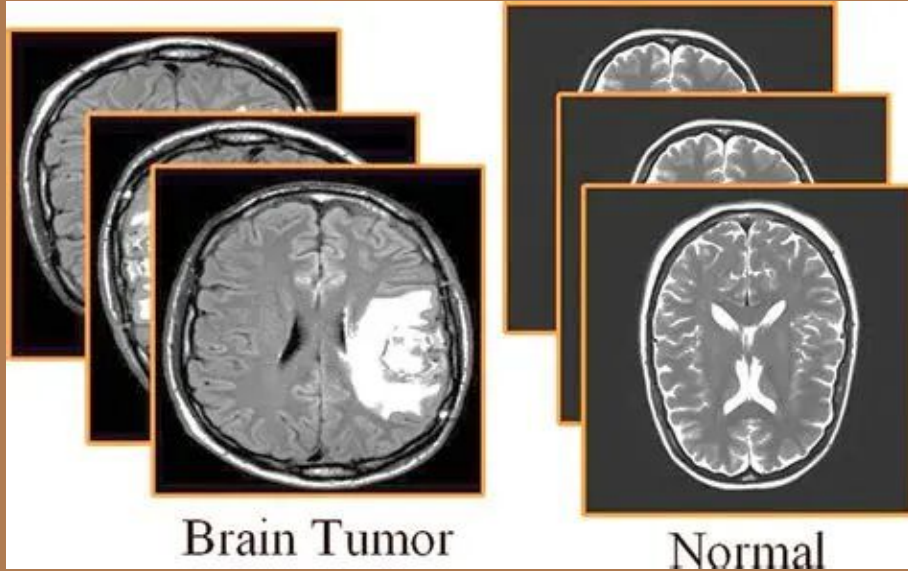


Brain Tumor Classification with Deep Learning

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Problem

NeuroScan Diagnostics has been contracted by a San Diego based hospital to develop a deep learning model for brain tumor classification using MRI data to help their radiology department make faster and more accurate classifications. They are focusing on classifying glioma tumors, meningioma tumors, pituitary tumors, or no tumor.

Context

NeuroScan Diagnostics, is based in San Diego, CA, and is a leader in AI powered medical imaging and diagnostics. San Diego is renowned for its cutting edge research in neurology and biomedical sciences, making it the perfect environment for innovating advanced tumor detection models.

Success Metrics

Accurate and timely classification of tumors based on MRI scans. The model must have high evaluation metric scores for precision, recall, F1- score, and accuracy.

Constraints

MRI scan quality, patient positioning, and imaging equipment may affect the reliability of the model's predictions.

Stakeholders

Dr. Olivia Matthews will provide clinical expertise to ensure the model aligns with real world radiology practices

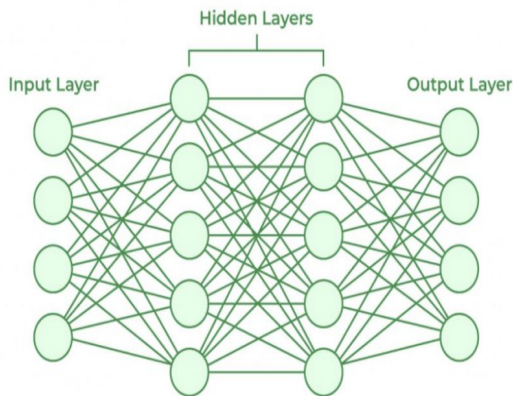
Type of Problem

This is a supervised learning image classification task focused on detecting brain tumor types from MRI scans. Will be solved by using deep learning models.

Why Deep Learning

Deep learning models are machine learning models that use layers of interconnected nodes (neurons) to learn from data. The “deep” part comes from having many layers, each layer extracts more abstract features.

DEEP LEARNING MODELS



Data Description

- Downloaded from Kaggle
- The training set contains 3,310 images, while the test set includes 394 images.
- Each training and testing folder had four folders inside with images of the tumors. Each folder was named after the tumor represented in the images.
- Each image is a 2D grayscale scan with a resolution of 240x240 pixels.

Project Workflow

- Step 1:** Data Wrangling and Pre-Processing
- Step 2:** Exploratory Data Analysis (EDA)
- Step 3:** Model Selection & Training
- Step 4:** Model Predictions and Evaluations
- Step 5:** Model Optimization
- Step 6:** Testing the Final Model

Building on the previously described dataset, the following steps were taken for deep learning model training.

Data Extraction

- Used Python `zipfile` library to extract contents
- Organized into folders per class
- Paths mapped using label driven for loops

Image Preprocessing

- Grayscale conversion for consistent visualization (`cv2.IMREAD_GRAYSCALE`)
- Resized to **224×224** for model compatibility
- Applied **CLAHE** for localized contrast enhancement
- Normalized pixel values to [0,1] scale

Data Preparation

- Processed images stored in `X_train, X_test`
- Corresponding labels stored in `y_train, y_test`
- `tqdm` progress bar used for efficiency tracking

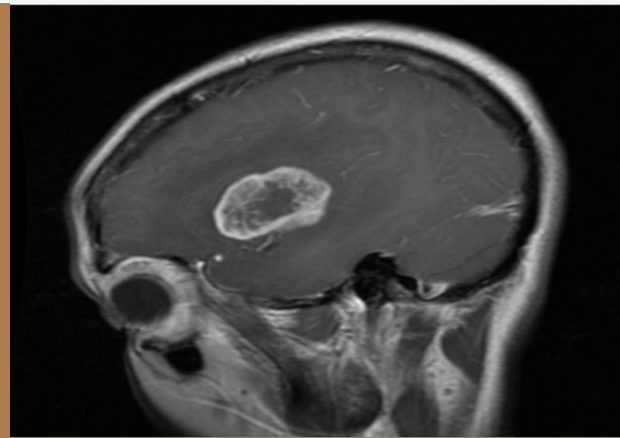
Data Wrangling and Pre-Processing

```
labels = ['glioma_tumor', 'meningioma_tumor', 'no_tumor', 'pituitary_tumor']
```

```
X_train = []  
y_train = []
```

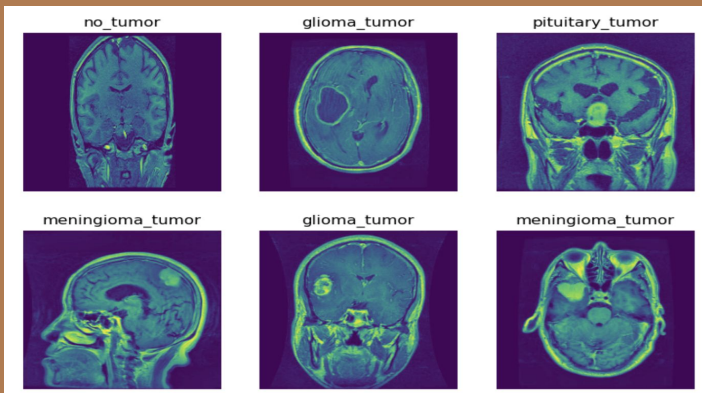
```
image_size = 224  
for i in labels:  
    folderPath = os.path.join('dataset_extracted/Tumor Data', 'Training', i)  
    for j in tqdm(os.listdir(folderPath)):  
        img = cv2.imread(os.path.join(folderPath,j),cv2.IMREAD_GRAYSCALE)  
        img = cv2.resize(img,(image_size, image_size))  
        clahe = cv2.createCLAHE(clipLimit=2.0, tileGridSize=(8,8))  
        img = clahe.apply(img) # Apply CLAHE for controlled contrast enhancement  
        img = img / 255.0 # Normalize pixel values to range [0, 1]  
        X_train.append(img)  
        y_train.append(i)
```

Image Before
transformations



Visual Checks After Transformations

- Random MRI samples printed from training/testing sets
- CLAHE preprocessing improved contrast in low-detail regions



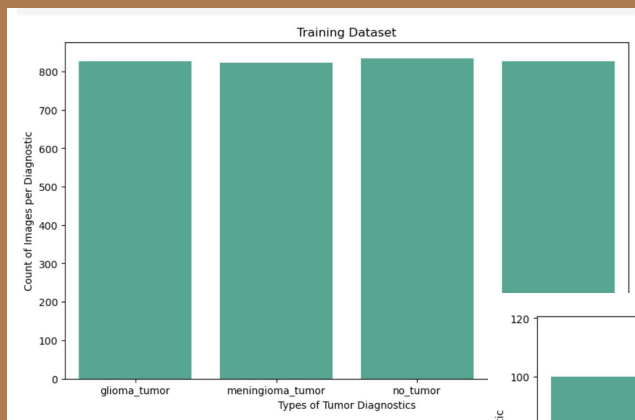
Dataset Shape

- **Training set:** 3,310 images at 224×224 pixels
- **Test set:** 394 images at 224×224 pixels

Exploratory Data Analysis

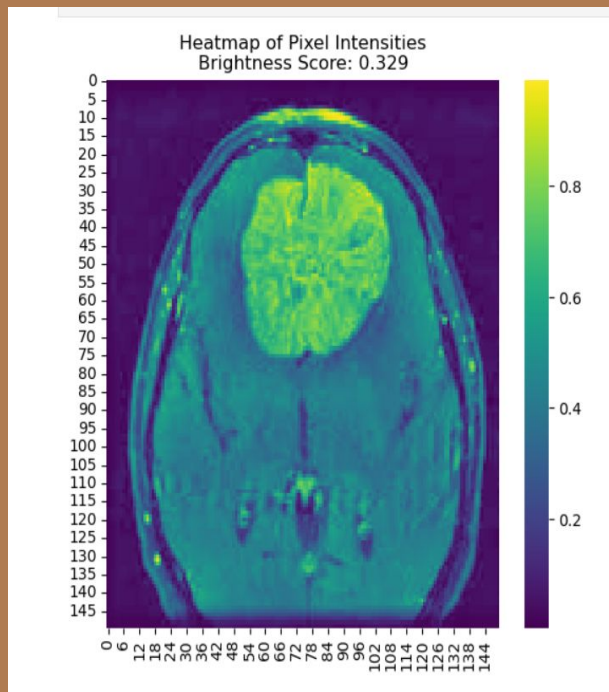
Class Balances

- **Training data:** Balanced across 4 categories
- **Testing data:** Imbalanced relied on precision, recall, F1-score for fair evaluation



Pixel Intensity Heatmaps

- Visualized brightness across scans
- Bright regions linked to potential tumor presence
- Aids interpretation and supports quality assurance before model training



RGB Conversion

- Converted grayscale images to 3-channel RGB
- Image arrays renamed: `X_train_rgb, X_test_rgb`
- Ensures compatibility with ImageNet-pretrained CNN models

Label Preparation

- Used `LabelEncoder()` for numeric conversion of categories
- Created both encoded (`y_train_encoded, y_test_encoded`) and one-hot versions (`y_train_cat, y_test_cat`)

Exploratory Data Analysis

ResNet50 Custom Model Setup

- Pretrained on **ImageNet**
- Used `include_top=False` to remove default classifier
- `res_net_model.trainable = False` keep all the weights in `res_net_model` unchanged during training
- Added **GlobalAveragePooling2D** to compress features
- Dropout(0.5) for regularization
- Dense(128) layer with **ReLU** activation
- Dropout(0.25) for regularization
- Dense(4) with **Softmax** activation for 4-class prediction
- Compiled with **Adam**, **categorical cross-entropy**, and **accuracy**
- Trained on `X_train_rgb` and `y_train_cat`
- Purpose: Balanced depth with strong feature learning, suited for smaller dataset

Model Selection & Training

DenseNet121 Custom Model Setup

- Pretrained on **ImageNet**
- Used `include_top=False` to replace default classifier
- Dense(64) layer with **ReLU** activation
- Dropout(0.5) for regularization
- Dense(4) with **Softmax** for final prediction
- Compiled with **Adam**, **categorical cross-entropy**, and **accuracy**
- Trained on `X_train_rgb` and `y_train_cat`
- Purpose: Test deeper architecture vs. smaller neuron count for performance

Xception Custom Model Setup

- Pretrained on **ImageNet**
- Used `include_top=False` to insert custom classifier
- Added **GlobalAveragePooling2D** layer for shape and texture focus
- Dense(64) layer with **ReLU** activation
- Dropout(0.3) for light regularization
- Dense(4) with **Softmax** activation for class prediction
- Compiled with **Adam**, **categorical cross-entropy**, and **accuracy**
- Trained on `X_train_rgb` and `y_train_cat`
- Purpose: Explore modular feature extraction and channel wise learning

Model Predictions and Evaluations

Prediction Strategy

- Created prediction function for modular evaluation
- Used `np.argmax` on model outputs to identify class predictions

Evaluation Strategy

- Created a function called `evaluate()` for model performance
 - Used `classification_report` from `sklearn` to extract:
 - **Precision, Recall, F1-Score** converted to percentages
 - Focused on clinically relevant metrics due to test set imbalance
- Added separate `accuracy()` function

ResNet50 Evaluation Summary

- **Precision:** 64%
- **Recall:** 59%
- **F1-Score:** 60%
- **Accuracy:** 59%
- Struggled to classify tumors reliably
- Fewer layers with more neurons led to overfitting
- **Conclusion:** Underperformed with medical images (MRI scans).

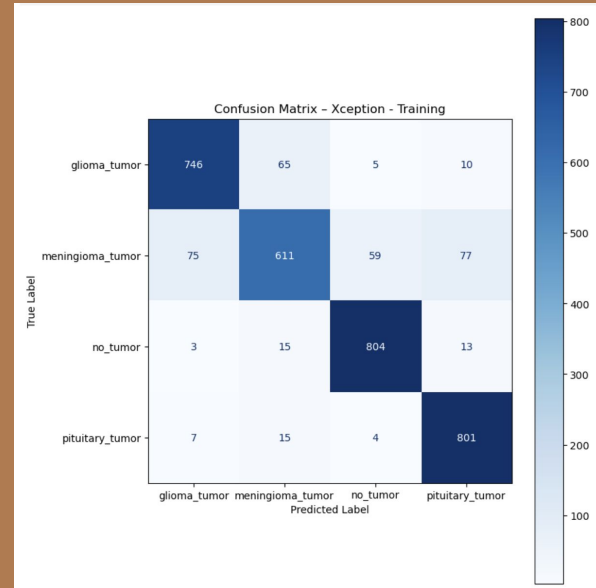
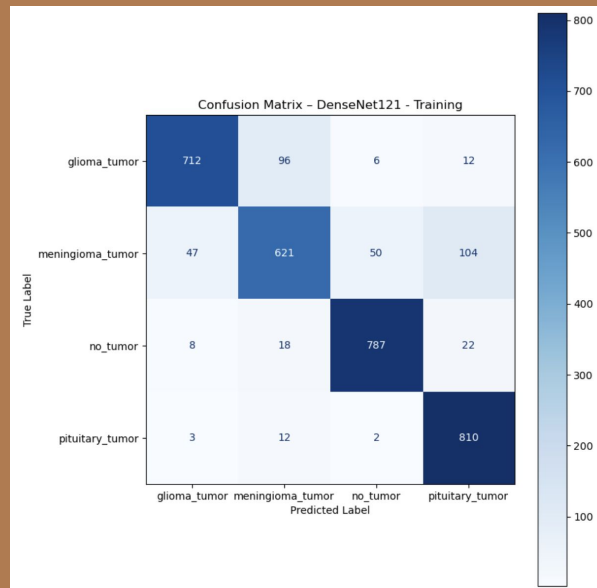
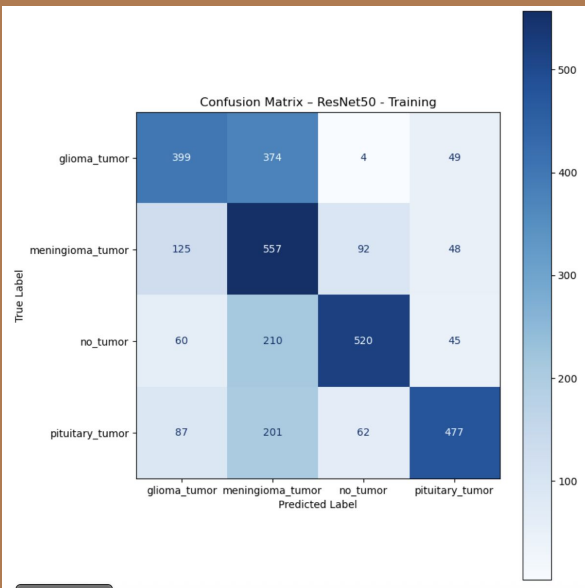
DenseNet121 Evaluation Summary

- **Precision:** 88.54%
- **Recall:** 88%
- **F1-Score:** 88%
- **Accuracy:** 88%
- Deep architecture captured complex tumor patterns
- Balanced generalization across all classes
- **Conclusion:** Strong performance with MRI scans.

Xception Evaluation Summary

- **Precision:** 89.35%
- **Recall:** 89%
- **F1-Score:** 89%
- **Accuracy:** 89%
- Modular learning boosted subtle detail detection
- Slight edge over DenseNet121 in all metrics
- **Conclusion:** Top-performing model ideal for further fine-tuning

Confusion Matrix

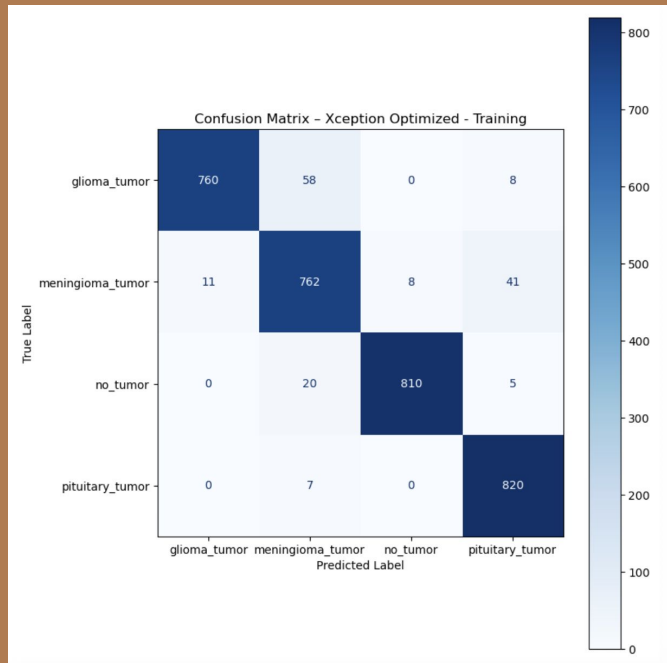


- **DenseNet121** slightly outperformed Xception on *meningioma* and *pituitary* tumor detection
- Correctly classified 9–10 more images in those categories
- Sparked interest in fine-tuning **Xception** to match or exceed that performance

Model Optimization

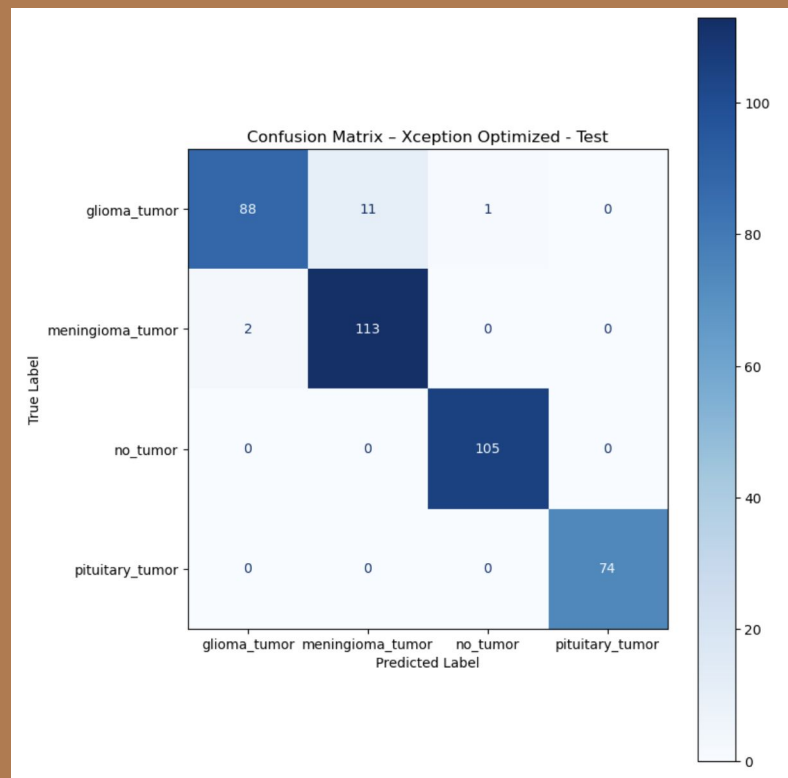
Manual Optimization: Xception Model

- Increased Dense layer size from **64 to 256 neurons**
- Reduced dropout rate from **30% to 10%**
- Model architecture unchanged beyond hyperparameters
- Achieved significant performance boost:
 - **Precision:** 95%
 - **Recall:** 95%
 - **F1-Score:** 95%
 - **Accuracy:** 95%
- Confusion matrix shows improved predictions across all 4 tumor classes



Testing the Final Model

- Evaluated on **394 test images**, preprocessed identically to training data
- Achieved strong generalization on unseen data:
 - **Precision:** 97%
 - **Recall:** 96%
 - **F1-Score:** 97%
 - **Accuracy:** 96%
- Consistent correct classifications across all four classes
- Minimal misclassifications suggest **no overfitting or underfitting**
- Confirms the model's reliability for real world application.



Recommendations

- **Streamline Workflow:** Automate MRI scan classification to free up clinicians for personalized treatment planning.
- **Support Research:** Analyze tumor patterns and demographics to uncover trends in patient susceptibility.
- **Enable Early Detection:** Integrate as a screening tool for identifying tumors in high risk individuals.

Suggestions For Improvement

Class-Specific Fine-Tuning

- Retrain only on glioma and meningioma samples using a smaller model or the last few layers of Xception
- Helps the model learn subtle differences it may be glossing over in full multiclass training

