

Machine Learning Lab 9: Cancer classification using SVM

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Roll No: 2448513

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```
In [52]: import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
warnings.filterwarnings('ignore')
```

```
In [15]: import os

for dirname, _, filenames in os.walk('data\Training'):
    for filename in filenames:
        print(os.path.join(dirname, filename))
```

Data Preprocessing:

```
In [43]: import os
import cv2

path = r'data/Training'
classes = {'no_tumor': 0, 'pituitary_tumor': 1, 'glioma_tumor': 2, 'meningioma_tumo
X = []
Y = []

for cls in classes:
    pth = os.path.join(path, cls)
    for j in os.listdir(pth):
        img = cv2.imread(os.path.join(pth, j), 0)
        img = cv2.resize(img, (200, 200))
        X.append(img)
        Y.append(classes[cls])
```

```
In [17]: X = np.array(X)
Y = np.array(Y)
```

```
In [ ]: pd.Series(Y).value_counts()
```

```
Out[ ]:   count
```

1	827
2	826
3	822
0	395

dtype: int64

```
In [18]: X_updated = X.reshape(len(X), -1)
```

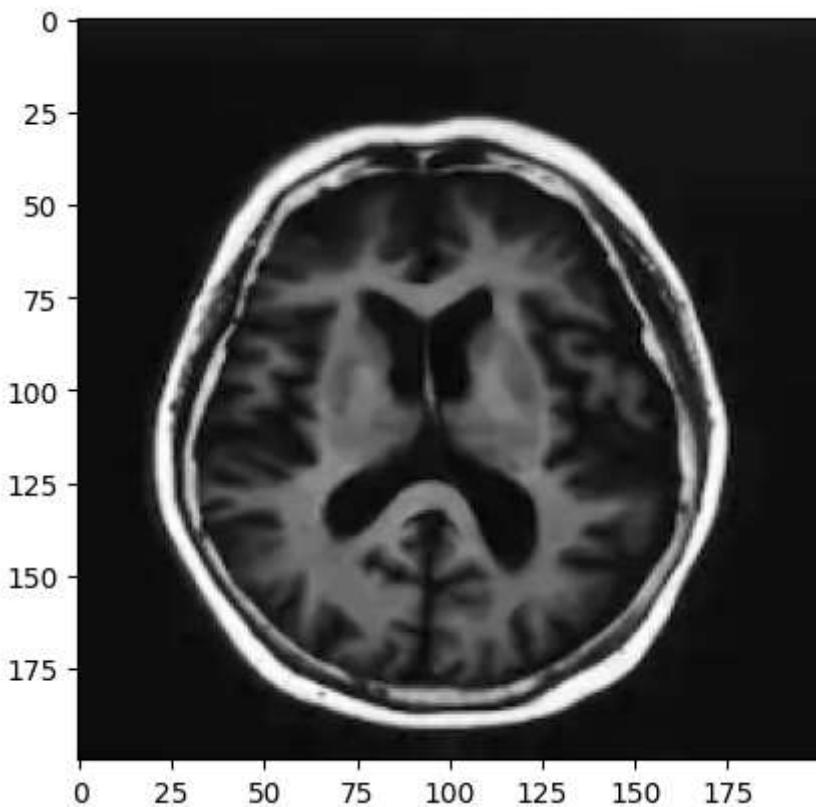
```
In [19]: X.shape, X_updated.shape
```

```
Out[19]: ((2870, 200, 200), (2870, 40000))
```

Data Exploration and Visualization:

```
In [20]: plt.imshow(X[0], cmap='gray')
```

```
Out[20]: <matplotlib.image.AxesImage at 0x7facc1edc880>
```



Model Building and Training:

```
In [21]: xtrain, xtest, ytrain, ytest = train_test_split(X_updated, Y, random_state=10, test_
```

```
In [22]: xtrain.shape, xtest.shape
```

```
Out[22]: ((2296, 40000), (574, 40000))
```

```
In [23]: print(xtrain.max(), xtrain.min())
print(xtest.max(), xtest.min())
xtrain = xtrain/255
xtest = xtest/255
print(xtrain.max(), xtrain.min())
print(xtest.max(), xtest.min())
```

```
255 0
255 0
1.0 0.0
1.0 0.0
```

```
In [24]: from sklearn.svm import SVC
```

Hyperparameter Tuning:

```
In [31]: sv = SVC(kernel='sigmoid')
sv.fit(xtrain, ytrain)
```

```
print("Training Score:", sv.score(xtrain, ytrain))
print("Testing Score:", sv.score(xtest, ytest))
```

Training Score: 0.32229965156794427
 Testing Score: 0.2926829268292683

```
In [32]: sv = SVC(kernel='rbf')
sv.fit(xtrain, ytrain)

print("Training Score:", sv.score(xtrain, ytrain))
print("Testing Score:", sv.score(xtest, ytest))
```

Training Score: 0.9425087108013938
 Testing Score: 0.8292682926829268

```
In [33]: sv = SVC(kernel='poly')
sv.fit(xtrain, ytrain)

print("Training Score:", sv.score(xtrain, ytrain))
print("Testing Score:", sv.score(xtest, ytest))
```

Training Score: 0.9838850174216028
 Testing Score: 0.8501742160278746

```
In [34]: sv = SVC(kernel='linear')
sv.fit(xtrain, ytrain)

print("Training Score:", sv.score(xtrain, ytrain))
print("Testing Score:", sv.score(xtest, ytest))
```

Training Score: 1.0
 Testing Score: 0.8240418118466899

Prediction:

```
In [35]: pred = sv.predict(xtest)
```

```
In [36]: misclassified=np.where(ytest!=pred)
misclassified
```

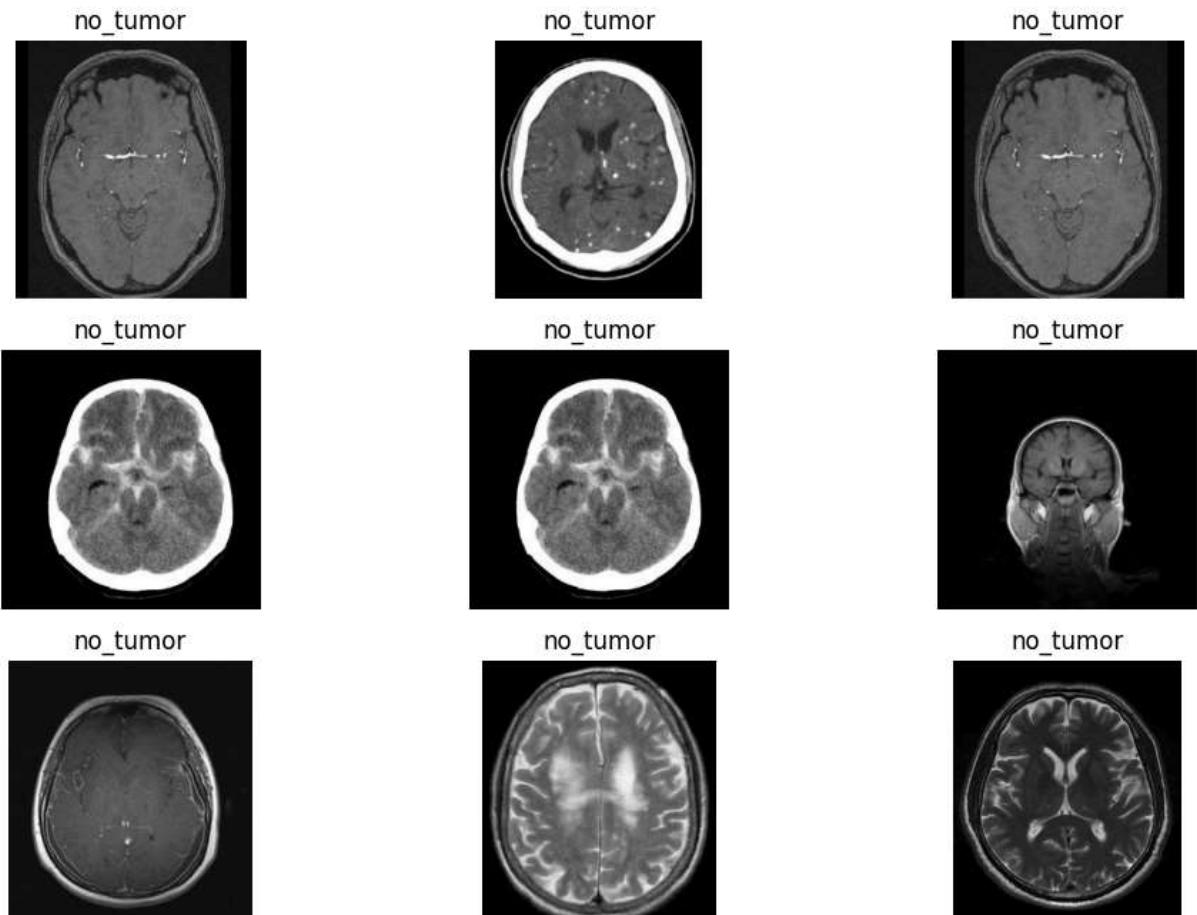
```
Out[36]: array([ 2,  7, 19, 27, 29, 40, 41, 42, 48, 60, 68, 72, 85,
   93, 104, 107, 113, 120, 125, 126, 127, 129, 135, 142, 149, 152,
   156, 163, 164, 165, 173, 179, 182, 194, 201, 204, 214, 218, 228,
   230, 233, 237, 239, 246, 248, 250, 253, 258, 264, 265, 269, 273,
   286, 287, 288, 302, 317, 323, 336, 339, 352, 355, 356, 359, 364,
   375, 376, 381, 392, 397, 399, 400, 402, 403, 405, 408, 409, 415,
   425, 427, 436, 438, 440, 444, 449, 455, 463, 476, 480, 483, 485,
   488, 493, 495, 503, 512, 516, 525, 536, 539, 570]),)
```

