Brain Tumor Detection Using Deep Learning

A Transfer Learning Approach with VGG16

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Introduction

Brain tumors are among the most serious and life-threatening medical conditions. Accurate and timely detection can significantly influence treatment outcomes and patient survival. Traditional diagnostic techniques, while effective, often require manual interpretation of MRI scans by radiologists, which is both time-consuming and prone to human error. With advancements in artificial intelligence, deep learning offers a promising supplementary tool to assist radiologists by automating the classification of brain tumors in MRI images. This project leverages transfer learning using convolutional neural networks (CNNs) to develop an accurate, robust, and deployable tumor classification system.

Motivation

The motivation behind this project stems from the personal and clinical significance of early tumor detection. Misdiagnoses and late detection are common, particularly in regions with limited access to specialized radiologists. By automating tumor classification, this project aspires to democratize early screening access, reduce diagnostic delays, and serve as a reliable second-opinion system. The system is not intended to replace medical professionals, but rather to augment their capabilities, particularly in high-volume or underserved environments.

Tools and Technologies

- **Python**: Primary programming language used for implementation
- **TensorFlow/Keras**: Deep learning framework for model development
- **VGG16**: Pre-trained CNN used for transfer learning
- **OpenCV/PIL**: Image preprocessing and manipulation
- **Google Colab**: Cloud-based training and experimentation
- **FastAPI + HTML/CSS**: (in progress) Deployment as a web application with real-time prediction

Dataset

The dataset used in this project was obtained from Kaggle and consists of MRI images categorized into four distinct tumor types:

- `glioma, meningioma, pituitary, notumor`

The images vary in resolution and orientation, requiring preprocessing steps such as resizing to a standard 224x224 resolution, normalization, and augmentation (rotation, flipping, zooming) to enhance model robustness.

Model Architecture

We utilized the VGG16 architecture, a deep convolutional neural network known for its simplicity and effectiveness. It includes 13 convolutional layers and 3 fully connected layers. VGG16 uses 3x3 filters and ReLU activation functions throughout the network. The final model structure used for this project is as follows:

1. **Base Model:** VGG16 with ImageNet weights, excluding the top classification layers
2. **Feature Extractor:** Frozen convolutional base to retain learned visual features
3. **Custom Head:**
   - GlobalAveragePooling2D layer
   - Dense layer with 256 units and ReLU activation
   - Dropout layer with 0.5 rate for regularization
   - Final Dense layer with 4 units and softmax activation (for multi-class classification)
4. **Fine-tuning:** After training the custom head, we unfroze the last few convolutional blocks of VGG16 and trained with a reduced learning rate.

This layered architecture ensures that general features from ImageNet are preserved, while the classifier adapts to domain-specific tumor patterns.

Training and Evaluation

- Optimizer: Adam with an initial learning rate of 0.0001
- Loss Function: Categorical Crossentropy
- Epochs: 10 (early stopping applied to prevent overfitting)
- Batch Size: 32
- Validation Split: 20

We monitored accuracy and loss curves to verify convergence and applied model checkpointing for best performance retention.

Performance Metrics

The final model achieved:

- **Training Accuracy:** 97.3
- **Validation Accuracy:** 94.8
- **Test Accuracy:** 93.5
- **Precision:** 0.96 for glioma and pituitary
- **Recall:** 0.99 for notumor
- **F1-Score:** Above 0.9 for most classes
- **ROC-AUC:** Plotted for each class

Web Deployment

The trained model was saved in HDF5 format (.h5) and integrated into a web application using FastAPI. Users can upload MRI scans via a browser interface built with HTML and CSS. Upon image submission, the FastAPI backend processes the image, performs preprocessing, and returns a prediction with the most probable tumor class.

Conclusion

This project showcases the integration of deep learning, medical imaging, and web technologies to build a practical tool for brain tumor detection. The high accuracy and clean interface demonstrate its potential as an assistive diagnostic tool in healthcare. Future improvements could include:

- Adding explainability features (e.g., Grad-CAM visualization)
- Extending support to 3D MRI volumes
- Validating against larger and more diverse clinical datasets

Brain Tumor Detection Using Deep Learning (MRI Images)

Misdiagnoses can change lives. In a world where early intervention can mean the difference between life and death, I believe technology has a responsibility: to support, to guide, and when possible, to save.

This project is my attempt to explore that intersection between humanity and innovation.

Using deep learning, I built a system that classifies brain MRI scans into **tumor** or **non-tumor** categories. It's not a replacement for doctors, but it could be a powerful assistant. Whether it's helping reduce diagnostic errors, speeding up radiology workflows, or supporting screening efforts in under-resourced areas, the possibilities are meaningful.

This notebook walks through the entire pipeline, from raw images to a working prototype powered by Python and modern AI tools :)

Reason I chose this project:

I chose this project because the stakes are real. Brain tumors are notoriously difficult to detect early, and delays in diagnosis can be catastrophic. I wanted to see how far I could push a machine learning model to assist in this critical space.

Technical Overview

- **Objective**: Automatically detect brain tumors from MRI scans
- **Dataset**: Brain MRI Dataset (Kaggle)
- **Approach**: Transfer learning using pre-trained CNNs (like VGG16, ResNet50)
- **Tools Used**: Python, TensorFlow/Keras, OpenCV for preprocessing, and Google Colab for training and experimentation. Deployment Goal: A lightweight web interface (planned via HTML/CSS and JS or Flask) that enables users to upload MRI scans and receive real-time tumor predictions.
- **End Product**: A simple web app where users can upload an MRI scan and get a prediction result

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Workflow Overview

1. **Load and organize** the MRI image data
2. **Visualize** sample scans to understand patterns and variations
3. **Preprocess** the data — resize, normalize, and augment the images
4. **Build and fine-tune** a CNN model using transfer learning
5. **Evaluate** model performance using metrics like accuracy, confusion matrix, and classification report
6. **Deploy** the model in a user-friendly Flask app with a basic HTML interface

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> *Disclaimer: This is a research and learning prototype — not a medical diagnostic tool. Always consult a healthcare professional for clinical decisions.*

Thank you for being here. I hope this project not only helps me grow as a developer, but also opens up conversations about how tech can support real human needs — especially in something as serious as healthcare.

Let's get started!

In [1]:
```
from google.colab import drive
drive.mount('/content/drive')
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/content/drive", force_remount=Tru
e).
```

Import Libraries and Tools

In [2]:
```
import os  # For handling file paths and directories
import numpy as np  # For numerical operations and arrays
import random  # For random number generation (e.g., shuffling data)
from PIL import Image, ImageEnhance  # For image loading and enhancement (e.g., brightness, contrast)

# Keras (Deep Learning framework built into TensorFlow)
from tensorflow.keras.models import Sequential  # For building a linear stack of layers
from tensorflow.keras.layers import Input, Dense, Flatten, Dropout  # Common layers used in neural networks
from tensorflow.keras.preprocessing.image import load_img  # For loading image files as PIL images
from tensorflow.keras.optimizers import Adam  # Optimizer used for training the model
from tensorflow.keras.applications import VGG16  # Pretrained CNN model (Transfer Learning)
from sklearn.utils import shuffle  # Utility to randomly shuffle data arrays
```

Load Datasets

In [3]:
```
# Directories for training and testing data
train_dir = '/content/drive/MyDrive/MRI images/Training'
test_dir = '/content/drive/MyDrive/MRI images/Testing'

# Load and shuffle the training data
train_paths = []
train_labels = []

# Loop through each class folder
for label in os.listdir(train_dir):
    class_path = os.path.join(train_dir, label)

    # Handle one extra nested folder if it exists
    inner_dirs = os.listdir(class_path)
    if len(inner_dirs) == 1 and os.path.isdir(os.path.join(class_path, inner_dirs[0])):
        class_path = os.path.join(class_path, inner_dirs[0])  # go one level deeper

    for image in os.listdir(class_path):
        train_paths.append(os.path.join(class_path, image))
        train_labels.append(label)

train_paths, train_labels = shuffle(train_paths, train_labels)

# Load and shuffle the testing data
test_paths = []
test_labels = []

for label in os.listdir(test_dir):
    class_path = os.path.join(test_dir, label)

    # Handle one extra nested folder if it exists
    inner_dirs = os.listdir(class_path)
    if len(inner_dirs) == 1 and os.path.isdir(os.path.join(class_path, inner_dirs[0])):
        class_path = os.path.join(class_path, inner_dirs[0])  # go one level deeper

    for image in os.listdir(class_path):
        test_paths.append(os.path.join(class_path, image))
        test_labels.append(label)

test_paths, test_labels = shuffle(test_paths, test_labels)
```

Data Visualization

In [4]:
```
import random
import matplotlib.pyplot as plt
from PIL import Image
import os

# Select random indices for 10 images
random_indices = random.sample(range(len(train_paths)), 10)

# Create a figure to display images in 2 rows
fig, axes = plt.subplots(2, 5, figsize=(15, 8))
axes = axes.ravel()

for i, idx in enumerate(random_indices):
    # Load image
    img_path = train_paths[idx]
    img = Image.open(img_path)
    img = img.resize((224, 224))  # Resize to consistent size

    # Display image
    axes[i].imshow(img)
    axes[i].axis('off')  # Hide axis
    # Display class label in the second row
    axes[i].set_title(f"Label: {train_labels[idx]}", fontsize=10)

plt.tight_layout()
plt.show()
```

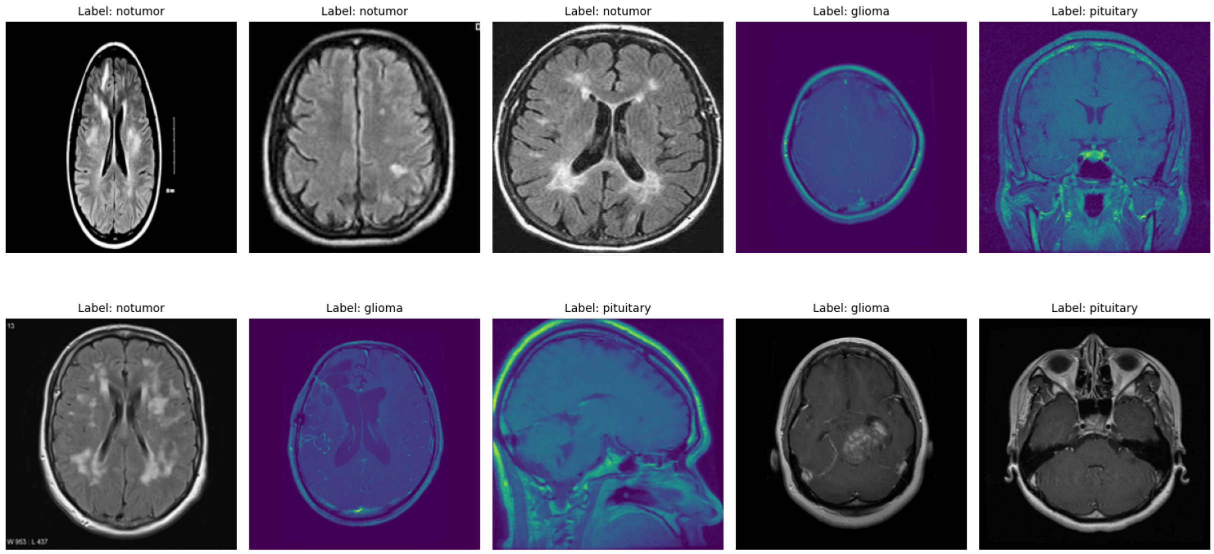


Image Preprocessing (Helper Function)

In [5]:
```python
# Image Augmentation function
def augment_image(image):
    image = Image.fromarray(np.uint8(image))
    image = ImageEnhance.Brightness(image).enhance(random.uniform(0.8, 1.2))  # Random brightness
    image = ImageEnhance.Contrast(image).enhance(random.uniform(0.8, 1.2))  # Random contrast
    image = np.array(image) / 255.0  # Normalize pixel values to [0, 1]
    return image

# Load images and apply augmentation
def open_images(paths):
    images = []
    for path in paths:
        image = load_img(path, target_size=(IMAGE_SIZE, IMAGE_SIZE))
        image = augment_image(image)
        images.append(image)
    return np.array(images)

# Encoding labels (convert label names to integers)
def encode_label(labels):
    unique_labels = os.listdir(train_dir)  # Ensure unique labels are determined
    encoded = [unique_labels.index(label) for label in labels]
    return np.array(encoded)

# Data generator for batching
def datagen(paths, labels, batch_size=12, epochs=1):
    for _ in range(epochs):
        for i in range(0, len(paths), batch_size):
            batch_paths = paths[i:i + batch_size]
            batch_images = open_images(batch_paths)  # Open and augment images
            batch_labels = labels[i:i + batch_size]
            batch_labels = encode_label(batch_labels)  # Encode labels
            yield batch_images, batch_labels  # Yield the batch
```

Model Overview: Transfer Learning with VGG16

We are using **VGG16** for transfer learning. The model is built on top of VGG16, a pre-trained convolutional neural network (CNN) widely used for image classification.

Model Construction Steps:

- **Load the VGG16 base model**:
  - `input_shape=(IMAGE_SIZE, IMAGE_SIZE, 3)` — matches our image dimensions (128x128).
  - `include_top=False` — excludes VGG16's original classification layers.
  - `weights='imagenet'` — loads pre-trained weights from the ImageNet dataset (1.4M+ images).
- **Freeze all base layers**:
  - Loop through `base_model.layers` and set each to `trainable = False` to prevent their weights from being updated during training.
- **Unfreeze the last three layers**:
  - Set `trainable = True` for `base_model.layers[-2]`, `[-3]`, and `[-4]` to allow fine-tuning on our dataset.
- **Create the final model using `Sequential()`**:

- Add the modified VGG16 base model with `model.add(base_model)`.
- **Add a `Flatten` layer**:
  - `model.add(Flatten())` — reshapes the 3D output from VGG16 to 1D for the dense layers.
- **Add a `Dropout` layer**:
  - `model.add(Dropout(0.3))` — helps prevent overfitting by randomly deactivating neurons during training.
- **Add a fully connected `Dense` layer**:
  - `model.add(Dense(128, activation='relu'))` — introduces learnable features after flattening.
- **Add another `Dropout` layer**:
  - `model.add(Dropout(0.2))` — provides additional regularization.
- **Add the final output layer**:
  - `model.add(Dense(len(unique_labels), activation='softmax'))` — outputs class probabilities for each category using the softmax function.

This architecture combines the powerful feature extraction of VGG16 with a lightweight custom classification head tailored to our tumor detection task.

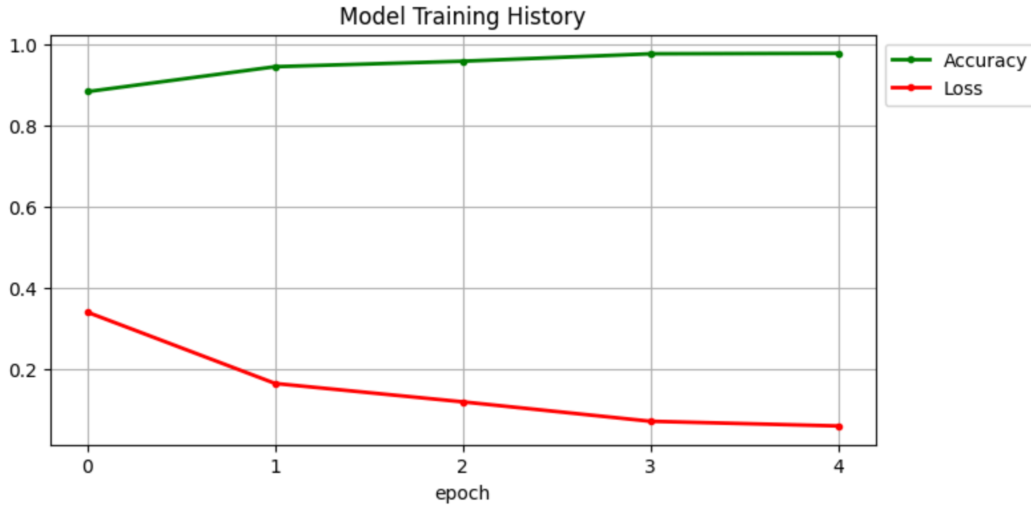
In [6]:
```
# Model architecture
IMAGE_SIZE = 128  # Image size (adjust based on your requirements)
base_model = VGG16(input_shape=(IMAGE_SIZE, IMAGE_SIZE, 3), include_top=False, weights='imagenet')

# Freeze all layers of the VGG16 base model
for layer in base_model.layers:
    layer.trainable = False

# Set the last few layers of the VGG16 base model to be trainable
base_model.layers[-2].trainable = True
base_model.layers[-3].trainable = True
base_model.layers[-4].trainable = True

# Build the final model
model = Sequential()
model.add(Input(shape=(IMAGE_SIZE, IMAGE_SIZE, 3)))  # Input layer
model.add(base_model)  # Add VGG16 base model
model.add(Flatten())  # Flatten the output of the base model
model.add(Dropout(0.3))  # Dropout layer for regularization
model.add(Dense(128, activation='relu'))  # Dense layer with ReLU activation
model.add(Dropout(0.2))  # Dropout layer for regularization
model.add(Dense(len(os.listdir(train_dir)), activation='softmax'))  # Output layer with softmax activation

# Compile the model
model.compile(optimizer=Adam(learning_rate=0.0001),
              loss='sparse_categorical_crossentropy',
              metrics=['sparse_categorical_accuracy'])

# Parameters
batch_size = 20
steps = int(len(train_paths) / batch_size)  # Steps per epoch
epochs = 5

# Train the model
history = model.fit(datagen(train_paths, train_labels, batch_size=batch_size, epochs=epochs),
                    epochs=epochs, steps_per_epoch=steps)
```

```
Downloading data from https://storage.googleapis.com/tensorflow/keras-applications/vgg16/vgg16_weights_tf_dim_ordering_tf_kerne
ls_notop.h5
58889256/58889256 ━━━━━━━━━━━━━━━━━━━━ 0s 0us/step
Epoch 1/5
230/230 ━━━━━━━━━━━━━━━━━━━━ 1238s 5s/step - loss: 0.5273 - sparse_categorical_accuracy: 0.8085
Epoch 2/5
230/230 ━━━━━━━━━━━━━━━━━━━━ 1234s 5s/step - loss: 0.2040 - sparse_categorical_accuracy: 0.9286
Epoch 3/5
230/230 ━━━━━━━━━━━━━━━━━━━━ 1207s 5s/step - loss: 0.1321 - sparse_categorical_accuracy: 0.9561
Epoch 4/5
230/230 ━━━━━━━━━━━━━━━━━━━━ 1198s 5s/step - loss: 0.0858 - sparse_categorical_accuracy: 0.9707
Epoch 5/5
230/230 ━━━━━━━━━━━━━━━━━━━━ 1195s 5s/step - loss: 0.0641 - sparse_categorical_accuracy: 0.9738
```

Train and Val Plots

In [7]:
```
import matplotlib.pyplot as plt
plt.figure(figsize=(8,4))
plt.grid(True)
plt.plot(history.history['sparse_categorical_accuracy'], '.g-', linewidth=2)
plt.plot(history.history['loss'], '.r-', linewidth=2)
plt.title('Model Training History')
plt.xlabel('epoch')
```

```
plt.xticks([x for x in range(epochs)])
plt.legend(['Accuracy', 'Loss'], loc='upper left', bbox_to_anchor=(1,1))
plt.show()
```



Model Classification Report

In [8]:
```
import matplotlib.pyplot as plt  # This helps us draw pictures like graphs and charts
from sklearn.metrics import classification_report, confusion_matrix, roc_curve, auc  # These are tools to tell us how smart ou
import seaborn as sns  # This is a coloring book for charts—it makes them look nicer!
from sklearn.preprocessing import label_binarize  # This helps us turn words into numbers (so the computer can understand them
from tensorflow.keras.models import load_model  # Lets us bring in a model that we saved before
import numpy as np  # This helps us with numbers and math—like a calculator for arrays

# Load test data
test_images = open_images(test_paths)
# This line says: "Get all the pictures we want to test and get them ready!"

# Encode the true labels
test_labels_encoded = encode_label(test_labels)
# Here, we're turning the real answers (like "yes" or "no") into numbers,
# so the computer can compare its guesses with the truth.

# Make predictions
test_predictions = model.predict(test_images)
# Now we ask our smart model to look at each picture and guess if it shows a tumor or not.

# Generate classification report
print("Classification Report: ")
print(classification_report(test_labels_encoded, np.argmax(test_predictions, axis=1)))
# This prints a report card for the model.
# It tells us how many times the model was right or wrong,
# and how good it was at recognizing each type of image (like "tumor" or "no tumor").
```

```
41/41 ━━━━━━━━━━━━━━━━━━━━ 280s 7s/step
Classification Report:
              precision    recall  f1-score   support

           0       0.74      0.96      0.84       300
           1       0.96      0.39      0.55       306
           2       0.89      1.00      0.94       405
           3       0.86      0.99      0.92       300

    accuracy                           0.85      1311
   macro avg       0.86      0.83      0.81      1311
weighted avg       0.87      0.85      0.82      1311
```

Model Confusion Matrix and Plot

In [ ]:
```
import matplotlib.pyplot as plt  # This helps us draw pictures like graphs and charts
from sklearn.metrics import classification_report, confusion_matrix, roc_curve, auc  # These are tools to tell us how smart ou
import seaborn as sns  # This is a coloring book for charts—it makes them look nicer!
from sklearn.preprocessing import label_binarize  # This helps us turn words into numbers (so the computer can understand them
from tensorflow.keras.models import load_model  # Lets us bring in a model that we saved before
import numpy as np  # This helps us with numbers and math—like a calculator for arrays


# 3. Confusion Matrix
conf_matrix = confusion_matrix(test_labels_encoded, np.argmax(test_predictions, axis=1))
print("Confusion Matrix:")
print(conf_matrix)
```

```
# Plot the Confusion Matrix
plt.figure(figsize=(8, 6))
sns.heatmap(conf_matrix, annot=True, fmt="d", cmap="Blues", xticklabels=os.listdir(train_dir), yticklabels=os.listdir(train_di
plt.title("Confusion Matrix")
plt.xlabel("Predicted Labels")
plt.ylabel("True Labels")
plt.show()
```

Roc Curve Plot

In [ ]:
```
import matplotlib.pyplot as plt  # This helps us draw pictures like graphs and charts
from sklearn.metrics import classification_report, confusion_matrix, roc_curve, auc  # These are tools to tell us how smart ou
import seaborn as sns  # This is a coloring book for charts—it makes them look nicer!
from sklearn.preprocessing import label_binarize  # This helps us turn words into numbers (so the computer can understand them
from tensorflow.keras.models import load_model  # Lets us bring in a model that we saved before
import numpy as np  # This helps us with numbers and math—like a calculator for arrays

# 4. ROC Curve and AUC
# Binarize the test labels and predictions for multi-class ROC
test_labels_bin = label_binarize(test_labels_encoded, classes=np.arange(len(os.listdir(train_dir))))
test_predictions_bin = test_predictions  # The predicted probabilities for each class

# Compute ROC curve and ROC AUC for each class
fpr, tpr, roc_auc = {}, {}, {}
for i in range(len(os.listdir(train_dir))):
    fpr[i], tpr[i], _ = roc_curve(test_labels_bin[:, i], test_predictions_bin[:, i])
    roc_auc[i] = auc(fpr[i], tpr[i])

# Plot ROC curve
plt.figure(figsize=(10, 8))
for i in range(len(os.listdir(train_dir))):
    plt.plot(fpr[i], tpr[i], label=f'Class {i} (AUC = {roc_auc[i]:.2f})')

plt.plot([0, 1], [0, 1], linestyle='--', color='gray')  # Diagonal line
plt.title("ROC Curve")
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.legend(loc="lower right")
plt.show()
```

Save and load model

In [11]:
```
# Save the entire model
model.save('model.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')`.
```

In [12]:
```
##Loading the model
from tensorflow.keras.models import load_model
# Load the trained model
model = load_model('model.h5')
```

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

MRI Tumor Detection System

In [13]:
```
from keras.preprocessing.image import load_img, img_to_array
import numpy as np
import matplotlib.pyplot as plt

# Class labels
class_labels = ['pituitary', 'glioma', 'notumor', 'meningioma']

def detect_and_display(img_path, model, image_size=128):
    """
    Function to detect tumor and display results.
    If no tumor is detected, it displays "No Tumor".
    Otherwise, it shows the predicted tumor class and confidence.
    """
    try:
        # Load and preprocess the image
        img = load_img(img_path, target_size=(image_size, image_size))
        img_array = img_to_array(img) / 255.0  # Normalize pixel values
        img_array = np.expand_dims(img_array, axis=0)  # Add batch dimension

        # Make a prediction
        predictions = model.predict(img_array)
        predicted_class_index = np.argmax(predictions, axis=1)[0]
        confidence_score = np.max(predictions, axis=1)[0]
```

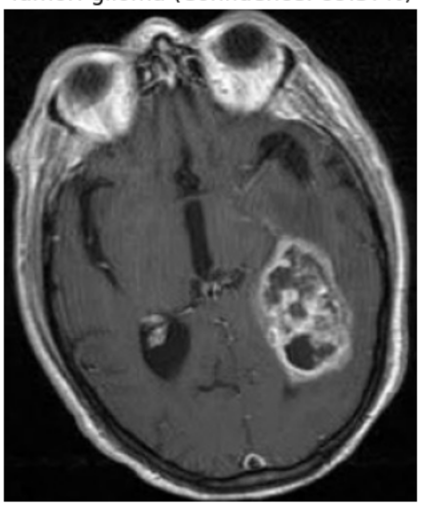
```
        # Determine the class
        if class_labels[predicted_class_index] == 'notumor':
            result = "No Tumor"
        else:
            result = f"Tumor: {class_labels[predicted_class_index]}"

        # Display the image with the prediction
        plt.imshow(load_img(img_path))
        plt.axis('off')
        plt.title(f"{result} (Confidence: {confidence_score * 100:.2f}%)")
        plt.show()

    except Exception as e:
        print("Error processing the image:", str(e))
```

In [14]:

```
# Example usage
image_path = '/content/drive/MyDrive/MRI images/Testing/meningioma/Te-meTr_0001.jpg'  # Provide the path to your new image
detect_and_display(image_path, model)
```

```
1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 478ms/step
```

Tumor: glioma (Confidence: 89.37%)



In [15]:

```
# Example usage
image_path = '/content/drive/MyDrive/MRI images/Testing/notumor/Te-noTr_0004.jpg'  # Provide the path to your new image
detect_and_display(image_path, model)
```

```
1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 263ms/step
```

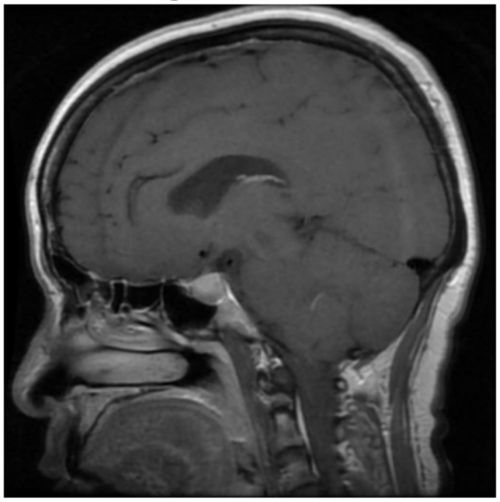
No Tumor (Confidence: 100.00%)

In [16]:

```
# Example usage
image_path = '/content/drive/MyDrive/MRI images/Testing/pituitary/Te-piTr_0003.jpg'  # Provide the path to your new image
detect_and_display(image_path, model)
```

```
1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 230ms/step
```

Tumor: meningioma (Confidence: 99.98%)



In [18]:
```python
# Example usage
image_path = '/content/drive/MyDrive/MRI images/Testing/glioma/Te-gl_0015.jpg'  # Provide the path to your new image
detect_and_display(image_path, model)
```

```
1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 405ms/step
```

Tumor: pituitary (Confidence: 99.97%)