

## Load Modules

```
In [23]: import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
```

## Prepare/collect data

```
In [24]: import os

path = os.listdir('brain_tumor/Training/')
classes = {'no_tumor':0, 'pituitary_tumor':1}
classes
```

```
Out[24]: {'no_tumor': 0, 'pituitary_tumor': 1}
```

```
In [25]: import cv2
X = []
Y = []
for cls in classes:
    pth = 'brain_tumor/Training/'+cls
    for j in os.listdir(pth):
        img = cv2.imread(pth+'/'+j, 0)
        img = cv2.resize(img, (200,200))
        X.append(img)
        Y.append(classes[cls])
# plt.imshow(X[0], cmap='gray')
```

```
In [26]: X = np.array(X)
Y = np.array(Y)

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

```
In [27]: np.unique(Y)
```

```
Out[27]: array([0, 1])
```

```
In [28]: pd.Series(Y).value_counts()
```

```
Out[28]: 1    827
0    395
dtype: int64
```

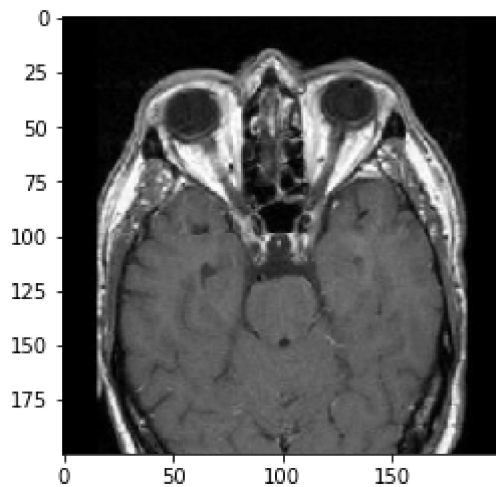
```
In [29]: X.shape, X_updated.shape
```

```
Out[29]: ((1222, 200, 200), (1222, 40000))
```

## Visualize data

```
In [30]: plt.imshow(X[0], cmap='gray')
```

```
Out[30]: <matplotlib.image.AxesImage at 0x272617a6d00>
```



## Prepare data

```
In [31]: X_updated = X.reshape(len(X), -1)
X_updated.shape
```

```
Out[31]: (1222, 40000)
```

## Split Data

```
In [32]: xtrain, xtest, ytrain, ytest = train_test_split(X_updated, Y, random_state=10,
                                                         test_size=.20)
```

```
In [33]: xtrain.shape, xtest.shape
```

```
Out[33]: ((977, 40000), (245, 40000))
```

## Feature Scaling

```
In [35]: 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
```

## Feature Selection: PCA

```
In [37]: from sklearn.decomposition import PCA
```

```
In [46]: print(xtrain.shape, xtest.shape)

pca = PCA(.98)
pca_train = pca.fit_transform(xtrain)
pca_test = pca.transform(xtest)
pca_train = xtrain
pca_test = xtest
```

```
(977, 40000) (245, 40000)
```

```
In [47]: print(pca_train.shape, pca_test.shape)
print(pca.n_components_)
print(pca.n_features_)
```

```
(977, 40000) (245, 40000)
621
40000
```

## Train Model

```
In [49]: from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
```

```
In [50]: import warnings
warnings.filterwarnings('ignore')

lg = LogisticRegression(C=0.1)
lg.fit(xtrain, ytrain)
```

Out[50]: LogisticRegression(C=0.1)

```
In [52]: sv = SVC()
sv.fit(xtrain, ytrain)
```

Out[52]: SVC()

## Evaluation

```
In [53]: print("Training Score:", lg.score(xtrain, ytrain))
print("Testing Score:", lg.score(xtest, ytest))
```

Training Score: 1.0  
Testing Score: 0.9591836734693877

```
In [54]: print("Training Score:", sv.score(xtrain, ytrain))
print("Testing Score:", sv.score(xtest, ytest))
```

Training Score: 0.9938587512794268  
Testing Score: 0.963265306122449

## Prediction

```
In [55]: pred = sv.predict(xtest)
```

```
In [56]: misclassified=np.where(ytest!=pred)
misclassified
```

Out[56]: (array([ 36, 51, 68, 120, 212, 214, 220, 227, 239], dtype=int64),)

```
In [57]: print("Total Misclassified Samples: ",len(misclassified[0]))
print(pred[36],ytest[36])
```

Total Misclassified Samples: 9  
0 1

## TEST MODEL

