diabetes-1

October 2, 2024

1 By prisca

2 i used all the classification to detect which model best suit this dataset

[2]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import sklearn
```

[3]:
```
df=pd.read_csv(r'C:\Users\USER\Documents\dataset\diabetes-Data.csv')
```

[4]:
```
df.head()
```

[4]:

	Id	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	\
0	1	6	148	72	35	0	33.6	
1	2	1	85	66	29	0	26.6	
2	3	8	183	64	0	0	23.3	
3	4	1	89	66	23	94	28.1	
4	5	0	137	40	35	168	43.1	

	DiabetesPedigreeFunction	Age	Outcome
0	0.627	50	1
1	0.351	31	0
2	0.672	32	1
3	0.167	21	0
4	2.288	33	1

[5]:
```
df.shape
```

[5]:
```
(2768, 10)
```

[6]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2768 entries, 0 to 2767
```

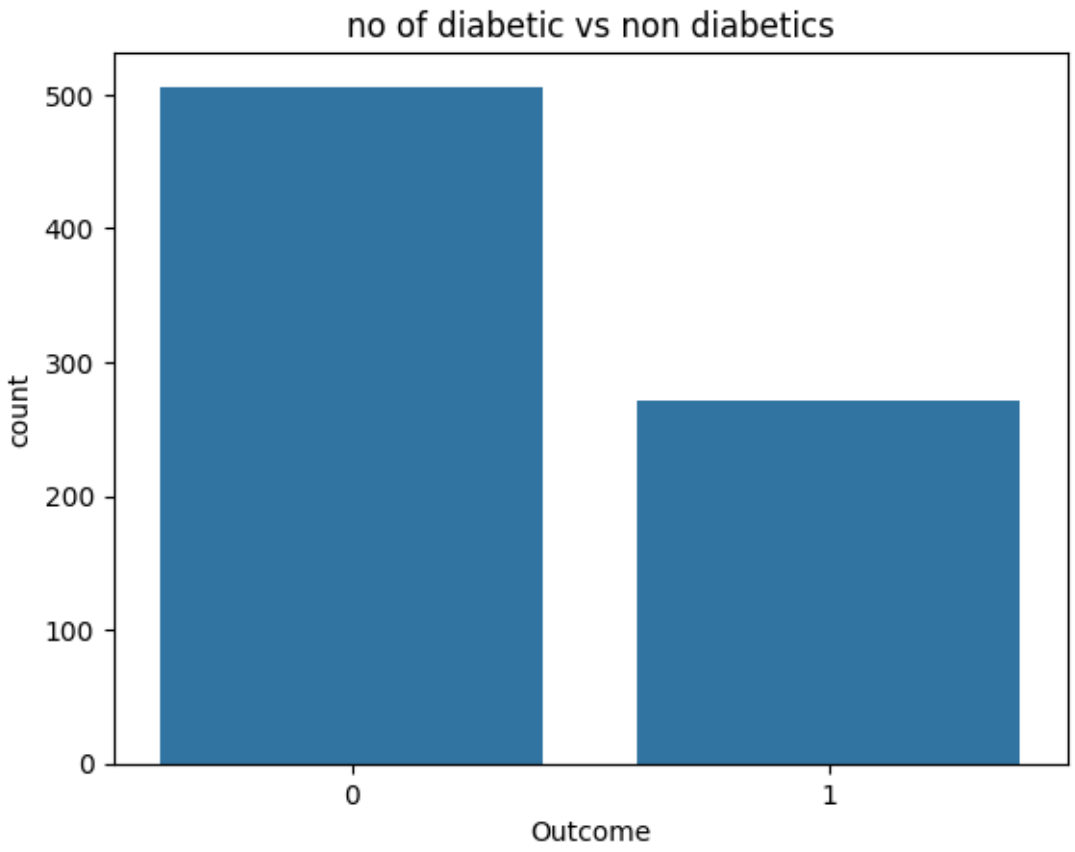
```
Data columns (total 10 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   Id                        2768 non-null   int64
 1   Pregnancies               2768 non-null   int64
 2   Glucose                   2768 non-null   int64
 3   BloodPressure             2768 non-null   int64
 4   SkinThickness             2768 non-null   int64
 5   Insulin                   2768 non-null   int64
 6   BMI                       2768 non-null   float64
 7   DiabetesPedigreeFunction  2768 non-null   float64
 8   Age                       2768 non-null   int64
 9   Outcome                   2768 non-null   int64
dtypes: float64(2), int64(8)
memory usage: 216.4 KB
```

[7]:
```
df.columns
```

[7]:
```
Index(['Id', 'Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness',
       'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

[79]:
```
sns.countplot(x='Outcome',data=df)
plt.title('no of diabetic vs non diabetics')
```

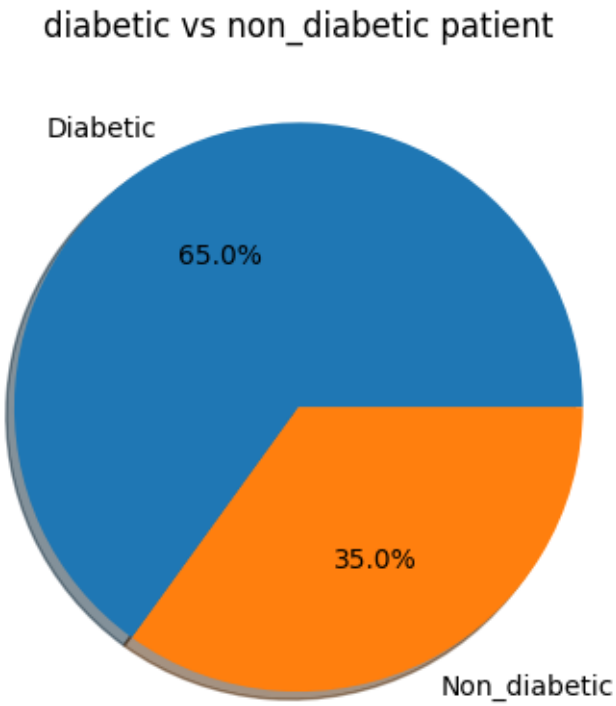
[79]:
```
Text(0.5, 1.0, 'no of diabetic vs non diabetics')
```



[82]:
```
df6=df['Outcome'].value_counts()
```

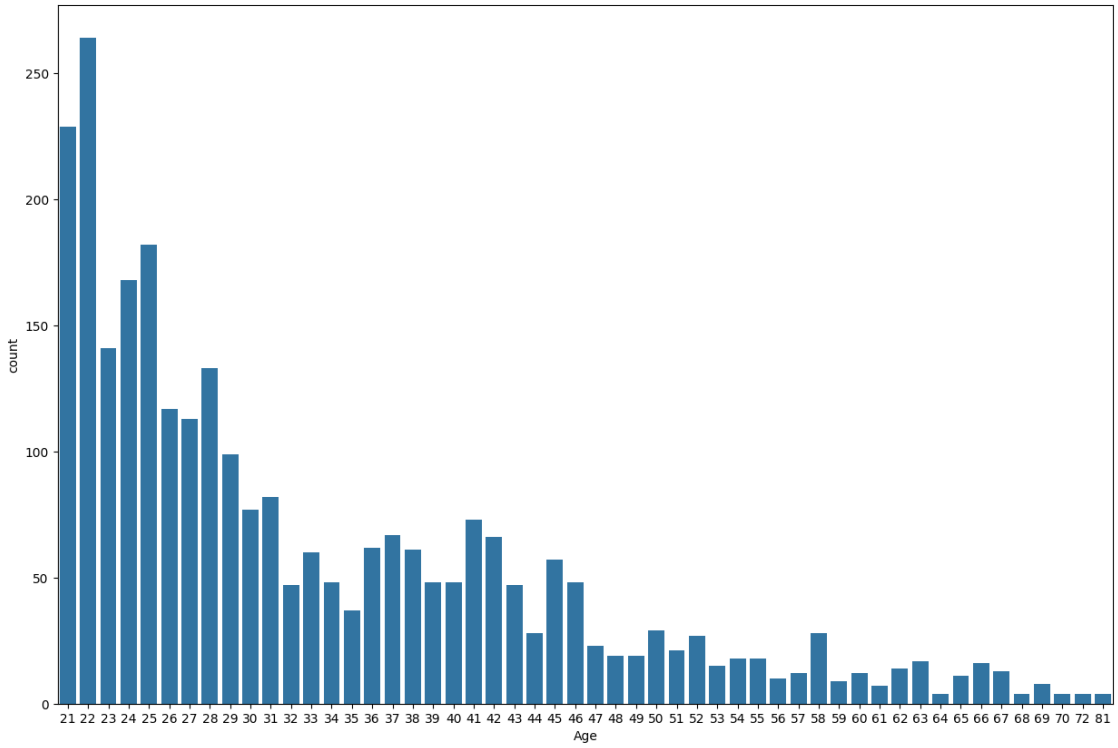
[90]:
```
plt.pie(df6, labels=['Diabetic','Non_diabetic'], autopct='%1.1f%%',shadow=True)
plt.savefig('diabetic.jpg',pad_inches=0.8,bbox_inches='tight')
plt.title('diabetic vs non_diabetic patient')    # over 65% patient are diabetic
```

[90]:
```
Text(0.5, 1.0, 'diabetic vs non_diabetic patient')
```



[9]:
```
fig, ax=plt.subplots(figsize=(15,10))
sns.countplot(x='Age',data=df)
```

[9]:
```
<Axes: xlabel='Age', ylabel='count'>
```



[10]:
```
df['Age'].mean()
```

[10]:
```
33.13222543352601
```

[11]:
```
df.head()
```

[11]:

	Id	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	\
0	1	6	148	72	35	0	33.6	
1	2	1	85	66	29	0	26.6	
2	3	8	183	64	0	0	23.3	
3	4	1	89	66	23	94	28.1	
4	5	0	137	40	35	168	43.1	

	DiabetesPedigreeFunction	Age	Outcome
0	0.627	50	1
1	0.351	31	0
2	0.672	32	1
3	0.167	21	0
4	2.288	33	1

[12]:
```
df2=df.drop(['Id','Pregnancies'],axis=1,inplace=True)
```

[13]:
```
df.columns
```

[13]:
```
Index(['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI',
       'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

[14]:
```
df.columns=['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI',
       'Diabetes_degree', 'Age', 'Outcome']
```

[15]:
```
df5=df.drop(['SkinThickness'],axis=1,inplace=True)
```

[16]:
```
df.head(10)
```

[16]:

	Glucose	BloodPressure	Insulin	BMI	Diabetes_degree	Age	Outcome
0	148	72	0	33.6	0.627	50	1
1	85	66	0	26.6	0.351	31	0
2	183	64	0	23.3	0.672	32	1
3	89	66	94	28.1	0.167	21	0
4	137	40	168	43.1	2.288	33	1
5	116	74	0	25.6	0.201	30	0
6	78	50	88	31.0	0.248	26	1
7	115	0	0	35.3	0.134	29	0
8	197	70	543	30.5	0.158	53	1
9	125	96	0	0.0	0.232	54	1

[17]:
```
df.isnull().sum() # no missing values
```

[17]:
```
Glucose             0
BloodPressure       0
Insulin             0
BMI                 0
Diabetes_degree     0
Age                 0
Outcome             0
dtype: int64
```

[18]:
```
df.duplicated().sum()
```

[18]:
```
1990
```

[19]:
```
df7=df.drop_duplicates(inplace=True) #  duplicates handled
```

[20]:
```
df.duplicated().sum()
```

[20]:
```
0
```

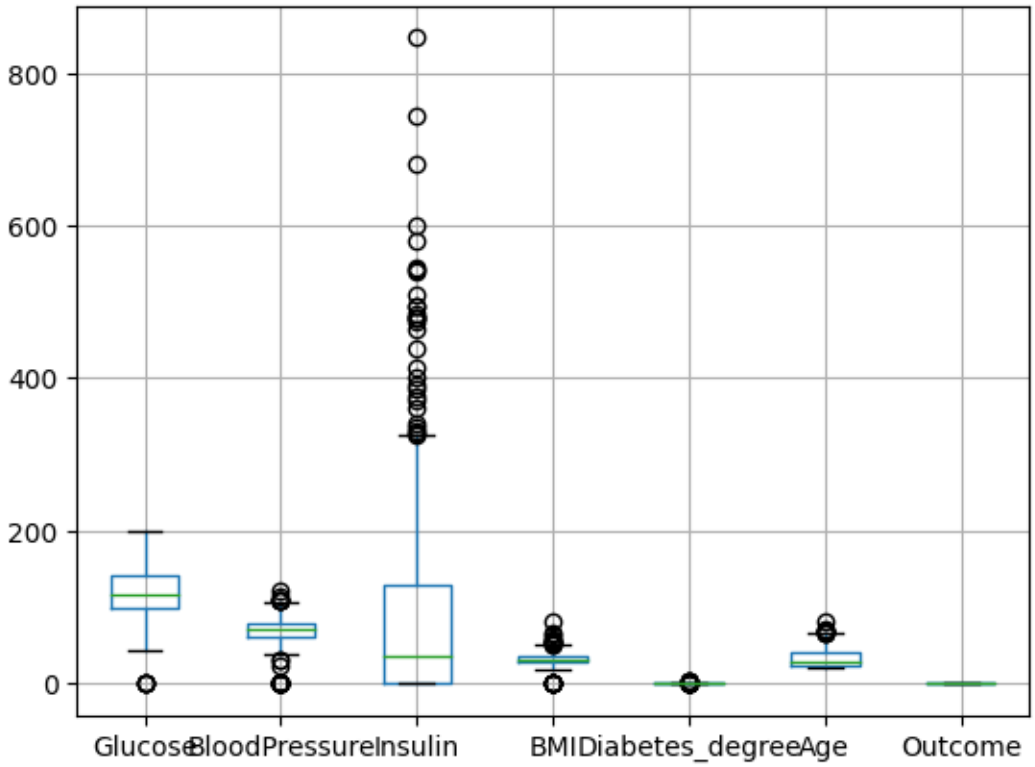
[21]:
```
df.head()
```

[21]:

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

[22]:
```
df.boxplot(column=['Glucose', 'BloodPressure', 'Insulin', 'BMI',␣
↪'Diabetes_degree', 'Age','Outcome'])
```

[22]: <Axes: >



2.1 handling outlier

[98]:
```
q1=df['Insulin'].quantile(0.25)
q3=df['Insulin'].quantile(0.75)
iqr=q3-q1
upperlimit=q3+(1.5*iqr)
lowerlimit=q1-(1.5*iqr)
upperlimit,lowerlimit
```

[98]: (325.0, -195.0)

[100]:
```
out=df.loc[(df['Insulin']>upperlimit)|(df['Insulin']<lowerlimit)]
```

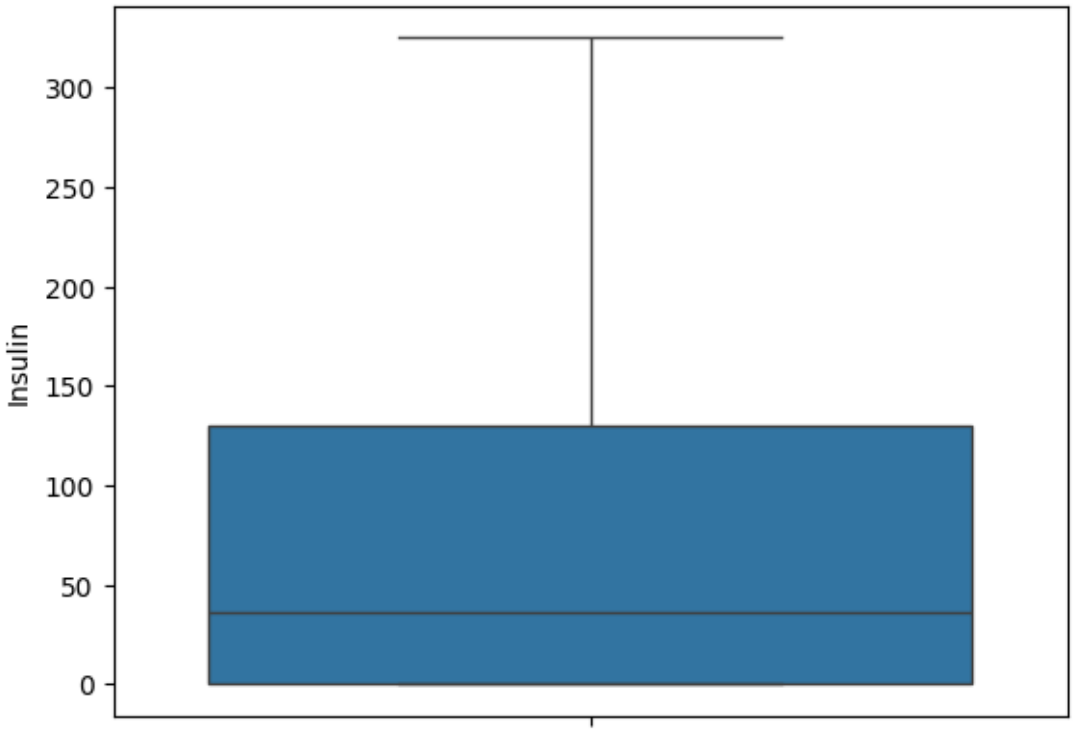
[101]:
```
len(out)
```

[101]: 30

[103]:
```
df.loc[(df['Insulin']>upperlimit),'Insulin']=upperlimit
df.loc[(df['Insulin']<lowerlimit),'Insulin']=lowerlimit
```

[104]:
```
sns.boxplot(df['Insulin'])
```

[104]: <Axes: ylabel='Insulin'>



[105]:
```
q1=df['BMI'].quantile(0.25)
q3=df['BMI'].quantile(0.75)
iqr=q3-q1
upperlimit=q3+(1.5*iqr)
lowerlimit=q1-(1.5*iqr)
upperlimit,lowerlimit
```

[105]: (50.949999999999996, 13.15)

[107]:
```
out_df=df.loc[(df['BMI']>upperlimit)|(df['BMI']<lowerlimit)]
```

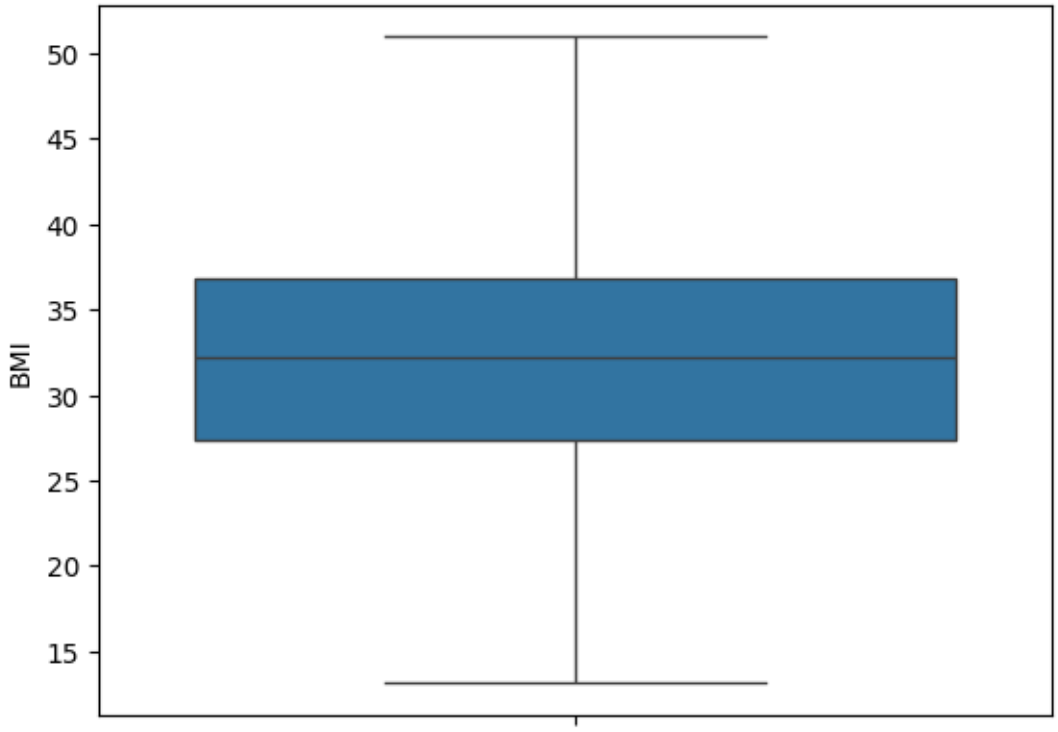
[108]:
```
len(out_df)
```

[108]: 22

[109]:
```
df.loc[(df['BMI']>upperlimit),'BMI']=upperlimit
df.loc[(df['BMI']<lowerlimit),'BMI']=lowerlimit
```

[110]:
```
sns.boxplot(df['BMI'])
```

[110]: <Axes: ylabel='BMI'>



[112]:
```
q1=df['BloodPressure'].quantile(0.25)
q3=df['BloodPressure'].quantile(0.75)
iqr=q3-q1
upperlimit=q3+(1.5*iqr)
lowerlimit=q1-(1.5*iqr)
upperlimit,lowerlimit
```

[112]: (107.0, 35.0)

[115]:
```
bloo_df=df.
  ↪loc[(df['BloodPressure']>upperlimit)|(df['BloodPressure']<lowerlimit)]
```

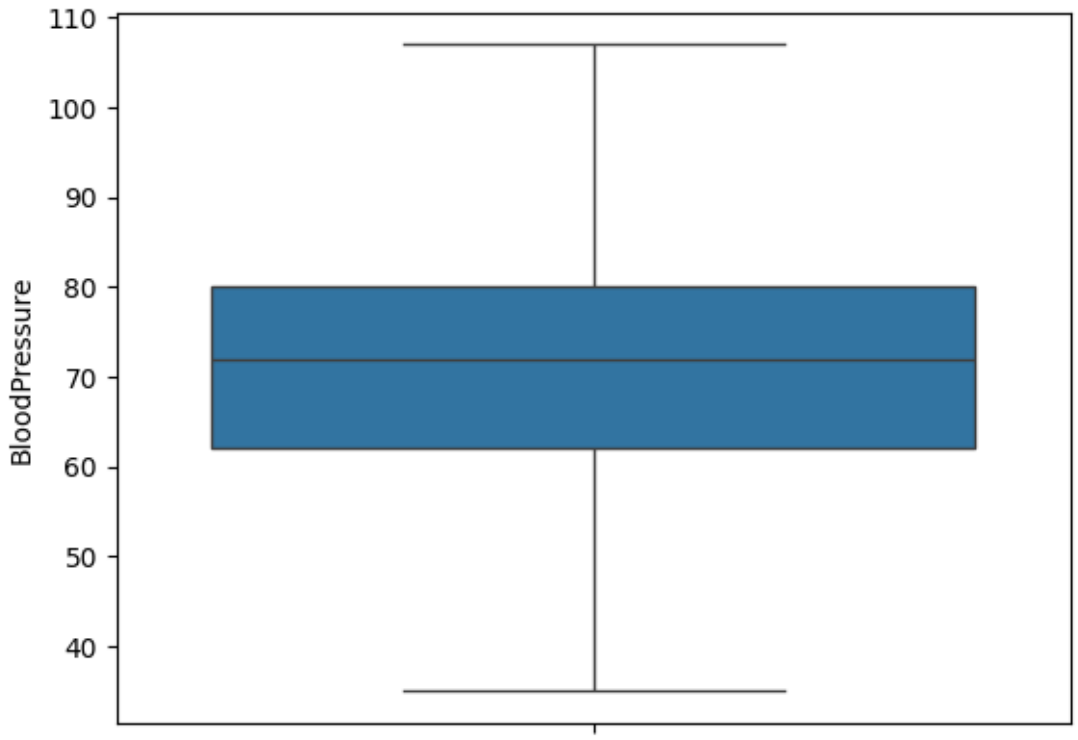
[116]:
```
len(bloo_df)
```

[116]: 0

[117]:
```
df.loc[(df['BloodPressure']>upperlimit),'BloodPressure']=upperlimit
df.loc[(df['BloodPressure']<lowerlimit),'BloodPressure']=lowerlimit
```

[118]:
```
sns.boxplot(df['BloodPressure'])
```

[118]: <Axes: ylabel='BloodPressure'>



[119]:
```
q1=df['Age'].quantile(0.25)
q3=df['Age'].quantile(0.75)
iqr=q3-q1
upperlimit=q3+(1.5*iqr)
lowerlimit=q1-(1.5*iqr)
upperlimit,lowerlimit
```

[119]: (66.5, -1.5)

[120]:
```
Age_df=df.loc[(df['BloodPressure']>upperlimit)|(df['BloodPressure']<lowerlimit)]
```

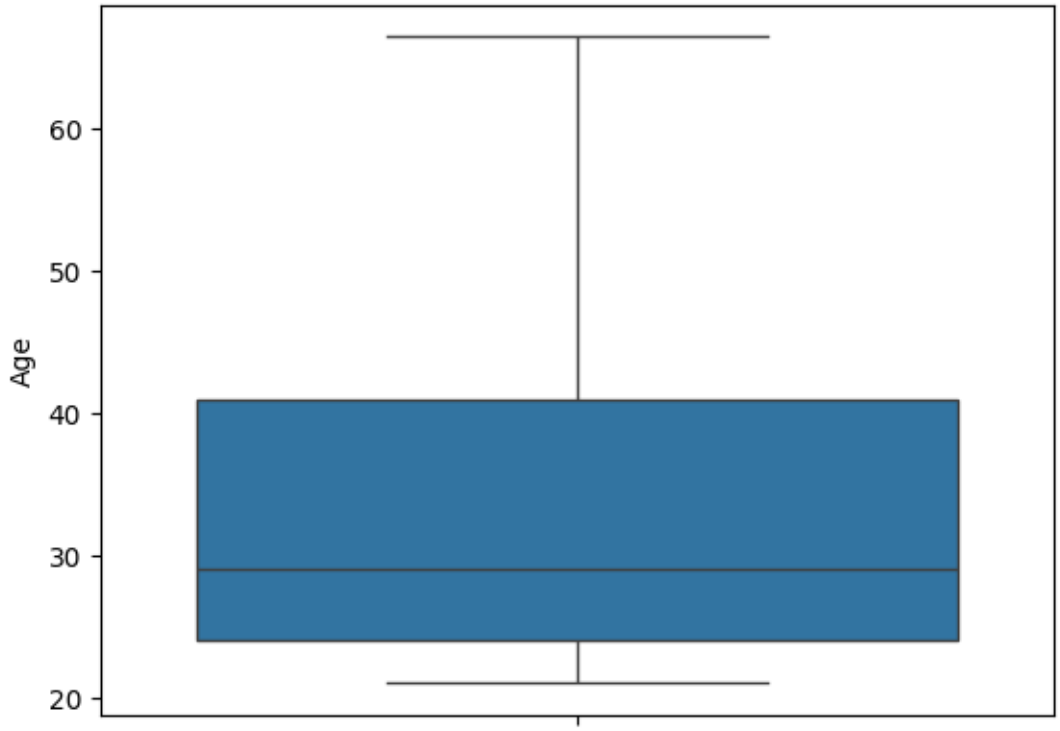
[121]:
```
len(Age_df)
```

[121]: 498

[122]:
```
df.loc[(df['Age']>upperlimit),'Age']=upperlimit
df.loc[(df['Age']<lowerlimit),'Age']=lowerlimit
```

[123]:
```
sns.boxplot(df['Age'])
```

[123]: <Axes: ylabel='Age'>



3 statistical analysis

[133]:
```
df.describe()
```

[133]:

	Glucose	BloodPressure	Insulin	BMI	Diabetes_degree	\
count	778.000000	778.000000	778.000000	778.000000	778.000000	
mean	121.199229	70.579692	74.615681	32.259897	0.471861	
std	31.990831	14.280945	94.543053	7.202884	0.330180	
min	0.000000	35.000000	0.000000	13.150000	0.078000	
25%	99.000000	62.000000	0.000000	27.325000	0.244000	
50%	117.000000	72.000000	36.000000	32.250000	0.374500	
75%	141.000000	80.000000	130.000000	36.775000	0.626750	
max	199.000000	107.000000	325.000000	50.950000	2.420000	

```
                Age     Outcome
count   778.000000  778.000000
mean     33.306555    0.349614
std      11.659594    0.477155
min      21.000000    0.000000
25%      24.000000    0.000000
50%      29.000000    0.000000
75%      41.000000    1.000000
max      66.500000    1.000000
```

4 correlation

[134]:
```
df.corr()
```

[134]:
```
                  Glucose  BloodPressure   Insulin       BMI  Diabetes_degree  \
Glucose          1.000000       0.181315  0.318247  0.237895         0.137337
BloodPressure    0.181315       1.000000  0.044089  0.255752         0.031285
Insulin          0.318247       0.044089  1.000000  0.208445         0.191229
BMI              0.237895       0.255752  0.208445  1.000000         0.135974
Diabetes_degree  0.137337       0.031285  0.191229  0.135974         1.000000
Age              0.264498       0.306607 -0.058915  0.048321         0.034873
Outcome          0.459152       0.122449  0.120865  0.291450         0.172160

                     Age   Outcome
Glucose          0.264498  0.459152
BloodPressure    0.306607  0.122449
Insulin         -0.058915  0.120865
BMI              0.048321  0.291450
Diabetes_degree  0.034873  0.172160
Age              1.000000  0.248594
Outcome          0.248594  1.000000
```

[24]:
```
df.columns
```

[24]:
```
Index(['Glucose', 'BloodPressure', 'Insulin', 'BMI', 'Diabetes_degree', 'Age',
       'Outcome'],
      dtype='object')
```

5 Model building

[26]:
```
from sklearn.linear_model import LogisticRegression
from sklearn .tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import RandomForestClassifier
```

```
from sklearn.svm import SVC
```

[27]:
```
x=df[['Glucose', 'BloodPressure', 'Insulin', 'BMI', 'Diabetes_degree', 'Age']]
y=df['Outcome']
```

6 Data splitting

[156]:
```
from sklearn.model_selection import train_test_split
```

[157]:
```
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.
↪2,random_state=42)
```

[158]:
```
from sklearn .preprocessing import StandardScaler
```

[159]:
```
x_train.shape, x_test.shape
```

[159]:
```
((622, 6), (156, 6))
```

[160]:
```
y_train.shape,y_test.shape
```

[160]:
```
((622,), (156,))
```

7 scaling the data

[129]:
```
scaler=StandardScaler()
```

[130]:
```
x_train=scaler. fit_transform(x_train)
```

[131]:
```
x_test=scaler.transform(x_test)
```

[36]:
```
y_train.shape,x_train.shape
```

[36]:
```
((622,), (622, 6))
```

[37]:
```
tree=DecisionTreeClassifier()
knn=KNeighborsClassifier(n_neighbors=5)
sv=SVC()
log=LogisticRegression()
rm=RandomForestClassifier()
```

[38]:
```
knn.fit(x_train,y_train)
log.fit(x_train,y_train)
```

[38]:
```
LogisticRegression()
```

[39]:
```
tree.fit(x_train,y_train)
knn.fit(x_train,y_train)
sv.fit(x_train,y_train)
rm.fit(x_train,y_train)
```

[39]:
```
RandomForestClassifier()
```

[40]:
```
ypred1=tree.predict(x_test)
ypred2=knn.predict(x_test)
ypred3=sv.predict(x_test)
ypred4=rm.predict(x_test)
ypred5=log.predict(x_test)
```

8 Model Evaluation

[41]:
```
from sklearn import metrics
```

[136]:
```
metrics.accuracy_score(ypred1,y_test) # decision tree
```

[136]:
```
0.6923076923076923
```

[137]:
```
metrics.accuracy_score(ypred2,y_test) # knn
```

[137]:
```
0.7628205128205128
```

[138]:
```
metrics.accuracy_score(ypred3,y_test) # svm
```

[138]:
```
0.7948717948717948
```

[139]:
```
metrics.accuracy_score(ypred4,y_test) # randomforest
```

[139]:
```
0.7628205128205128
```

[140]:
```
metrics.accuracy_score(ypred5,y_test) # losgistics regression
```

[140]:
```
0.7564102564102564
```

[141]:
```
tree.score(x_train,y_train)
```

[141]:
```
1.0
```

[142]:
```
knn.score(x_train,y_train)
```

[142]:
```
0.8135048231511254
```

[143]:
```
rm.score(x_train,y_train)
```

[143]:
```
1.0
```

[144]:
```
sv.score(x_train,y_train)
```

[144]:
```
0.8247588424437299
```

[145]:
```
log.score(x_train,y_train)
```

[145]:
```
0.7781350482315113
```

[52]:
```
treee=pd.DataFrame({'actual':y_test,
                    'predicted':ypred1})
```

[146]:
```
treee
```

[146]:

	actual	predicted
595	1	1
587	0	0
543	0	0
644	0	0
487	0	1
..	…	…
351	0	0
79	0	0
148	0	0
333	0	0
168	0	1

[156 rows x 2 columns]

[147]:
```
knnn=pd.DataFrame({'actual':y_test,
                    'predicted':ypred2})
```

[148]:
```
knnn
```

[148]:

	actual	predicted
595	1	1
587	0	0
543	0	0
644	0	0
487	0	1
..	…	…
351	0	0
79	0	0
148	0	0
333	0	0
168	0	0

```
[156 rows x 2 columns]
```

[56]:
```
svv=pd.DataFrame({'actual':y_test,
                  'predicted':ypred3})
```

[57]:
```
svv
```

[57]:
```
     actual  predicted
595       1          1
587       0          0
543       0          0
644       0          0
487       0          1
..      …         …
351       0          0
79        0          0
148       0          0
333       0          0
168       0          0

[156 rows x 2 columns]
```

[58]:
```
logg=pd.DataFrame({'actual':y_test,
                  'predicted':ypred5})
```

[149]:
```
logg
```

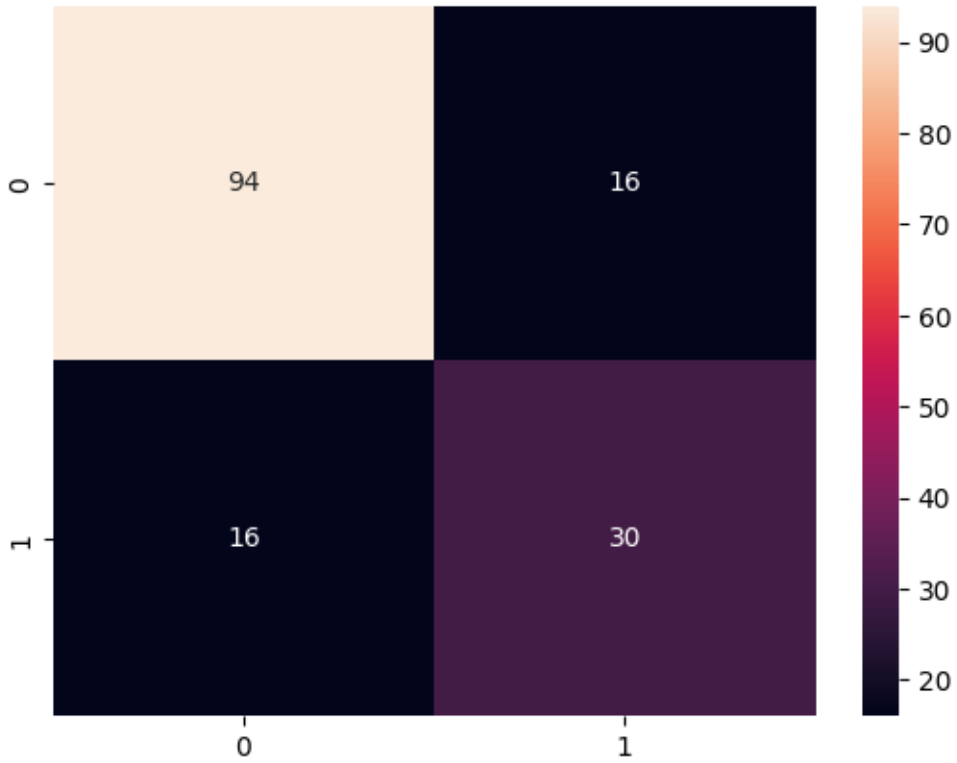
[149]:
```
     actual  predicted
595       1          1
587       0          0
543       0          0
644       0          0
487       0          1
..      …         …
351       0          0
79        0          0
148       0          1
333       0          0
168       0          0

[156 rows x 2 columns]
```

[60]:
```
from sklearn .metrics import confusion_matrix
```

[61]:
```
sv_cf=confusion_matrix(ypred3,y_test)
```

[150]:
```
sns.heatmap(sv_cf,annot=True,color='green')
```

[150]: <Axes: >

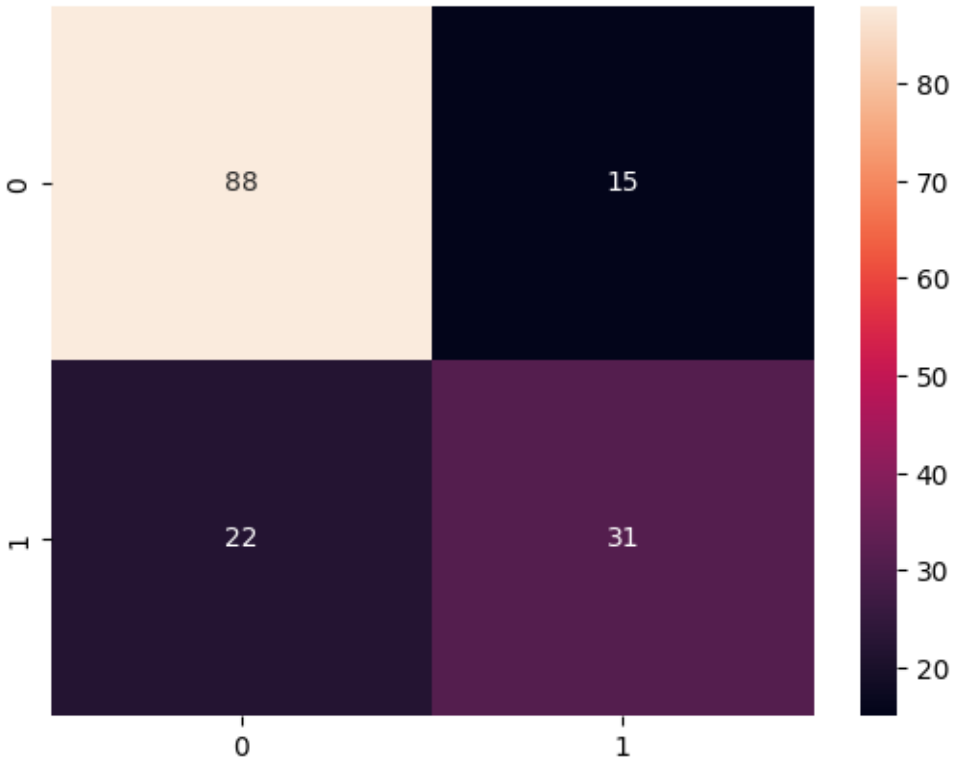


[151]:
```
# 0 was predicted correctly 94 times and wrong 16 times
# 1 was predicted corrcetly 30 times and wrong 16 times
```

[152]:
```
knn_cf=confusion_matrix(ypred2,y_test)
```

[153]:
```
sns.heatmap(knn_cf,annot=True,)
```

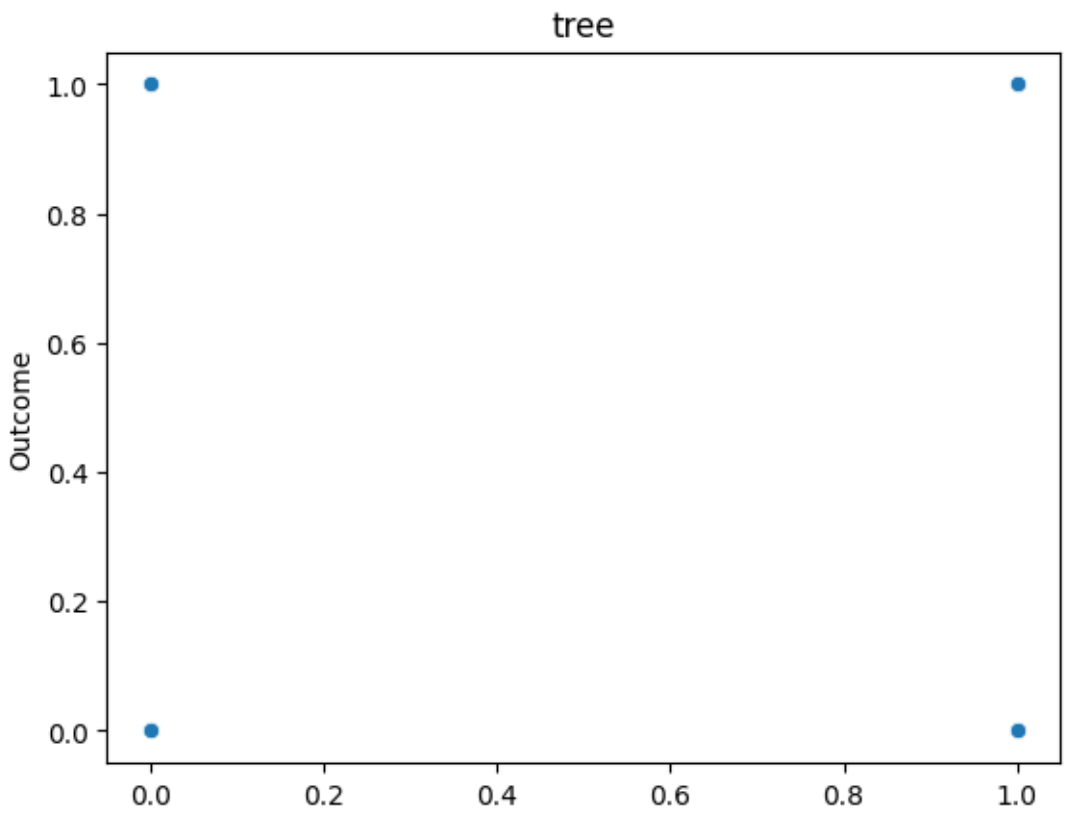
[153]: <Axes: >



[66]:
```
# 0 correctly predicted 88 times amd 15 times wrong
# 1 correctly predicted 31 times and 22 times wrong
```

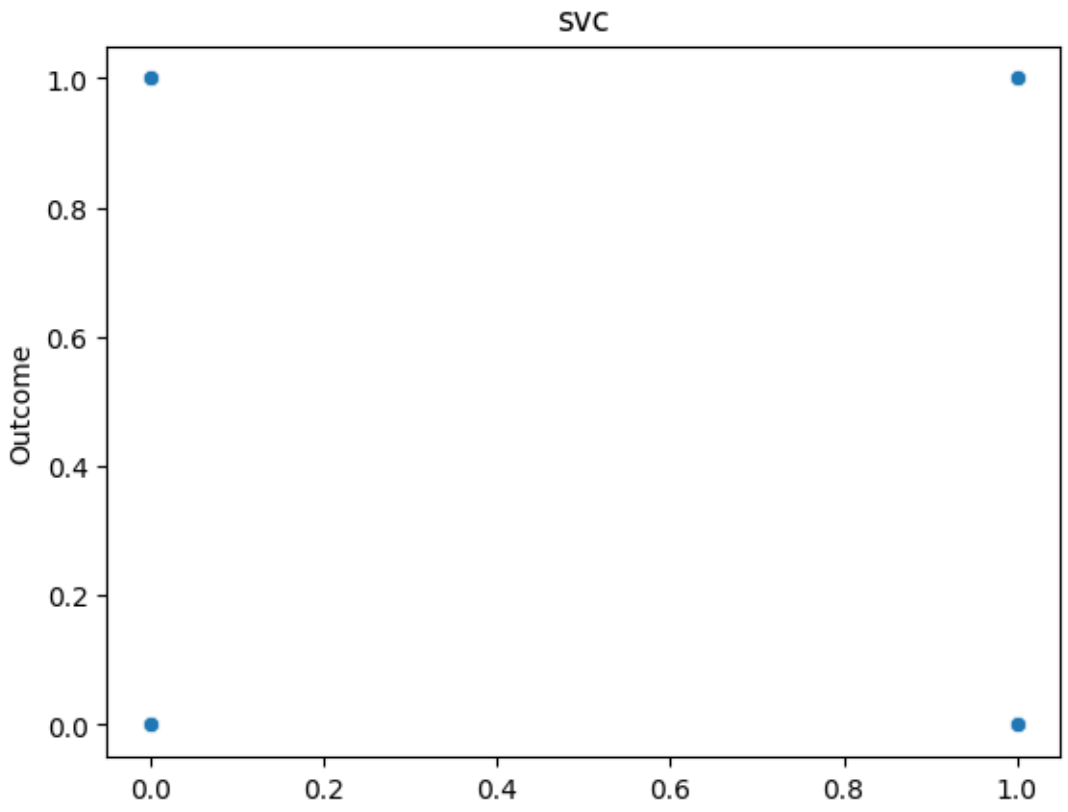
[67]:
```
sns.scatterplot(x=ypred1,y=y_test)
plt.title('tree')
```

[67]: Text(0.5, 1.0, 'tree')



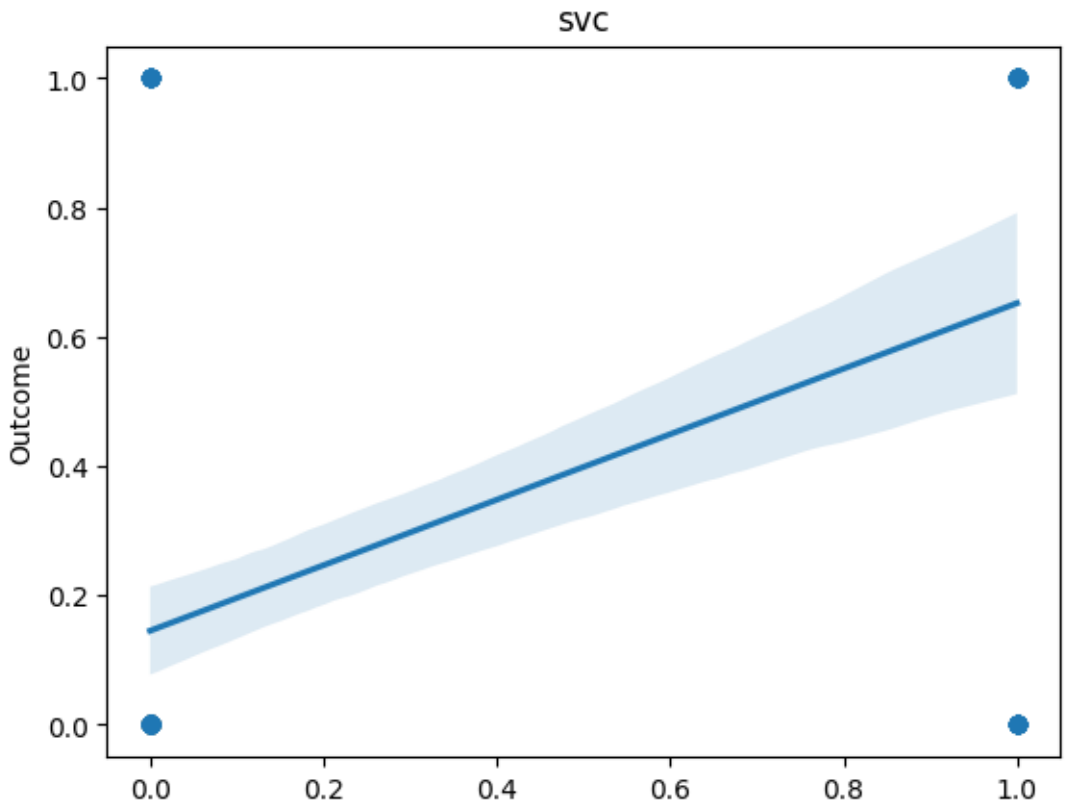
[68]:
```
sns.scatterplot(x=ypred3,y=y_test)
plt.title('svc')
```

[68]: Text(0.5, 1.0, 'svc')



[154]:
```
sns.regplot(x=ypred3,y=y_test)
plt.title('svc')
```

[154]: Text(0.5, 1.0, 'svc')



9 svc model gave higher accuracy and is chosen

10 Model testing

[161]:
```
sv.predict(scaler.transform([[183,        64,        0        ,23.3,        0.
↪672        ,32        ]]))
```

```
C:\Users\USER\anaconda3\envs\tf_env\lib\site-packages\sklearn\base.py:465:
UserWarning: X does not have valid feature names, but StandardScaler was fitted
with feature names
  warnings.warn(
```

[161]:
```
array([1], dtype=int64)
```

[162]:
```
sv.predict(scaler.transform([[116,        74,        0,        25.6,        0.
↪201,        30        ]])) #corrcetly predicted
```

```
C:\Users\USER\anaconda3\envs\tf_env\lib\site-packages\sklearn\base.py:465:
UserWarning: X does not have valid feature names, but StandardScaler was fitted
with feature names
```

```
  warnings.warn(
```

[162]:
```
array([0], dtype=int64)
```

[ ]:
```
```

[163]:
```
sv.predict(scaler.transform([[137,        40        ,168,        43.1,        2.
↪288,        33        ]]))  #corrcetly predicted
```

```
C:\Users\USER\anaconda3\envs\tf_env\lib\site-packages\sklearn\base.py:465:
UserWarning: X does not have valid feature names, but StandardScaler was fitted
with feature names
  warnings.warn(
```

[163]:
```
array([1], dtype=int64)
```

[77]:
```
# Conclusion:
## model fitted and predicted well
## there is 65% of diabetic patient , simply means diabeties is gradually␣
↪increasing and people should watch out for their health.

# Recommendation:
## Patient should check their health regulary.
## they should also have personalized sugar checking device  in their home.
## no self treatment.
## Always talk to your doctor.
## Drink water regularly.
```