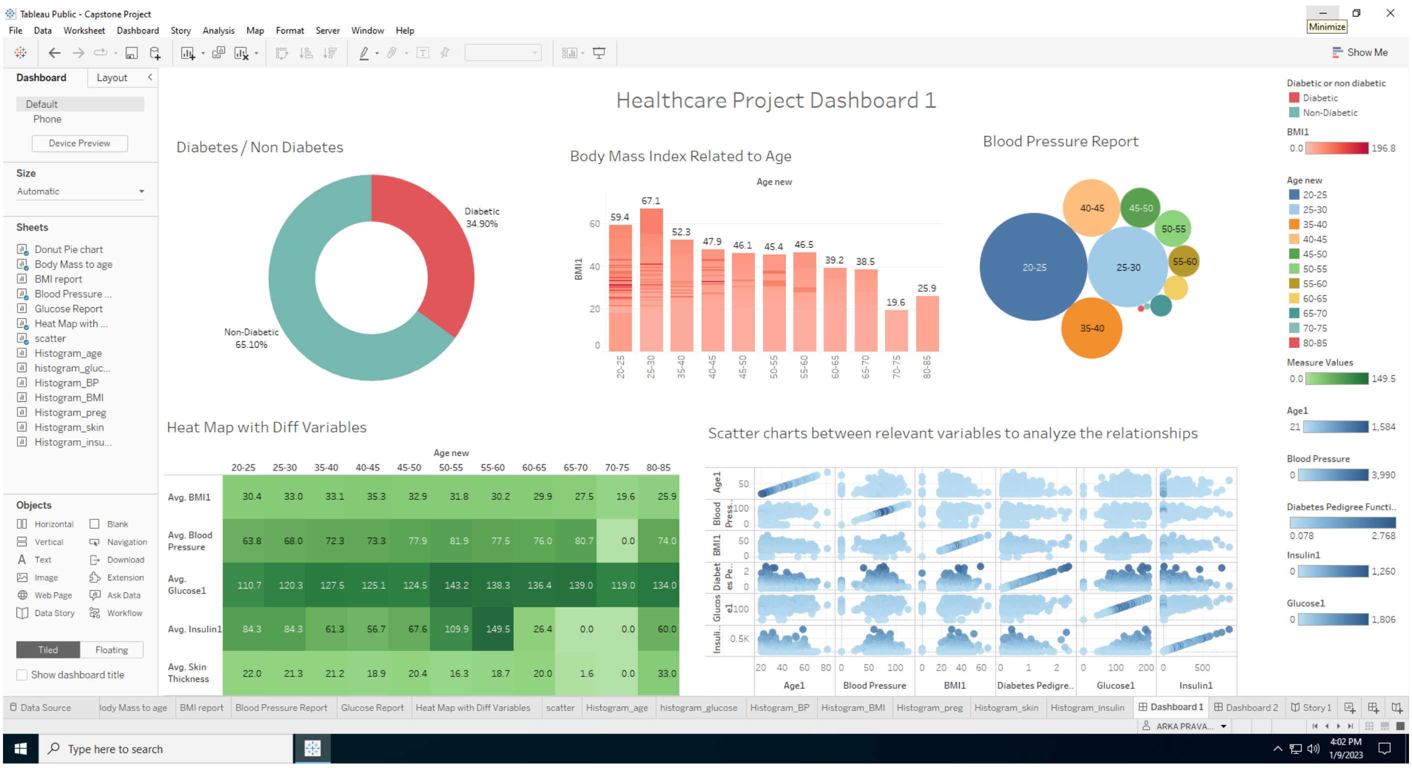
4) Heatmap of correlation analysis among the relevant variables

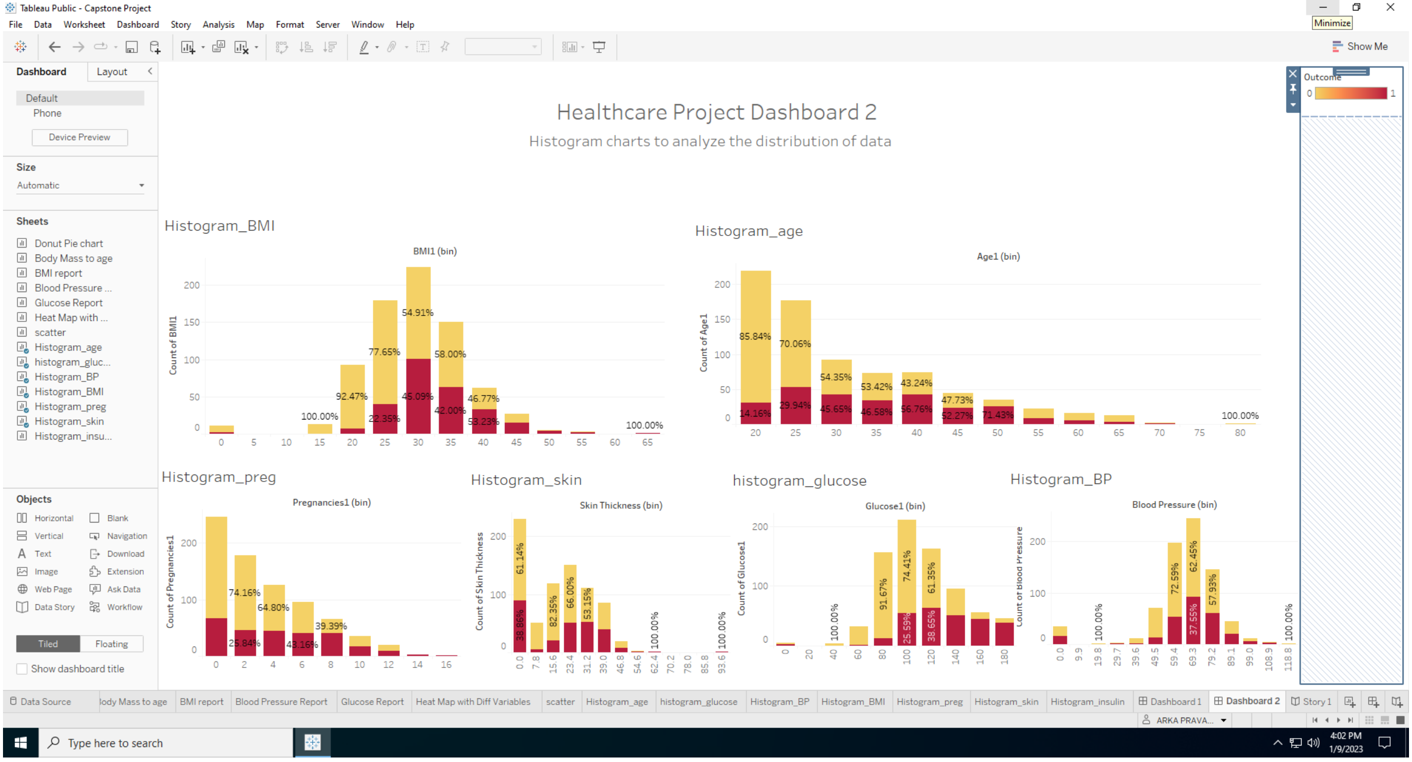


5) Create bins of these age values: 20-25, 25-30, 30-35, etc. Analyze different variables for these age brackets using a bubble chart



And Finally we have created two Dashboards to display these analysis in one place





And this concludes our analysis on NIDDK (National Institute of Diabetes and Digestive and Kidney Diseases) data.

Type *Markdown* and LaTeX: α^2