

Brain_Tumor_Detection_Classification

Load Modules

In [4]:

```
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 [8]:

```
import os

path = os.listdir(r'D:\Softwares\21\Anuj\D_S\Projects\Code1 Clause\brain-tumor-detection-classes')
classes = {'no_tumor': 0, 'pituitary_tumor': 1}
```

In [10]:

```
import cv2

X = []
Y = []
for cls in classes:
    pth = r'D:\Softwares\21\Anuj\D_S\Projects\Code1 Clause\brain-tumor-detection-master\b
    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])
```

In [11]:

```
np.unique(Y)
```

Out[11]:

```
array([0, 1])
```

In [12]:

```
X = np.array(X)
Y = np.array(Y)
```

In [13]:

```
pd.Series(Y).value_counts()
```

Out[13]:

```
1    827
0    395
dtype: int64
```

In [14]:

```
X.shape
```

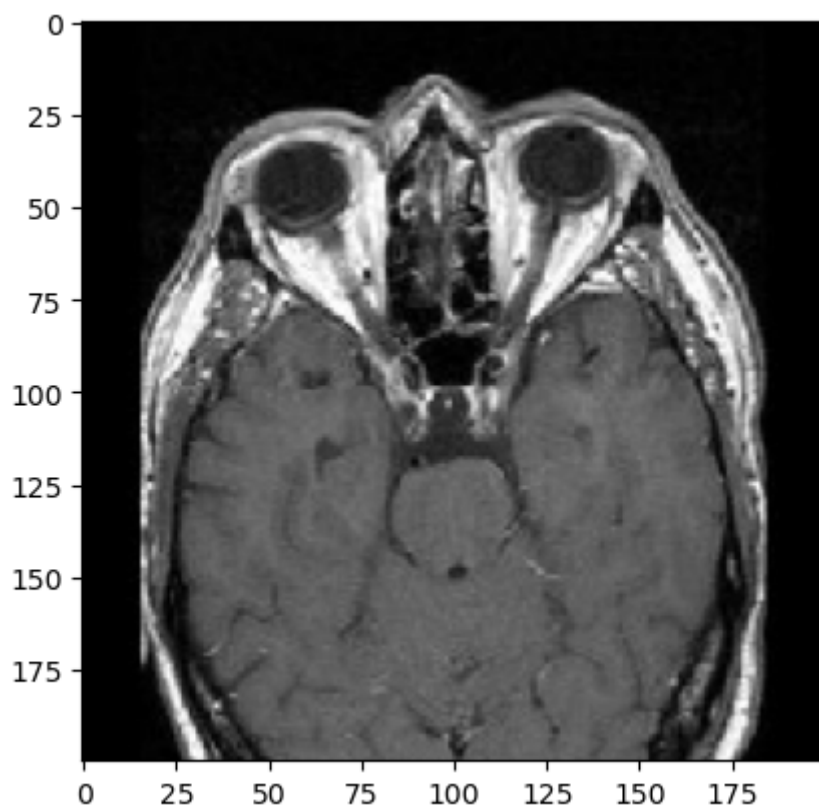
Out[14]:

```
(1222, 200, 200)
```

Visualize data

In [16]:

```
plt.imshow(X[0], cmap = 'gray')
plt.show()
```



Prepare Data

In [17]:

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

Out[17]:

```
(1222, 40000)
```

Split Data

In [18]:

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

In [19]:

```
xtrain.shape, xtest.shape
```

Out[19]:

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

Feature Scaling

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
```

Feature Selection: PCA

In [24]:

```
from sklearn.decomposition import PCA
```

In [26]:

```
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 [27]:

```
#print(pca_train.shape, pca_test.shape)
#print(pca.n_components_)
#print(pca.n_features_)
```

Train Model

In [30]:

```
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
```

In [31]:

```
import warnings
warnings.filterwarnings('ignore')

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

Out[31]:

```
▼ LogisticRegression
LogisticRegression(C=0.1)
```

In [32]:

```
sv = SVC()
sv.fit(pca_train, ytrain)
```

Out[32]:

```
▼ SVC
SVC()
```

Evaluation

In [33]:

```
print("Training Score:", lg.score(pca_train, ytrain))
print("Testing Score:", lg.score(pca_test, ytest))
```

