Brain Tumor Detection Classification

Load Module

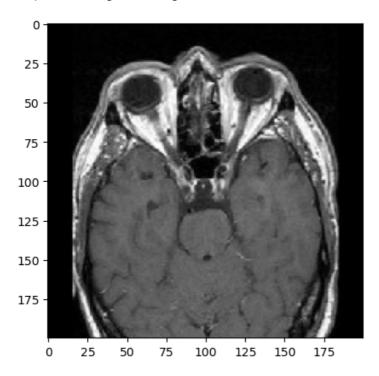
```
In [1]: import numpy as np
    import pandas as pd
    import matplotlib.pyplot as plt
    from sklearn.model_selection import train_test_split
    from sklearn.metrics import accuracy_score
```

```
Prepare/Collect Data
In [2]: import os
        path = os.listdir('F:/A DATA SCIENCE 2023/Brain Tumor Detection Classification/Training/')
        classes = {'no_tumor':0, 'pituitary_tumor':1}
In [3]: import cv2
        X = []
        Y = []
        for cls in classes:
            pth = 'F:/A DATA SCIENCE 2023/Brain Tumor Detection Classification/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])
In [4]: np.unique(Y)
Out[4]: array([0, 1])
In [5]: X = np.array(X)
        Y = np.array(Y)
In [6]: pd.Series(Y).value_counts()
Out[6]: 1
             827
             395
        dtype: int64
In [7]: X.shape
Out[7]: (1222, 200, 200)
```

Visualize Data

```
In [8]: plt.imshow(X[0], cmap='gray')
```

Out[8]: <matplotlib.image.AxesImage at 0x224fc080550>



Prepare Data

```
In [9]: X_updated = X.reshape(len(X), -1)
X_updated.shape
Out[9]: (1222, 40000)
```

Split Data

```
In [10]: xtrain, xtest, ytrain, ytest = train_test_split(X_updated, Y, random_state=10, test_size=.2
In [11]: xtrain.shape, xtest.shape
Out[11]: ((977, 40000), (245, 40000))
```

Feature Scaling

1.0 0.0

Feature Selection: PCA

```
In [13]: | from sklearn.decomposition import PCA
In [14]: print(xtrain.shape, xtest.shape)
         pca = PCA(.98)
         pca_train = xtrain
         pca_test = xtest
         (977, 40000) (245, 40000)
         Train Model
In [15]: from sklearn.linear model import LogisticRegression
         from sklearn.svm import SVC
In [16]: import warnings
         warnings.filterwarnings('ignore')
         lg = LogisticRegression(C=0.1)
         lg.fit(pca_train, ytrain)
Out[16]:
             LogisticRegression
          LogisticRegression(C=0.1)
In [17]: sv = SVC()
         sv.fit(pca_train, ytrain)
Out[17]:
         ▼ SVC
          sv¢()
         Evaluation
In [18]: print("Training Score:", lg.score(pca_train, ytrain))
         print("Testing Score:", lg.score(pca_test, ytest))
         Training Score: 1.0
         Testing Score: 0.9591836734693877
In [19]: 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 [20]:
         pred = sv.predict(pca_test)
         np.where(ytest != pred)
Out[20]: (array([ 36, 51, 68, 120, 212, 214, 220, 227, 239], dtype=int64),)
In [22]: pred[36]
Out[22]: 0
```

```
In [23]: ytest[36]
```

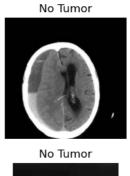
Out[23]: 1

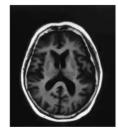
Test Model

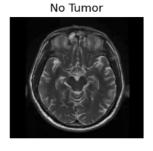
```
In [28]: dec = {0:'No Tumor', 1:'Positive Tumor'}

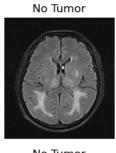
In [31]: plt.figure(figsize=(12,8))
    p = os.listdir('F:/A DATA SCIENCE 2023/Brain Tumor Detection Classification/Testing/')
    c=1
    for i in os.listdir('F:/A DATA SCIENCE 2023/Brain Tumor Detection Classification/Testing/no.
    plt.subplot(3,3,c)

    img = cv2.imread('F:/A DATA SCIENCE 2023/Brain Tumor Detection Classification/Testing/no.
    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
```

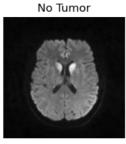


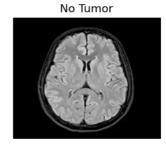


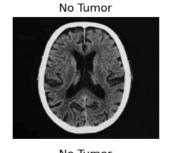


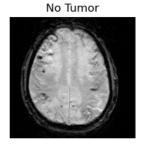












```
In [32]: plt.figure(figsize=(12,8))
p = os.listdir('F:/A DATA SCIENCE 2023/Brain Tumor Detection Classification/Testing/')
c=1
for i in os.listdir('F:/A DATA SCIENCE 2023/Brain Tumor Detection Classification/Testing/p:
    plt.subplot(4,4,c)

    img = cv2.imread('F:/A DATA SCIENCE 2023/Brain Tumor Detection Classification/Testing/p:
    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
```

Positive Tumor



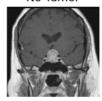
Positive Tumor



Positive Tumor



No Tumor



Positive Tumor



Positive Tumor



Positive Tumor



No Tumor



No Tumor



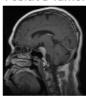
Positive Tumor



Positive Tumor



Positive Tumor



Positive Tumor



Positive Tumor



Positive Tumor



Positive Tumor