```
In [58]: dec = {0:'No Tumor', 1:'Positive Tumor'}
```

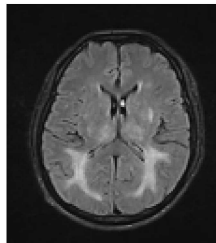
```
In [64]: plt.figure(figsize=(12,8))
p = os.listdir('brain_tumor/Testing/')
c=1
for i in os.listdir('brain_tumor/Testing/no_tumor/')[:9]:
    plt.subplot(3,3,c)

    img = cv2.imread('brain_tumor/Testing/no_tumor/'+i,0)
    img1 = cv2.resize(img, (200,200))
    img1 = img1.reshape(1,-1)/255
    p = sv.predict(img1)
    plt.title(dec[p[0]])
    plt.imshow(img, cmap='gray')
    plt.axis('off')
    c+=1
```

No Tumor



No Tumor



No Tumor



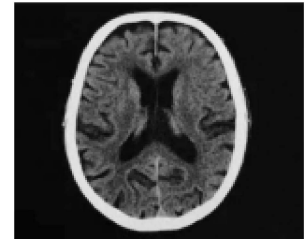
No Tumor



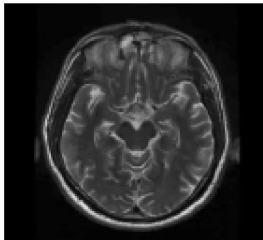
No Tumor



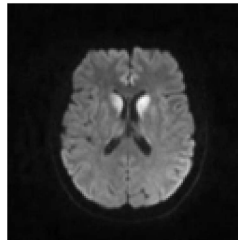
No Tumor



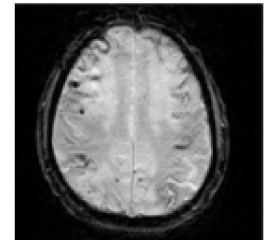
No Tumor



No Tumor



No Tumor

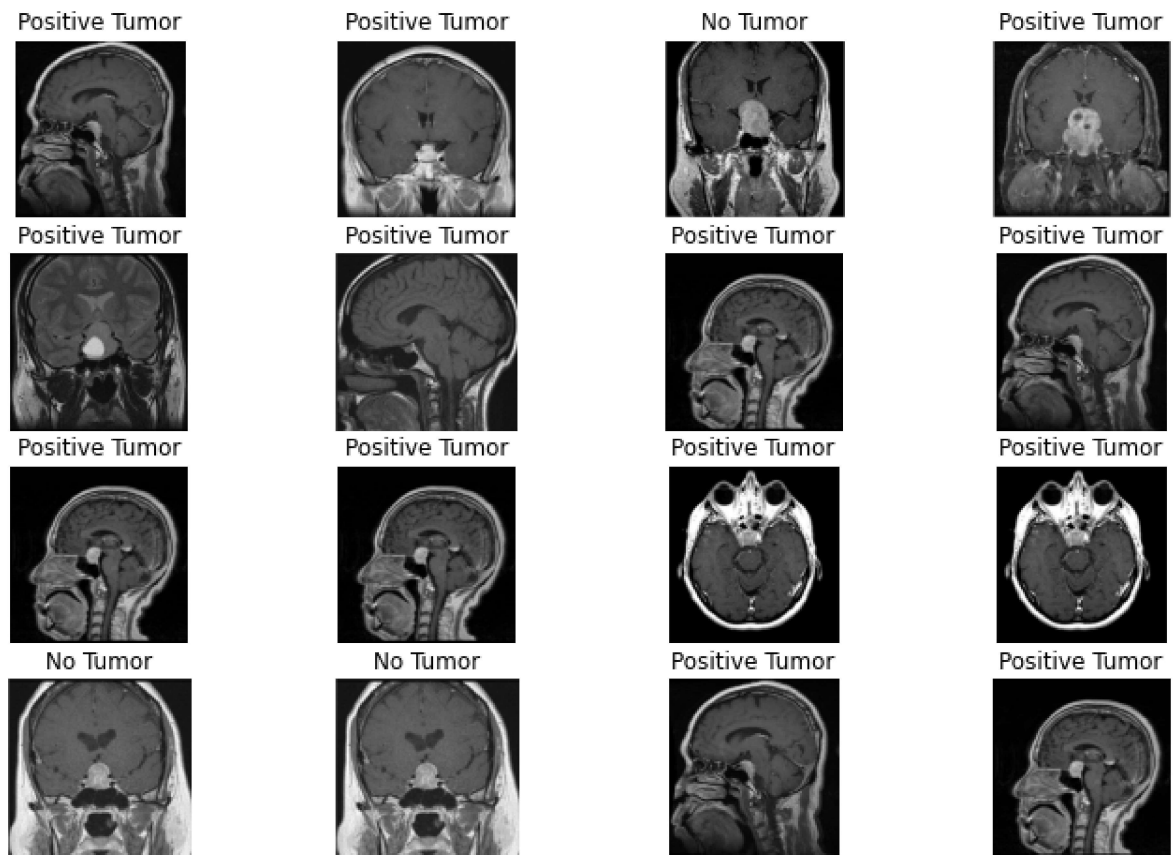


```

In [60]: plt.figure(figsize=(12,8))
p = os.listdir('brain_tumor/Testing/')
c=1
for i in os.listdir('brain_tumor/Testing/pituitary_tumor/')[:16]:
    plt.subplot(4,4,c)

    img = cv2.imread('brain_tumor/Testing/pituitary_tumor/'+i,0)
    img1 = cv2.resize(img, (200,200))
    img1 = img1.reshape(1,-1)/255
    p = sv.predict(img1)
    plt.title(dec[p[0]])
    plt.imshow(img, cmap='gray')
    plt.axis('off')
    c+=1

```



```

In [61]: # pip install opencv_python

```

```

In [62]: import pickle
pickle.dump(sv,open('model.pkl','wb'))

```

```

In [ ]:

```

```

In [ ]:

```

In [ ]: