```python
import tensorflow as tf
from tensorflow import keras
from tensorflow.keras import layers
from tensorflow.keras.preprocessing.image import ImageDataGenerator

IMG_SIZE=224
BATCH_SIZE=32

train_datagen=ImageDataGenerator(rescale=1./255,validation_split=0.2)

train_generator=train_datagen.flow_from_directory('/content/drive/
MyDrive/mydrive(internship)/Ramya /brain_tumor_dataset/train',
target_size=(IMG_SIZE,IMG_SIZE),
batch_size=BATCH_SIZE,
class_mode='binary',
subset='training',
)
```

```
Found 915 images belonging to 2 classes.
```

```python
val_generator=train_datagen.flow_from_directory('/content/drive/
MyDrive/mydrive(internship)/Ramya /brain_tumor_dataset/train',
target_size=(IMG_SIZE,IMG_SIZE),
batch_size=BATCH_SIZE,
class_mode='binary',
subset='validation')
```

```
Found 227 images belonging to 2 classes.
```

```python
model=keras.Sequential([
layers.Conv2D(32,
(3,3),activation='relu',input_shape=(IMG_SIZE,IMG_SIZE,3)),
layers.MaxPooling2D(2,2),
layers.Conv2D(64,(3,3),activation='relu'),
layers.MaxPooling2D(2,2),
layers.Conv2D(128,(3,3),activation='relu'),
layers.MaxPooling2D(2,2),
layers.Flatten(),
layers.Dense(128,activation='relu'),
layers.Dense(1,activation='sigmoid')
])

model.summary()
```

```
Model: "sequential_1"

┏━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━┳━━━━━━━━━━━━━━━━━━━━━━━━┳━━━━━━━━━━
━━━━━┓
┃ Layer (type)                     ┃ Output Shape           ┃
Param # ┃
┡━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━╇━━━━━━━━━━━━━━━━━━━━━━━━╇━━━━━━━━━━
```

```
─────┤
│ conv2d_3 (Conv2D)                │ (None, 222, 222, 32)   │
896 │
├─────────────────────────────────┼────────────────────────┼──────────
─────┤
│ max_pooling2d_3 (MaxPooling2D)   │ (None, 111, 111, 32)   │
0 │
├─────────────────────────────────┼────────────────────────┼──────────
─────┤
│ conv2d_4 (Conv2D)                │ (None, 109, 109, 64)   │
18,496 │
├─────────────────────────────────┼────────────────────────┼──────────
─────┤
│ max_pooling2d_4 (MaxPooling2D)   │ (None, 54, 54, 64)     │
0 │
├─────────────────────────────────┼────────────────────────┼──────────
─────┤
│ conv2d_5 (Conv2D)                │ (None, 52, 52, 128)    │
73,856 │
├─────────────────────────────────┼────────────────────────┼──────────
─────┤
│ max_pooling2d_5 (MaxPooling2D)   │ (None, 26, 26, 128)    │
0 │
├─────────────────────────────────┼────────────────────────┼──────────
─────┤
│ flatten_1 (Flatten)              │ (None, 86528)          │
0 │
├─────────────────────────────────┼────────────────────────┼──────────
─────┤
│ dense_2 (Dense)                  │ (None, 128)            │
11,075,712 │
├─────────────────────────────────┼────────────────────────┼──────────
─────┤
│ dense_3 (Dense)                  │ (None, 1)              │
129 │
└─────────────────────────────────┴────────────────────────┴──────────
─────┘
```

```
 Total params: 11,169,089 (42.61 MB)

 Trainable params: 11,169,089 (42.61 MB)

 Non-trainable params: 0 (0.00 B)
```

```
model.compile(optimizer='adam',loss='binary_crossentropy',metrics=['ac
curacy'])

model.fit(train_generator,epochs=5,validation_data=val_generator,batch
_size=BATCH_SIZE)
```

```
Epoch 1/5
29/29 ━━━━━━━━━━━━━━━━━━━━ 226s 8s/step - accuracy: 0.6486 - loss:
0.7830 - val_accuracy: 0.7004 - val_loss: 0.5329
Epoch 2/5
29/29 ━━━━━━━━━━━━━━━━━━━━ 121s 4s/step - accuracy: 0.7957 - loss:
0.4194 - val_accuracy: 0.7841 - val_loss: 0.4467
Epoch 3/5
29/29 ━━━━━━━━━━━━━━━━━━━━ 148s 4s/step - accuracy: 0.8873 - loss:
0.2751 - val_accuracy: 0.8502 - val_loss: 0.3397
Epoch 4/5
29/29 ━━━━━━━━━━━━━━━━━━━━ 131s 5s/step - accuracy: 0.9242 - loss:
0.2044 - val_accuracy: 0.9031 - val_loss: 0.2419
Epoch 5/5
29/29 ━━━━━━━━━━━━━━━━━━━━ 125s 4s/step - accuracy: 0.9620 - loss:
0.1127 - val_accuracy: 0.8018 - val_loss: 0.5079
```

```
<keras.src.callbacks.history.History at 0x790476ee5df0>
```

```
model.save('/content/drive/MyDrive/mydrive(internship)/Ramya
/brain_tumor_dataset/train.h5')
```

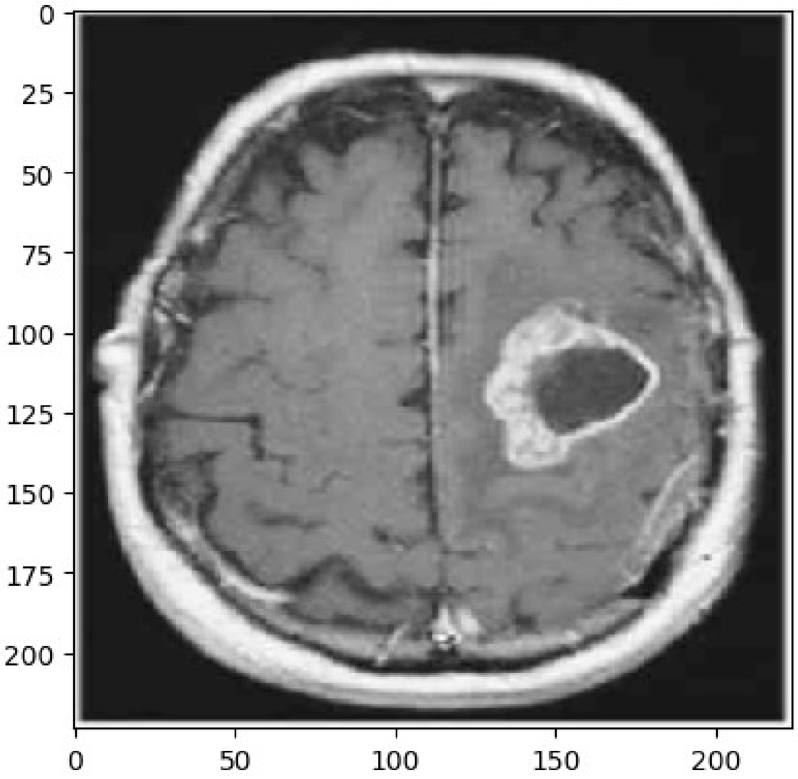
```
WARNING:absl:You are saving your model as an HDF5 file via
`model.save()` or `keras.saving.save_model(model)`. This file format
is considered legacy. We recommend using instead the native Keras
format, e.g. `model.save('my_model.keras')` or
`keras.saving.save_model(model, 'my_model.keras')`.
```

```
from tensorflow.keras.models import load_model
from tensorflow.keras.preprocessing import image
import matplotlib.pyplot as plt
import numpy as np
model=load_model('/content/drive/MyDrive/mydrive(internship)/Ramya
/brain_tumor_dataset/train.h5')
print("model loaded")
```

```
WARNING:absl:Compiled the loaded model, but the compiled metrics have
yet to be built. `model.compile_metrics` will be empty until you train
or evaluate the model.
```

```
model loaded
```

```
test_image_path='/content/drive/MyDrive/mydrive(internship)/Ramya
/brain_tumor_dataset/train/yes/Y1714.jpg'
img=image.load_img(test_image_path,target_size=(224,224))
plt.imshow(img)
plt.axis()
plt.show()
```



```
img_array=image.img_to_array(img)
img_array=np.expand_dims(img_array,axis=0)
img_array/=225
prediction=model.predict(img_array)
print(prediction)
```

```
1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 173ms/step
[[0.98168486]]
```

```
if prediction>=0.5:
  print("you have a brain tumor")
else:
  print("you do not have a brain tumor")
```

```
you have a brain tumor
```