```
In [44]: plt.figure(figsize=(12,8))
c=1
classes = {0 : 'no_tumor', 1: 'pituitary_tumor', 2: 'glioma_tumor', 3 : 'meningioma'
```

```

path=r'data/Testing/no_tumor'
for i in os.listdir(path)[:9]:
    img=cv2.imread(os.path.join(path,i),0)
    if img is not None:
        p=sv.predict(cv2.resize(img,(200,200)).reshape(1,-1)/255)
        plt.subplot(3,3,c)
        plt.title(classes.get(p[0], 'Unknown'))
        plt.imshow(img,cmap='gray')
        plt.axis('off')
        c+=1
    else:
        print(f"Fail to load image:{i}")
plt.show()

```

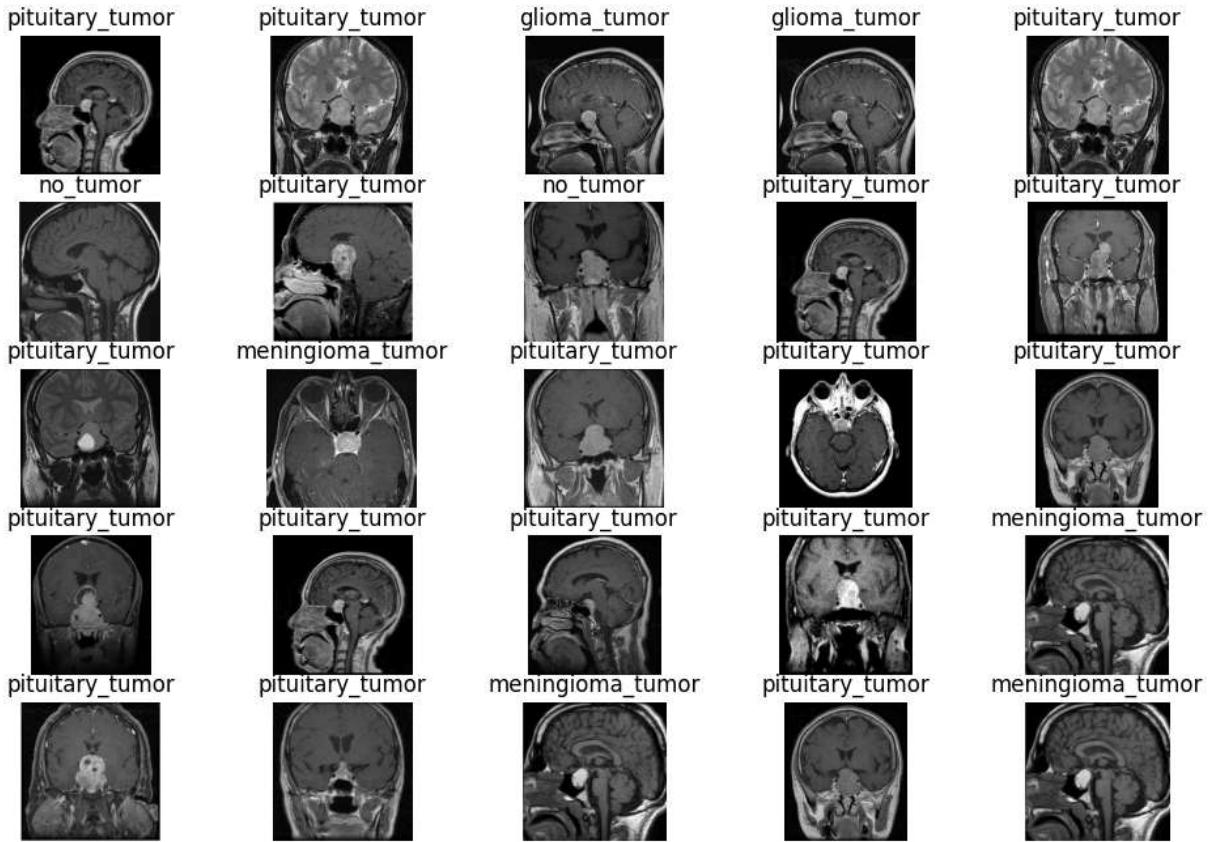


```

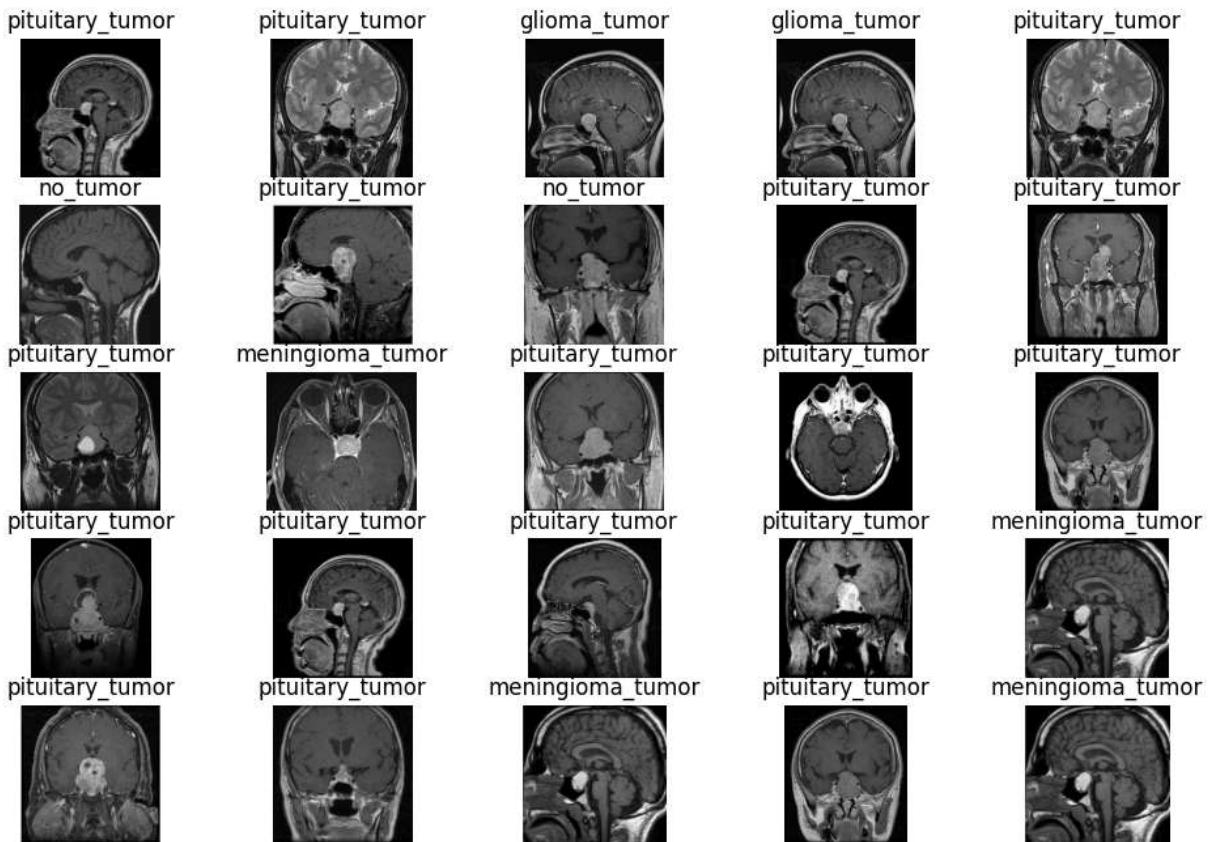
In [45]: plt.figure(figsize=(12,8))
c=1
path=r'data/Testing/pituitary_tumor'
for i in os.listdir(path)[:25]:
    img=cv2.imread(os.path.join(path,i),0)
    if img is not None:
        p=sv.predict(cv2.resize(img,(200,200)).reshape(1,-1)/255)
        plt.subplot(5,5,c)
        plt.title(classes.get(p[0], 'UnKnown'))
        plt.imshow(img,cmap='gray')
        plt.axis('off')
        c+=1;
    else:

```

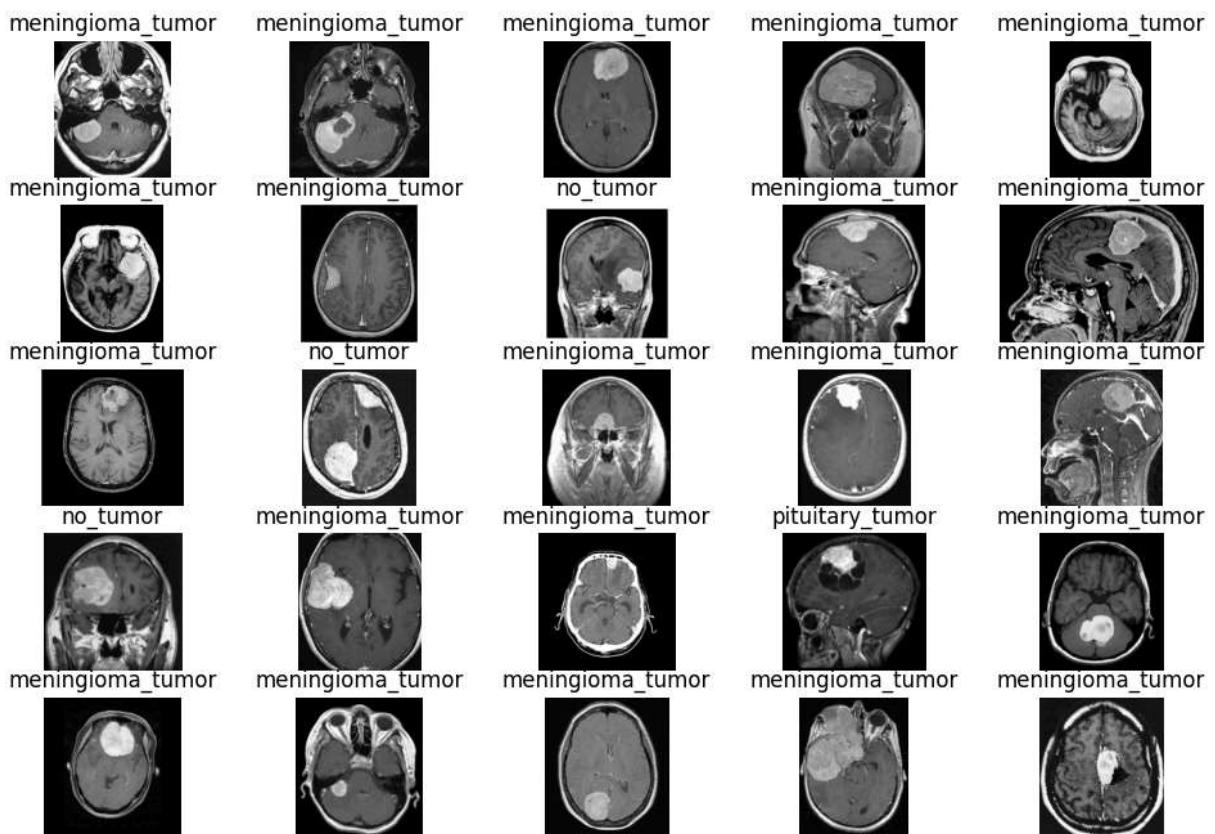
```
print(f"Failed to Load Image:{i}")
plt.show()
```



```
In [46]: plt.figure(figsize=(12,8))
c=1
path=r'data/Testing/pituitary_tumor'
for i in os.listdir(path)[:25]:
    img=cv2.imread(os.path.join(path,i),0)
    if img is not None:
        p=sv.predict(cv2.resize(img,(200,200)).reshape(1,-1)/255)
        plt.subplot(5,5,c)
        plt.title(classes.get(p[0], 'UnKnown'))
        plt.imshow(img,cmap='gray')
        plt.axis('off')
        c+=1;
    else:
        print(f"Failed to Load Image:{i}")
        plt.show()
```



```
In [48]: plt.figure(figsize=(12,8))
c=1
path=r'data/Testing/meningioma_tumor'
for i in os.listdir(path)[:25]:
    img=cv2.imread(os.path.join(path,i),0)
    if img is not None:
        p=sv.predict(cv2.resize(img,(200,200)).reshape(1,-1)/255)
        plt.subplot(5,5,c)
        plt.title(classes.get(p[0], 'UnKnown'))
        plt.imshow(img,cmap='gray')
        plt.axis('off')
        c+=1;
    else:
        print(f"Failed to Load Image:{i}")
plt.show()
```

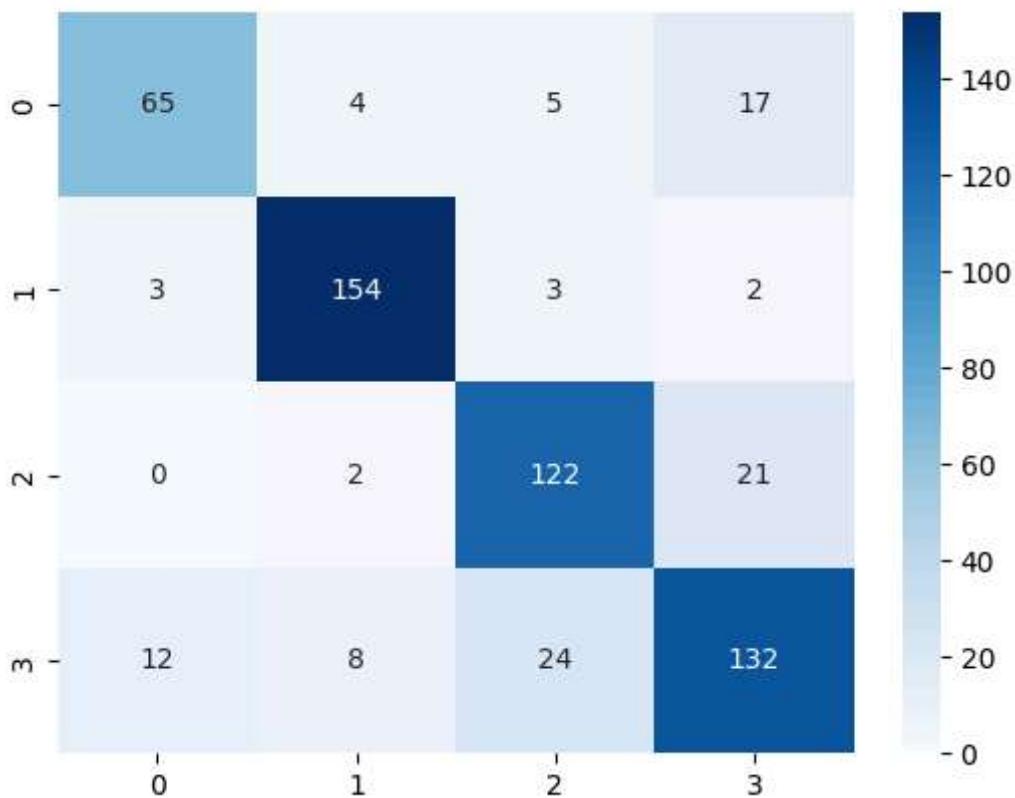


Model Evaluation

```
In [56]: from sklearn.metrics import confusion_matrix, classification_report, roc_auc_score,
```

```
In [57]: sns.heatmap(confusion_matrix(ytest, pred), annot=True, fmt='d', cmap='Blues')
```

```
Out[57]: <Axes: >
```



```
In [59]: print(classification_report(ytest, pred))
```

	precision	recall	f1-score	support
0	0.81	0.71	0.76	91
1	0.92	0.95	0.93	162
2	0.79	0.84	0.82	145
3	0.77	0.75	0.76	176
accuracy			0.82	574
macro avg	0.82	0.81	0.82	574
weighted avg	0.82	0.82	0.82	574

```
In [75]: import os
import cv2

path = r'data/Training'
classes = {'no_tumor': 0, 'pituitary_tumor': 1}
X = []
Y = []

for cls in classes:
    pth = os.path.join(path, cls)
    for j in os.listdir(pth):
        img = cv2.imread(os.path.join(pth, j), 0)
        img = cv2.resize(img, (200, 200))
        X.append(img)
        Y.append(classes[cls])

X = np.array(X)
```

```
Y = np.array(Y)

X_updated = X.reshape(len(X), -1)

xtrain, xtest, ytrain, ytest = train_test_split(X_updated, Y, random_state=10, test_size=0.2)

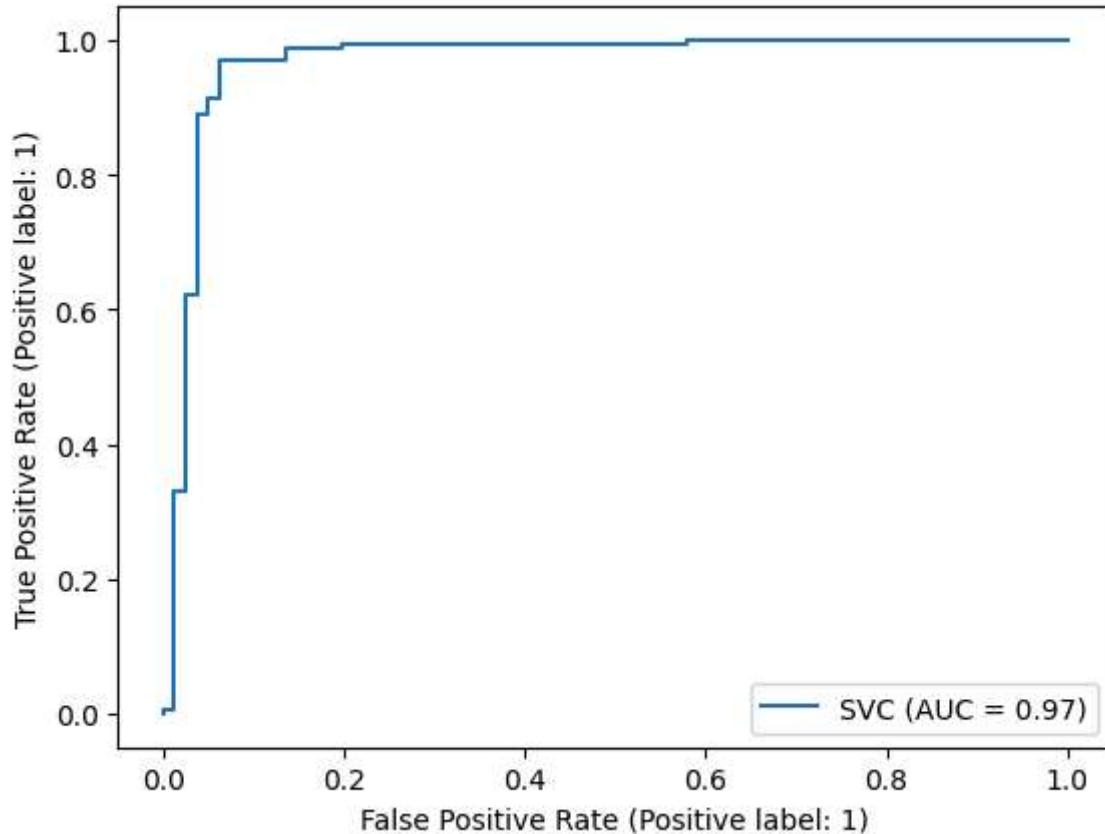
xtrain = xtrain/255
xtest = xtest/255

sv = SVC(kernel='linear')
sv.fit(xtrain, ytrain)

print("Training Score:", sv.score(xtrain, ytrain))
print("Testing Score:", sv.score(xtest, ytest))
```

Training Score: 1.0
Testing Score: 0.9428571428571428

In [79]: RocCurveDisplay.from_estimator(sv, xtest, ytest)
plt.show()



Model Interpretation

In [90]: sv.coef_[0]

Out[90]: array([-0.00490537, -0.0053542 , -0.00532606, ..., -0.00615709, -0.00505385, -0.00400225])

```
In [93]: sv.intercept_
```

```
Out[93]: array([1.1211504])
```

```
In [ ]:
```