Training Score: 1.0

Training Score: 0.9591836734693877

In [35]:

```
print("Training Score:", sv.score(pca_train, ytrain))
print("Testing Score:", sv.score(pca_test, ytest))
```

Training Score: 0.9938587512794268

Testing Score: 0.963265306122449

Prediction

In [38]:

```
pred = sv.predict(pca_test)
np.where(ytest != pred)
```

Out[38]:

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

In [39]:

```
pred[6]
```

Out[39]:

0

In [40]:

```
ytest[6]
```

Out[40]:

0

TEST MODEL

In [41]:

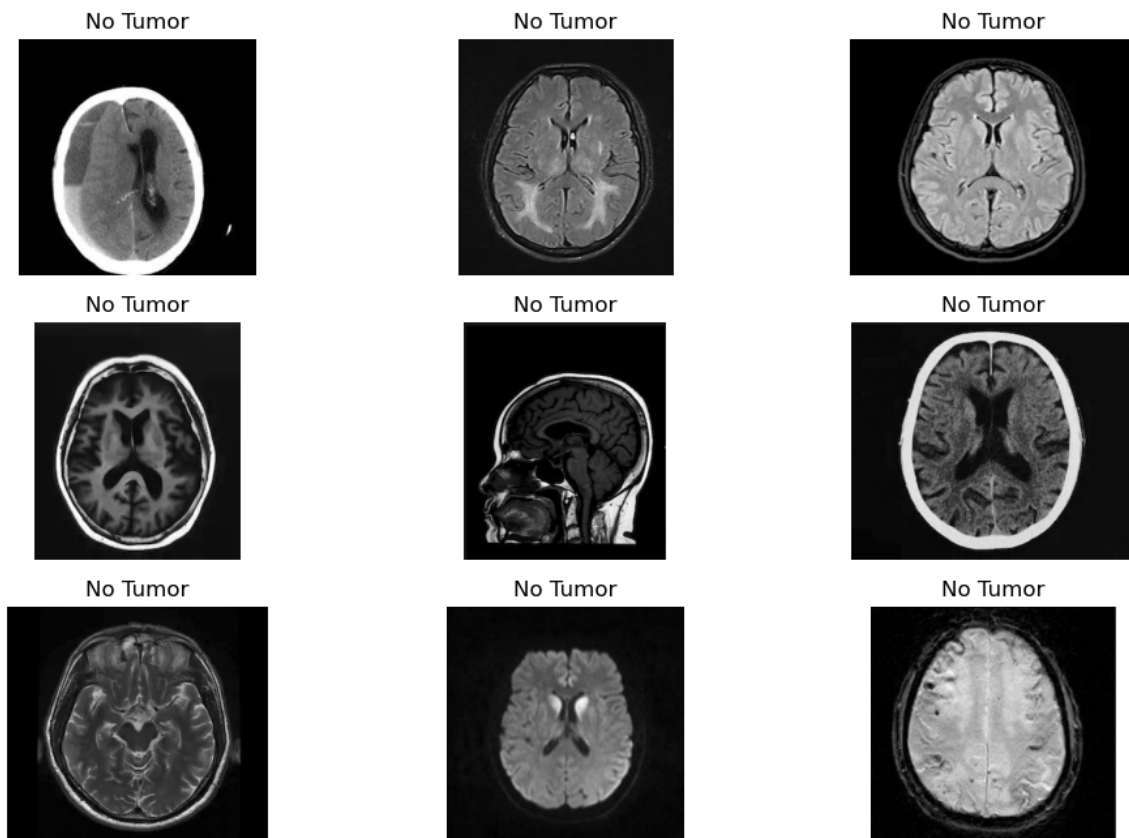
```
dec = {0: 'No Tumor', 1: 'Positive Tumor'}
```

In [50]:

```
plt.figure(figsize=(12, 8))
p = os.listdir('D:/Softwares/21/Anuj/D_S/Projects/Code1 Clause/brain-tumor-detection-master')
c = 1
for i in os.listdir('D:/Softwares/21/Anuj/D_S/Projects/Code1 Clause/brain-tumor-detection-master'):
    plt.subplot(3, 3, c)

    img = cv2.imread('D:/Softwares/21/Anuj/D_S/Projects/Code1 Clause/brain-tumor-detection-master/' + i)
    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

plt.show()
```



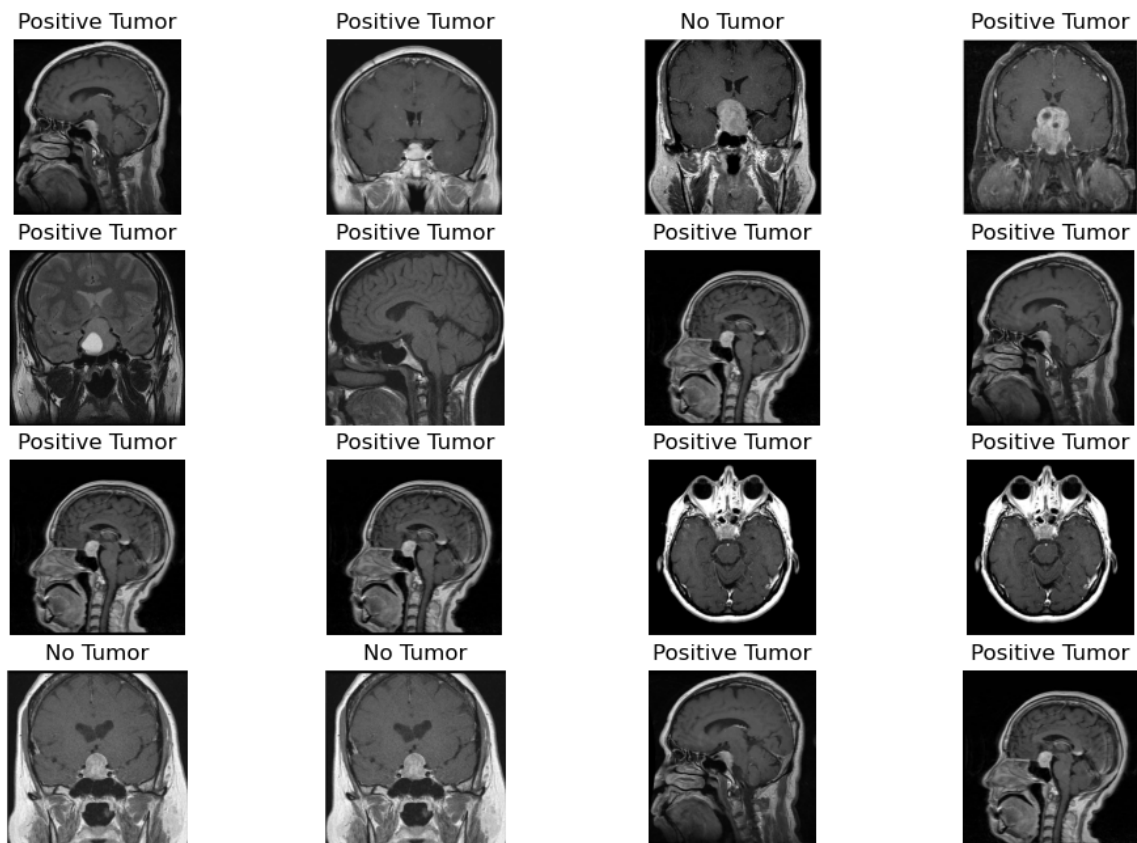
In [53]:

```
plt.figure(figsize=(12, 8))
p = os.listdir('D:/Softwares/21/Anuj/D_S/Projects/Code1 Clause/brain-tumor-detection-master')
c = 1

for i in os.listdir('D:/Softwares/21/Anuj/D_S/Projects/Code1 Clause/brain-tumor-detection-master'):
    plt.subplot(4, 4, c)

    img = cv2.imread('D:/Softwares/21/Anuj/D_S/Projects/Code1 Clause/brain-tumor-detection-master/' + i)
    if img is not None:
        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

plt.show()
```



In []: