```
from sklearn.svm import SVC
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.preprocessing import LabelEncoder
from sklearn.model_selection import train_test_split
from sklearn.metrics import
accuracy_score,classification_report,confusion_matrix,roc_auc_score,ro
c_curve,precision_score,recall_score

data=pd.read_csv("agaricus-lepiota.data",names=['poison','cap-
shape','cap-surface','cap-color','bruises','odor','gill-
attachment','gill-spacing','gill-size','gill-color','stalk-
shape','stalk-root','stalk-surface-above-ring','stalk-surface-below-
ring','stalk-color-above-ring','stalk-color-below-ring','veil-
type','veil-color',' ring-number','ring-type','spore-print-
color','population','habitat'])

data

     poison cap-shape cap-surface cap-color bruises odor gill-
attachment  \
0         p         x           s         n       t    p
f
1         e         x           s         y       t    a
f
2         e         b           s         w       t    l
f
3         p         x           y         w       t    p
f
4         e         x           s         g       f    n
f
...     ...       ...         ...       ...     ...  ...               .
..
8119      e         k           s         n       f    n
a
8120      e         x           s         n       f    n
a
8121      e         f           s         n       f    n
a
8122      p         k           y         n       f    y
f
8123      e         x           s         n       f    n
a

     gill-spacing gill-size gill-color  ... stalk-surface-below-
ring  \
0               c         n          k  ...                         s
```

```
1               c         b          k  ...                        s

2               c         b          n  ...                        s

3               c         n          n  ...                        s

4               w         b          k  ...                        s

...           ...       ...        ...  ...                      ...

8119            c         b          y  ...                        s

8120            c         b          y  ...                        s

8121            c         b          n  ...                        s

8122            c         n          b  ...                        k

8123            c         b          y  ...                        s


     stalk-color-above-ring stalk-color-below-ring veil-type veil-
color  \
0                         w                       w         p
w
1                         w                       w         p
w
2                         w                       w         p
w
3                         w                       w         p
w
4                         w                       w         p
w
...                     ...                     ...       ...        ..
.
8119                      o                       o         p
o
8120                      o                       o         p
n
8121                      o                       o         p
o
8122                      w                       w         p
w
8123                      o                       o         p
o

      ring-number ring-type spore-print-color population habitat
0               o         p                 k          s       u
1               o         p                 n          n       g
2               o         p                 n          n       m
```

```
3               o         p                    k          s       u
4               o         e                    n          a       g
...           ...       ...                  ...        ...     ...
8119            o         p                    b          c       l
8120            o         p                    b          v       l
8121            o         p                    b          c       l
8122            o         e                    w          v       l
8123            o         p                    o          c       l

[8124 rows x 23 columns]
```

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 8124 entries, 0 to 8123
Data columns (total 23 columns):
 #   Column                    Non-Null Count  Dtype 
---  ------                    --------------  ----- 
 0   poison                    8124 non-null   object
 1   cap-shape                 8124 non-null   object
 2   cap-surface               8124 non-null   object
 3   cap-color                 8124 non-null   object
 4   bruises                   8124 non-null   object
 5   odor                      8124 non-null   object
 6   gill-attachment           8124 non-null   object
 7   gill-spacing              8124 non-null   object
 8   gill-size                 8124 non-null   object
 9   gill-color                8124 non-null   object
 10  stalk-shape               8124 non-null   object
 11  stalk-root                8124 non-null   object
 12  stalk-surface-above-ring  8124 non-null   object
 13  stalk-surface-below-ring  8124 non-null   object
 14  stalk-color-above-ring    8124 non-null   object
 15  stalk-color-below-ring    8124 non-null   object
 16  veil-type                 8124 non-null   object
 17  veil-color                8124 non-null   object
 18   ring-number              8124 non-null   object
 19  ring-type                 8124 non-null   object
 20  spore-print-color         8124 non-null   object
 21  population                8124 non-null   object
 22  habitat                   8124 non-null   object
dtypes: object(23)
memory usage: 1.4+ MB
```

```
data.isnull().sum()
```

```
poison                      0
cap-shape                   0
cap-surface                 0
cap-color                   0
```

```
bruises                     0
odor                        0
gill-attachment             0
gill-spacing                0
gill-size                   0
gill-color                  0
stalk-shape                 0
stalk-root                  0
stalk-surface-above-ring    0
stalk-surface-below-ring    0
stalk-color-above-ring      0
stalk-color-below-ring      0
veil-type                   0
veil-color                  0
 ring-number                0
ring-type                   0
spore-print-color           0
population                  0
habitat                     0
dtype: int64
```

```
for column in data.columns:
    xx=data[column].value_counts()
    print(xx.index)
```

```
Index(['e', 'p'], dtype='object')
Index(['x', 'f', 'k', 'b', 's', 'c'], dtype='object')
Index(['y', 's', 'f', 'g'], dtype='object')
Index(['n', 'g', 'e', 'y', 'w', 'b', 'p', 'c', 'u', 'r'],
dtype='object')
Index(['f', 't'], dtype='object')
Index(['n', 'f', 'y', 's', 'a', 'l', 'p', 'c', 'm'], dtype='object')
Index(['f', 'a'], dtype='object')
Index(['c', 'w'], dtype='object')
Index(['b', 'n'], dtype='object')
Index(['b', 'p', 'w', 'n', 'g', 'h', 'u', 'k', 'e', 'y', 'o', 'r'],
dtype='object')
Index(['t', 'e'], dtype='object')
Index(['b', '?', 'e', 'c', 'r'], dtype='object')
Index(['s', 'k', 'f', 'y'], dtype='object')
Index(['s', 'k', 'f', 'y'], dtype='object')
Index(['w', 'p', 'g', 'n', 'b', 'o', 'e', 'c', 'y'], dtype='object')
Index(['w', 'p', 'g', 'n', 'b', 'o', 'e', 'c', 'y'], dtype='object')
Index(['p'], dtype='object')
Index(['w', 'n', 'o', 'y'], dtype='object')
Index(['o', 't', 'n'], dtype='object')
Index(['p', 'e', 'l', 'f', 'n'], dtype='object')
Index(['w', 'n', 'k', 'h', 'r', 'u', 'o', 'y', 'b'], dtype='object')
Index(['v', 'y', 's', 'n', 'a', 'c'], dtype='object')
Index(['d', 'g', 'p', 'l', 'u', 'm', 'w'], dtype='object')
```

```
data.drop(["cap-color","veil-type","stalk-root","stalk-
shape"],axis=1,inplace=True)

data
```

```
     poison cap-shape cap-surface bruises odor gill-attachment gill-
spacing  \
0         p         x           s       t    p               f
c
1         e         x           s       t    a               f
c
2         e         b           s       t    l               f
c
3         p         x           y       t    p               f
c
4         e         x           s       f    n               f
w
...     ...       ...         ...     ...  ...             ...
...
8119      e         k           s       f    n               a
c
8120      e         x           s       f    n               a
c
8121      e         f           s       f    n               a
c
8122      p         k           y       f    y               f
c
8123      e         x           s       f    n               a
c

     gill-size gill-color stalk-surface-above-ring stalk-surface-
below-ring  \
0            n          k                         s
s
1            b          k                         s
s
2            b          n                         s
s
3            n          n                         s
s
4            b          k                         s
s
...        ...        ...                       ...
...
8119         b          y                         s
s
8120         b          y                         s
s
8121         b          n                         s
s
```

```
8122         n           b                         s
k
8123         b           y                         s
s

     stalk-color-above-ring stalk-color-below-ring veil-color  ring-
number  \
0                          w                       w          w
o
1                          w                       w          w
o
2                          w                       w          w
o
3                          w                       w          w
o
4                          w                       w          w
o
...                      ...                     ...        ...
...
8119                       o                       o          o
o
8120                       o                       o          n
o
8121                       o                       o          o
o
8122                       w                       w          w
o
8123                       o                       o          o
o

     ring-type spore-print-color population habitat
0            p                 k          s       u
1            p                 n          n       g
2            p                 n          n       m
3            p                 k          s       u
4            e                 n          a       g
...        ...               ...        ...     ...
8119         p                 b          c       l
8120         p                 b          v       l
8121         p                 b          c       l
8122         e                 w          v       l
8123         p                 o          c       l

[8124 rows x 19 columns]

data.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 8124 entries, 0 to 8123
Data columns (total 19 columns):
```

```
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   poison                    8124 non-null   object
 1   cap-shape                 8124 non-null   object
 2   cap-surface               8124 non-null   object
 3   bruises                   8124 non-null   object
 4   odor                      8124 non-null   object
 5   gill-attachment           8124 non-null   object
 6   gill-spacing              8124 non-null   object
 7   gill-size                 8124 non-null   object
 8   gill-color                8124 non-null   object
 9   stalk-surface-above-ring  8124 non-null   object
 10  stalk-surface-below-ring  8124 non-null   object
 11  stalk-color-above-ring    8124 non-null   object
 12  stalk-color-below-ring    8124 non-null   object
 13  veil-color                8124 non-null   object
 14   ring-number              8124 non-null   object
 15  ring-type                 8124 non-null   object
 16  spore-print-color         8124 non-null   object
 17  population                8124 non-null   object
 18  habitat                   8124 non-null   object
dtypes: object(19)
memory usage: 1.2+ MB

data.describe()

       poison cap-shape cap-surface bruises  odor gill-attachment  \
count    8124      8124        8124    8124  8124             8124
unique      2         6           4       2     9                2
top         e         x           y       f     n                f
freq     4208      3656        3244    4748  3528             7914

       gill-spacing gill-size gill-color stalk-surface-above-ring  \
count          8124      8124       8124                     8124
unique            2         2         12                        4
top               c         b          b                        s
freq           6812      5612       1728                     5176

       stalk-surface-below-ring stalk-color-above-ring stalk-color-
below-ring  \
count                      8124                   8124
8124
unique                        4                      9
9
top                           s                      w
w
freq                       4936                   4464
4384

       veil-color  ring-number ring-type spore-print-color population
```

```
habitat
count        8124          8124       8124                8124        8124
8124
unique          4             3          5                   9           6
7
top             w             o          p                   w           v
d
freq         7924          7488       3968                2388        4040
3148
```

```
data.dtypes
```

```
poison                       object
cap-shape                    object
cap-surface                  object
bruises                      object
odor                         object
gill-attachment              object
gill-spacing                 object
gill-size                    object
gill-color                   object
stalk-surface-above-ring     object
stalk-surface-below-ring     object
stalk-color-above-ring       object
stalk-color-below-ring       object
veil-color                   object
 ring-number                 object
ring-type                    object
spore-print-color            object
population                   object
habitat                      object
dtype: object
```

```
le=LabelEncoder()
for column in data.columns:
    data[column]=le.fit_transform(data[column])
```

```
data.head()
```

```
   poison  cap-shape  cap-surface  bruises  odor  gill-attachment  \
0       1          5            2        1     6                1
1       0          5            2        1     0                1
2       0          0            2        1     3                1
3       1          5            3        1     6                1
4       0          5            2        0     5                1

   gill-spacing  gill-size  gill-color  stalk-surface-above-ring  \
0             0          1           4                         2
1             0          0           4                         2
2             0          0           5                         2
```

```
3              0           1            5                            2
4              1           0            4                            2

   stalk-surface-below-ring  stalk-color-above-ring  stalk-color-
below-ring  \
0                          2                       7
7
1                          2                       7
7
2                          2                       7
7
3                          2                       7
7
4                          2                       7
7

   veil-color   ring-number  ring-type  spore-print-color  population
habitat
0           2             1          4                  2           3
5
1           2             1          4                  3           2
1
2           2             1          4                  3           2
3
3           2             1          4                  2           3
5
4           2             1          0                  3           0
1

x=data.iloc[:,1:].values
y=data.iloc[:,0].values

x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.2,rando
m_state=42)

cl1=SVC(kernel="rbf",random_state=0,probability=True)
cl1.fit(x_train,y_train)

SVC(probability=True, random_state=0)

cl1.score(x_train,y_train)

0.9832281889521465

ypred1=cl1.predict(x_test)

acc1=accuracy_score(y_test,ypred1)

acc1

0.9833846153846154
```

```
print("pscore",precision_score(y_test,ypred1))
```

```
pscore 0.9934640522875817
```

```
print("rscore",recall_score(y_test,ypred1))
```

```
rscore 0.9718670076726342
```

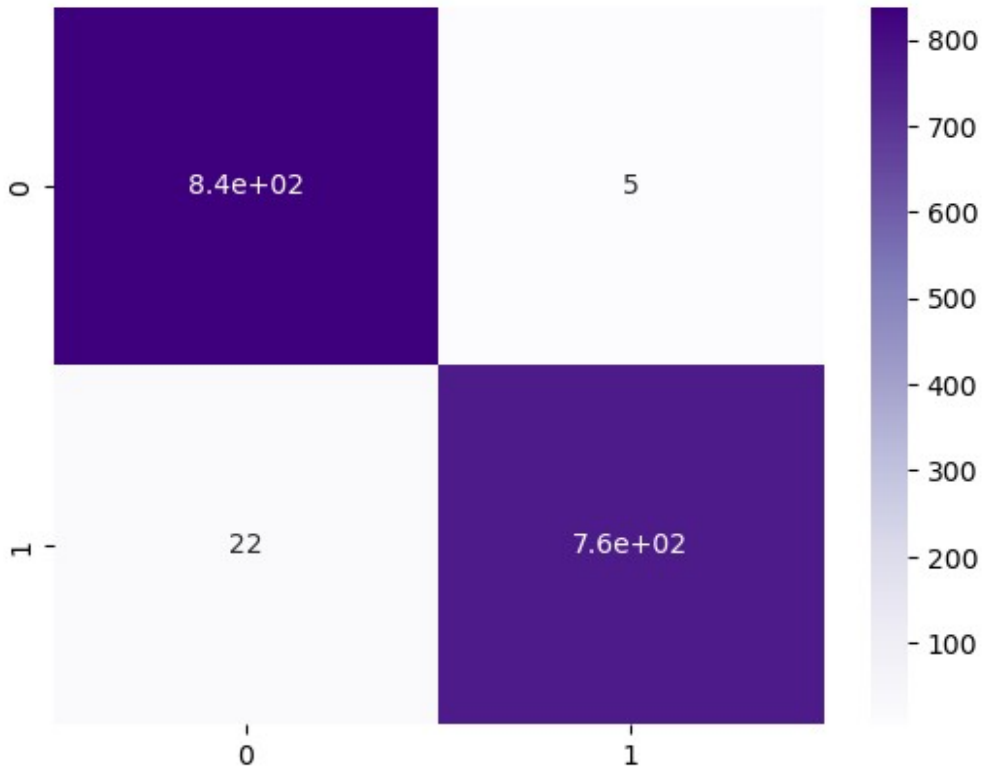
```
cm1=confusion_matrix(y_test,ypred1)
```

```
cm1
```

```
array([[838,   5],
       [ 22, 760]], dtype=int64)
```

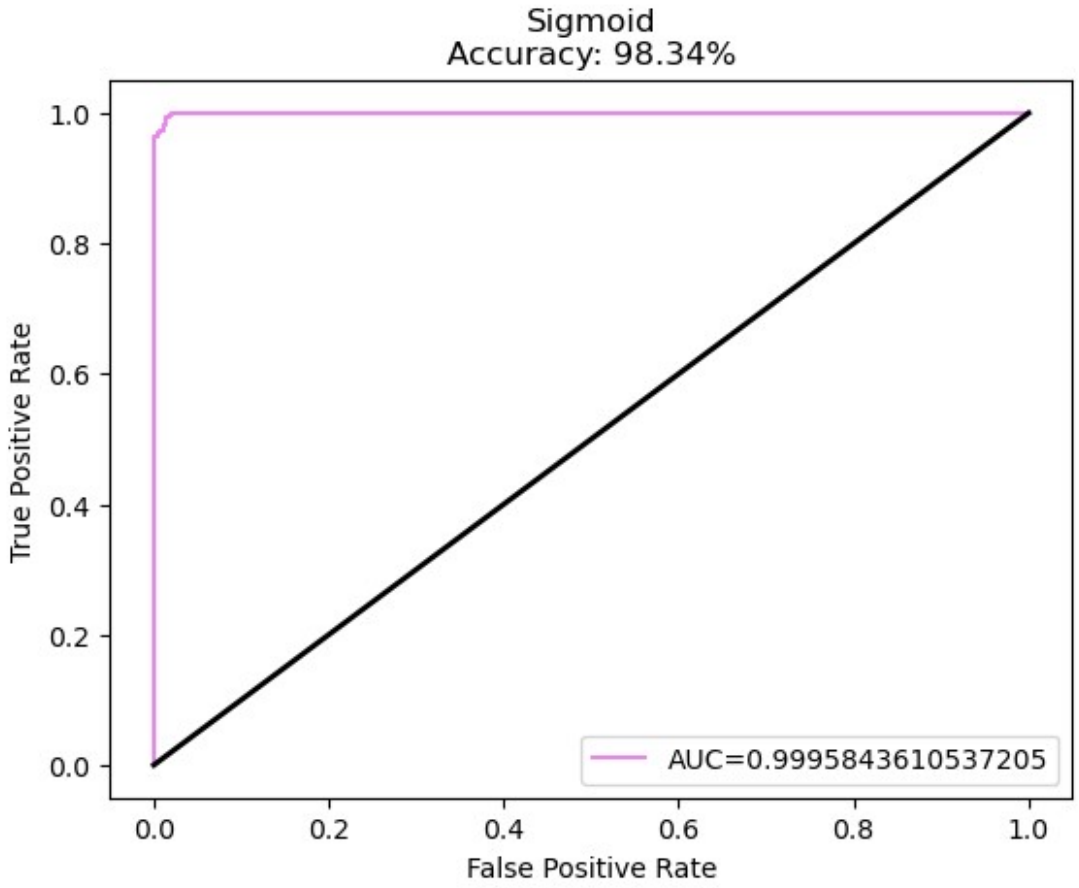
```
sns.heatmap(cm1,cmap='Purples',annot=True)
```

```
<Axes: >
```




```
import matplotlib.pyplot as plt
from sklearn import metrics
y_pred_proba = cl1.predict_proba(x_test)[::,1]
fpr, tpr, _ = metrics.roc_curve(y_test,  y_pred_proba)
auc = metrics.roc_auc_score(y_test, y_pred_proba)
plt.plot(fpr,tpr,label="AUC="+str(auc),color='violet')
plt.legend(loc=4)
```

```
plt.plot([0, 1], [0, 1], color='black', lw=2)
plt.ylabel('True Positive Rate')
plt.xlabel('False Positive Rate')
plt.title('Sigmoid\nAccuracy: {:.2f}%'.format(acc1 * 100))
plt.show()
```




```
cl2=SVC(kernel="linear",random_state=0,probability=True)
cl2.fit(x_train,y_train)
```

```
SVC(kernel='linear', probability=True, random_state=0)
```

```
cl2.score(x_train,y_train)
```

```
0.9524542237267272
```

```
ypred2=cl2.predict(x_test)
```

```
acc2=accuracy_score(y_test,ypred2)
acc2
```

```
0.9489230769230769
```

```
print("pscore",precision_score(y_test,ypred2))
```

```
pscore 0.9475032010243278
```

```
print("pscore",precision_score(y_test,ypred2))
```

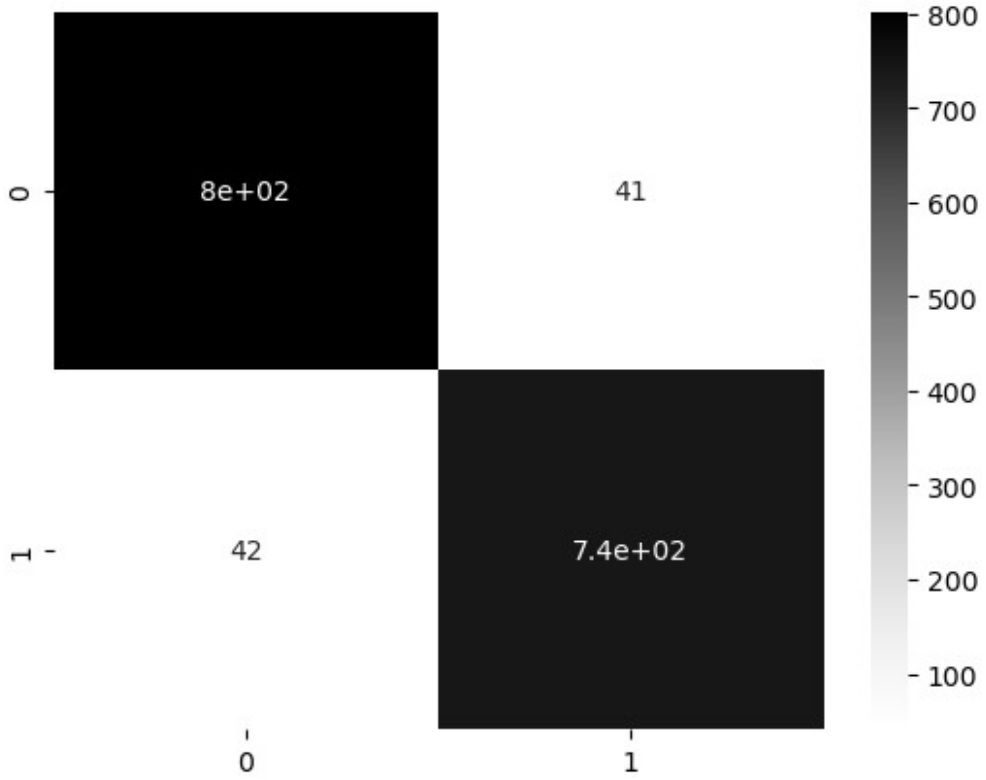
```
pscore 0.9475032010243278
```

```
cm2=confusion_matrix(y_test,ypred2)
cm2
```

```
array([[802,  41],
       [ 42, 740]], dtype=int64)
```

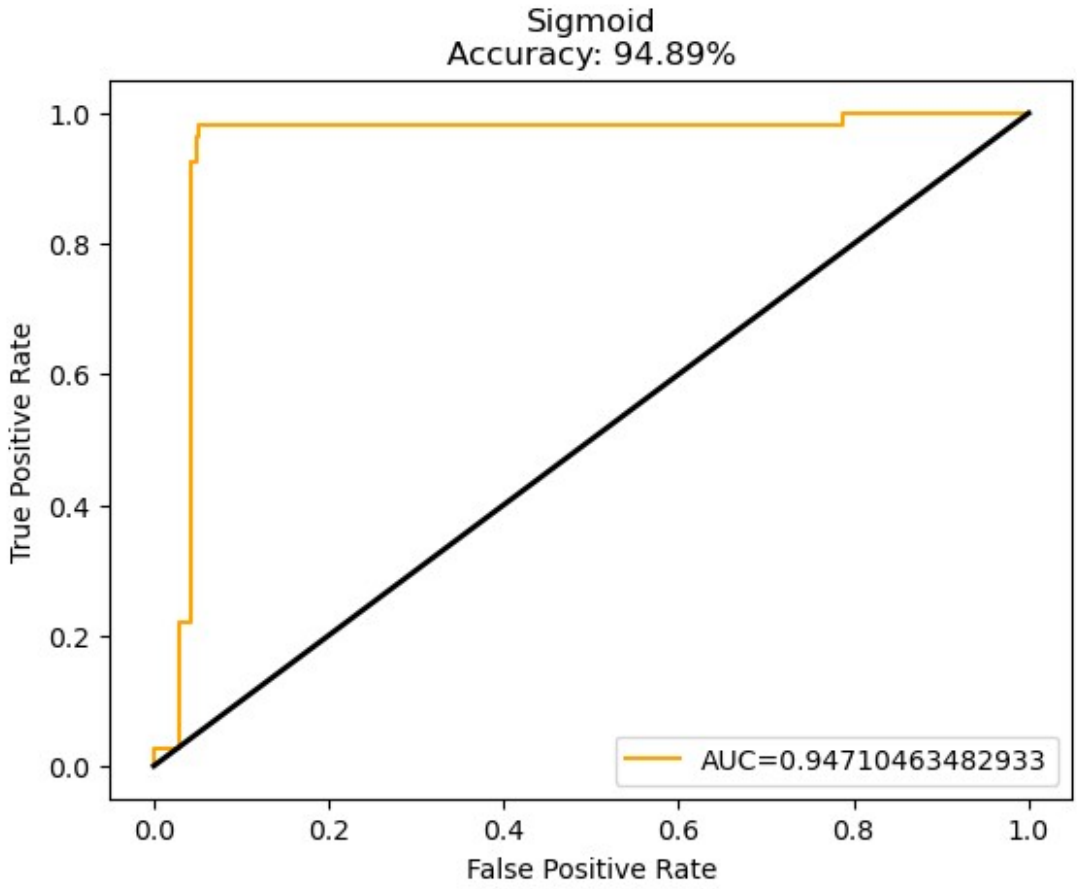
```
sns.heatmap(cm2,cmap='Greys',annot=True)
```

```
<Axes: >
```




```
import matplotlib.pyplot as plt
from sklearn import metrics
y_pred_proba = cl2.predict_proba(x_test)[::,1]
fpr, tpr, _ = metrics.roc_curve(y_test,  y_pred_proba)
auc = metrics.roc_auc_score(y_test, y_pred_proba)
plt.plot(fpr,tpr,label="AUC="+str(auc),color='orange')
plt.legend(loc=4)
plt.plot([0, 1], [0, 1], color='black', lw=2)
plt.ylabel('True Positive Rate')
plt.xlabel('False Positive Rate')
```

```
plt.title('Sigmoid\nAccuracy: {:.2f}%'.format(acc2* 100))
plt.show()
```




```
cl3=SVC(kernel="poly",random_state=0,probability=True)
cl3.fit(x_train,y_train)
```

```
SVC(kernel='poly', probability=True, random_state=0)
```

```
cl3.score(x_train,y_train)
```

```
0.9956916448684413
```

```
ypred3=cl3.predict(x_test)
```

```
acc3=accuracy_score(y_test,ypred3)
acc3
```

```
0.9969230769230769
```

```
print("pscore",precision_score(y_test,ypred3))
```

```
pscore 0.9949044585987261
```

```
print("rscore",precision_score(y_test,ypred3))
```

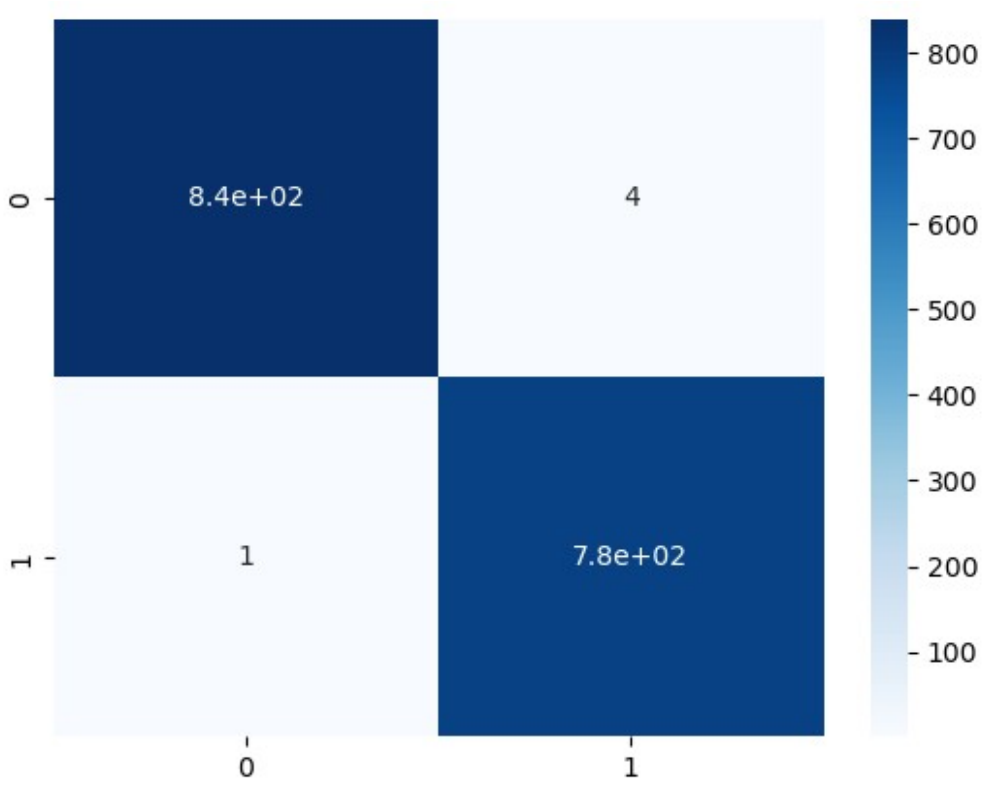
```
rscore 0.9949044585987261
```

```
cm3=confusion_matrix(y_test,ypred3)
cm3
```

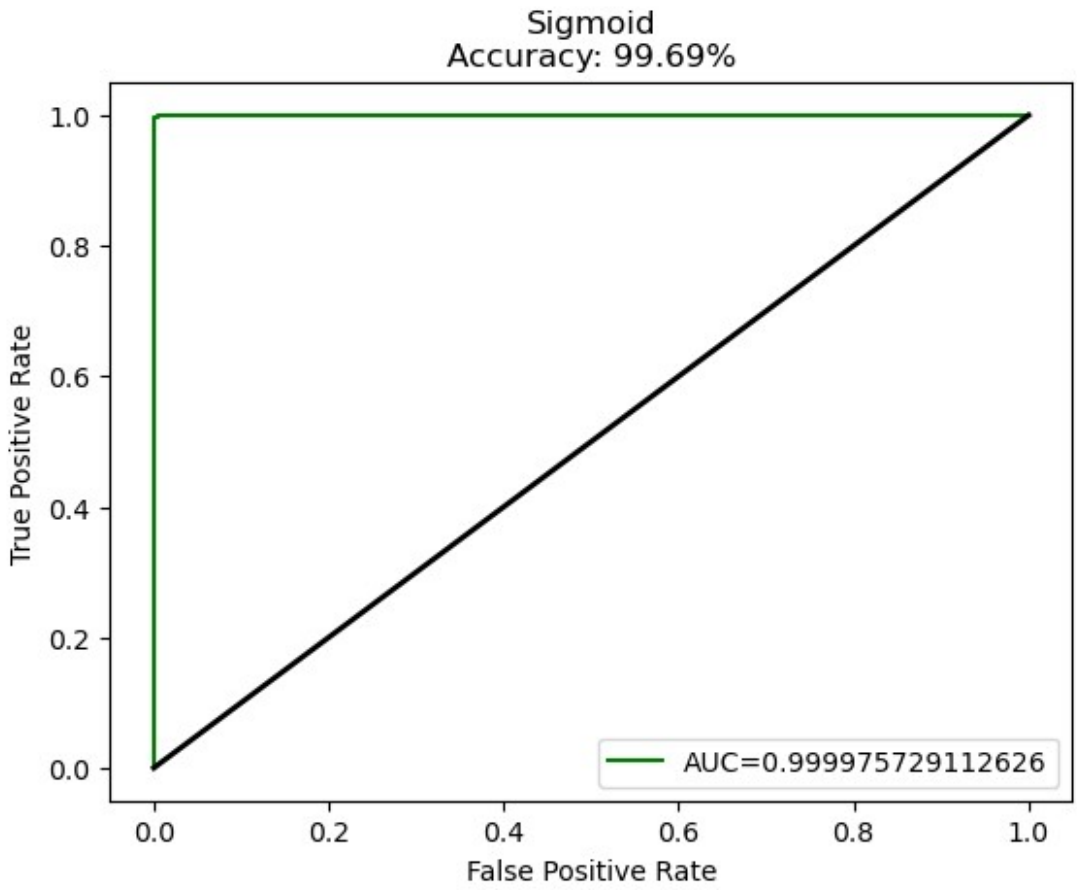
```
array([[839,   4],
       [  1, 781]], dtype=int64)
```

```
sns.heatmap(cm3,cmap='Blues',annot=True)
```

```
<Axes: >
```




```
import matplotlib.pyplot as plt
from sklearn import metrics
y_pred_proba = cl3.predict_proba(x_test)[::,1]
fpr, tpr, _ = metrics.roc_curve(y_test,  y_pred_proba)
auc = metrics.roc_auc_score(y_test, y_pred_proba)
plt.plot(fpr,tpr,label="AUC="+str(auc),color='green')
plt.legend(loc=4)
plt.plot([0, 1], [0, 1], color='black', lw=2)
plt.ylabel('True Positive Rate')
plt.xlabel('False Positive Rate')
plt.title('Sigmoid\nAccuracy: {:.2f}%'.format(acc3 * 100))
plt.show()
```




```
cl4=SVC(kernel="sigmoid",random_state=0,probability=True)
cl4.fit(x_train,y_train)
```

```
SVC(kernel='sigmoid', probability=True, random_state=0)
```

```
cl4.score(x_train,y_train)
```

```
0.4756116325588552
```

```
ypred4=cl4.predict(x_test)
```

```
acc4=accuracy_score(y_test,ypred4)
acc4
```

```
0.47015384615384614
```

```
print("pscore",precision_score(y_test,ypred4))
```

```
pscore 0.4496815286624204
```

```
print("rscore",precision_score(y_test,ypred4))
```

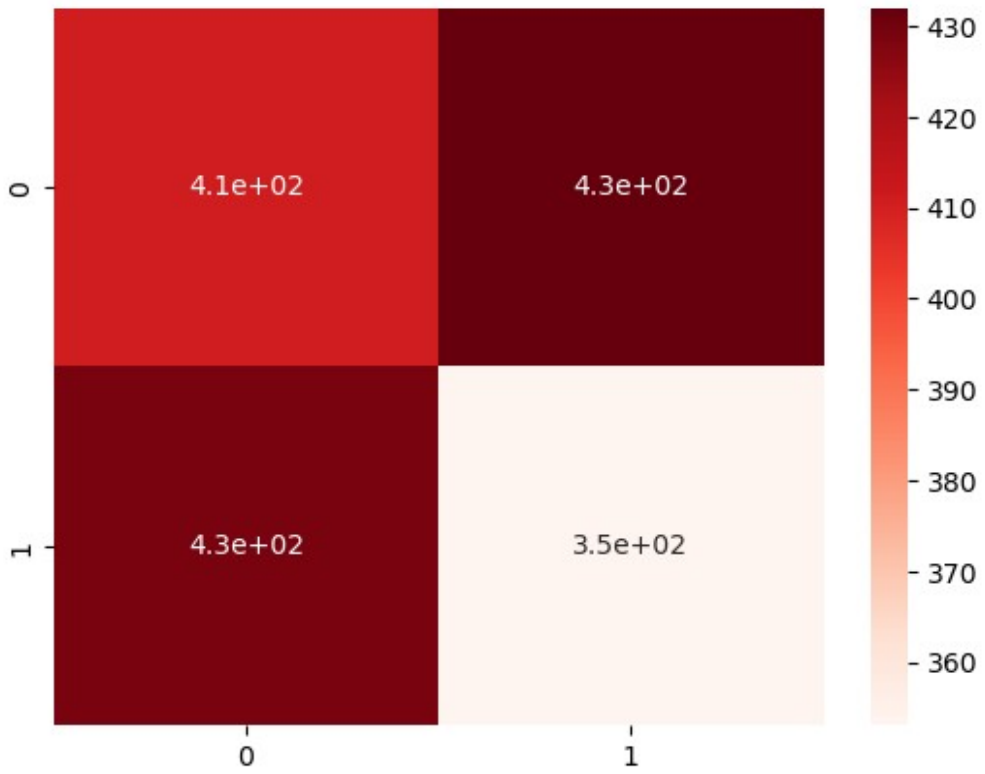
```
rscore 0.4496815286624204
```

```
cm4=confusion_matrix(y_test,ypred4)
cm4
```

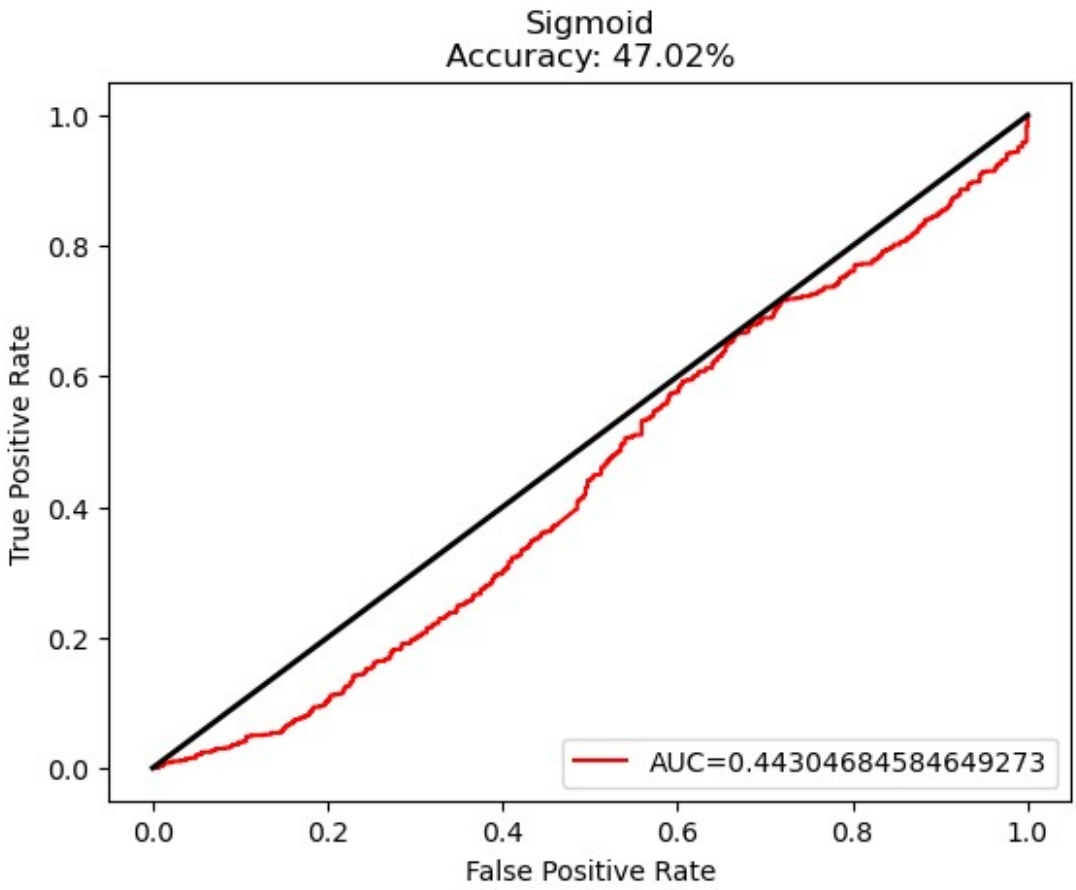
```
array([[411, 432],
       [429, 353]], dtype=int64)
```

```
sns.heatmap(cm4,cmap='Reds',annot=True)
```

```
<Axes: >
```




```
import matplotlib.pyplot as plt
from sklearn import metrics
y_pred_proba = cl4.predict_proba(x_test)[::,1]
fpr, tpr, _ = metrics.roc_curve(y_test,  y_pred_proba)
auc = metrics.roc_auc_score(y_test, y_pred_proba)
plt.plot(fpr,tpr,label="AUC="+str(auc),color='red')
plt.legend(loc=4)
plt.plot([0, 1], [0, 1], color='black', lw=2)
plt.ylabel('True Positive Rate')
plt.xlabel('False Positive Rate')
plt.title('Sigmoid\nAccuracy: {:.2f}%'.format(acc4 * 100))
plt.show()
```




```
pip install nbconvert

Requirement already satisfied: nbconvert in c:\users\new\anaconda3\
lib\site-packages (6.5.4)
Requirement already satisfied: lxml in c:\users\new\anaconda3\lib\
site-packages (from nbconvert) (4.9.3)
Requirement already satisfied: beautifulsoup4 in c:\users\new\
anaconda3\lib\site-packages (from nbconvert) (4.12.2)
Requirement already satisfied: bleach in c:\users\new\anaconda3\lib\
site-packages (from nbconvert) (4.1.0)
Requirement already satisfied: defusedxml in c:\users\new\anaconda3\
lib\site-packages (from nbconvert) (0.7.1)
Requirement already satisfied: entrypoints>=0.2.2 in c:\users\new\
anaconda3\lib\site-packages (from nbconvert) (0.4)
Requirement already satisfied: jinja2>=3.0 in c:\users\new\anaconda3\
lib\site-packages (from nbconvert) (3.1.2)
Requirement already satisfied: jupyter-core>=4.7 in c:\users\new\
anaconda3\lib\site-packages (from nbconvert) (5.3.0)
Requirement already satisfied: jupyterlab-pygments in c:\users\new\
anaconda3\lib\site-packages (from nbconvert) (0.1.2)
Requirement already satisfied: MarkupSafe>=2.0 in c:\users\new\
anaconda3\lib\site-packages (from nbconvert) (2.1.1)
```

```
Requirement already satisfied: mistune<2,>=0.8.1 in c:\users\new\
anaconda3\lib\site-packages (from nbconvert) (0.8.4)
Requirement already satisfied: nbclient>=0.5.0 in c:\users\new\
anaconda3\lib\site-packages (from nbconvert) (0.5.13)
Requirement already satisfied: nbformat>=5.1 in c:\users\new\
anaconda3\lib\site-packages (from nbconvert) (5.9.2)
Requirement already satisfied: packaging in c:\users\new\anaconda3\
lib\site-packages (from nbconvert) (23.1)
Requirement already satisfied: pandocfilters>=1.4.1 in c:\users\new\
anaconda3\lib\site-packages (from nbconvert) (1.5.0)
Requirement already satisfied: pygments>=2.4.1 in c:\users\new\
anaconda3\lib\site-packages (from nbconvert) (2.15.1)
Requirement already satisfied: tinycss2 in c:\users\new\anaconda3\lib\
site-packages (from nbconvert) (1.2.1)
Requirement already satisfied: traitlets>=5.0 in c:\users\new\
anaconda3\lib\site-packages (from nbconvert) (5.7.1)
Requirement already satisfied: platformdirs>=2.5 in c:\users\new\
anaconda3\lib\site-packages (from jupyter-core>=4.7->nbconvert)
(3.10.0)
Requirement already satisfied: pywin32>=300 in c:\users\new\anaconda3\
lib\site-packages (from jupyter-core>=4.7->nbconvert) (305.1)
Requirement already satisfied: jupyter-client>=6.1.5 in c:\users\new\
anaconda3\lib\site-packages (from nbclient>=0.5.0->nbconvert) (7.4.9)
Requirement already satisfied: nest-asyncio in c:\users\new\anaconda3\
lib\site-packages (from nbclient>=0.5.0->nbconvert) (1.5.6)
Requirement already satisfied: fastjsonschema in c:\users\new\
anaconda3\lib\site-packages (from nbformat>=5.1->nbconvert) (2.16.2)
Requirement already satisfied: jsonschema>=2.6 in c:\users\new\
anaconda3\lib\site-packages (from nbformat>=5.1->nbconvert) (4.17.3)
Requirement already satisfied: soupsieve>1.2 in c:\users\new\
anaconda3\lib\site-packages (from beautifulsoup4->nbconvert) (2.4)
Requirement already satisfied: six>=1.9.0 in c:\users\new\anaconda3\
lib\site-packages (from bleach->nbconvert) (1.16.0)
Requirement already satisfied: webencodings in c:\users\new\anaconda3\
lib\site-packages (from bleach->nbconvert) (0.5.1)
Requirement already satisfied: attrs>=17.4.0 in c:\users\new\
anaconda3\lib\site-packages (from jsonschema>=2.6->nbformat>=5.1-
>nbconvert) (23.2.0)
Requirement already satisfied: pyrsistent!=0.17.0,!=0.17.1,!
=0.17.2,>=0.14.0 in c:\users\new\anaconda3\lib\site-packages (from
jsonschema>=2.6->nbformat>=5.1->nbconvert) (0.18.0)
Requirement already satisfied: python-dateutil>=2.8.2 in c:\users\new\
anaconda3\lib\site-packages (from jupyter-client>=6.1.5-
>nbclient>=0.5.0->nbconvert) (2.8.2)
Requirement already satisfied: pyzmq>=23.0 in c:\users\new\anaconda3\
lib\site-packages (from jupyter-client>=6.1.5->nbclient>=0.5.0-
>nbconvert) (23.2.0)
Requirement already satisfied: tornado>=6.2 in c:\users\new\anaconda3\
lib\site-packages (from jupyter-client>=6.1.5->nbclient>=0.5.0-
```

```
>nbconvert) (6.3.2)
Note: you may need to restart the kernel to use updated packages.
```