Final Project Computer Vision

Brain Tumor Classification on Low Resolution Images

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Abstract—This project develops a computer-vision system to classify brain MRI slices into healthy or some tumor types classes using handcrafted texture features (GLCM and LBP) and the best machine learning model between Random Forest, Support Vector Machine (SVM), and XGBoost for classification. The pipeline includes dataset acquisition, preprocessing (resize, grayscale, histogram equalization, denoising, sharpening, normalization), feature extraction (quantized GLCM properties and uniform LBP histograms), feature scaling, model training, hyperparameter tuning, and evaluation on a held-out test set. Key contributions are a reproducible preprocessing pipeline, a lightweight explainable feature set suitable for limited-data regimes, and a Streamlit demo for interactive inference. The result shows SVM as a better model for this case with Accuracy: 90%; Precision: 90%; Macro F1: 89%; Recall: 89%. The system is intended for research/educational use and not for clinical diagnosis.

***Keywords*— Machine Learning, Tumor, Texture-based feature detection, XGBoost, Random Forest, SVM, Tumor Classification, Model Comparison, Model Evaluation**

I. Introduction

Brain tumors are among the most aggressive and life-threatening diseases globally, requiring rapid and precise diagnosis to maximize patient survival rates. Magnetic Resonance Imaging (MRI) is currently the gold standard for non-invasive brain tumor detection, offering detailed insights into soft tissue structures. However, the clinical interpretation of MRI scans is often complicated by artifacts, noise, and—crucially—variations in image resolution. In many developing regions or resource-constrained medical facilities, high-field MRI machines are not always available, resulting in lower-resolution scans that make fine-grained tumor differentiation difficult for human radiologists.

While Deep Learning (DL) models, particularly Convolutional Neural Networks (CNNs), have achieved state-of-the-art results in medical imaging, they often face two significant limitations. First, they are computationally expensive and data-hungry, requiring massive annotated datasets to avoid overfitting. Second, they operate as "black boxes," lacking the interpretability required for clinical trust. Furthermore, when applied to low-resolution images, standard CNNs often struggle to recover meaningful spatial features without extensive upsampling or super-resolution techniques.

To address these challenges, this project proposes a lightweight, texture-based machine learning pipeline designed specifically for classifying brain tumors (Glioma, Meningioma, and Pituitary) and healthy brain tissue. Instead of relying on raw pixel data, we leverage handcrafted feature extraction techniques—specifically Gray Level Co-occurrence Matrix (GLCM) and Local Binary Patterns (LBP). These descriptors are mathematically robust to changes in illumination and resolution, making them ideal for analyzing the structural heterogeneity of tumors in lower-quality images.

This study utilizes a curated dataset of 7,023 MRI slices to evaluate and compare the performance of three classical machine learning algorithms: Support Vector Machine (SVM), Random Forest (RF), and XGBoost. The primary objectives are:

1. To develop a reproducible preprocessing pipeline that standardizes variable-resolution MRI scans.
2. To extract discriminative texture features (GLCM and LBP) that quantify tumor heterogeneity.
3. To determine the most effective classification model for this specific feature set through rigorous hyperparameter tuning.

By focusing on feature engineering rather than raw computational power, this research aims to demonstrate that classical machine learning remains a competitive and highly efficient alternative for medical image classification, even in the era of Deep Learning.

II. Related Works

A. Texture-based MRI Classification

Traditional computer vision research has explored the use of hand made texture descriptors for medical imaging analysis for a very long time[1]. GLCM features, such as contrast, homogeneity, energy, and correlation, are often used due to their viability to quantify spatial relationships between pixel color and/or intensities. These descriptors are especially well-suited for grayscale medical images, where structural patterns rather than color information makes or breaks relevance to the subject image.

Similarly, LBP has proven very effective for characterizing micro-texture variations, making it suitable for identifying irregular tissue structures in MRI scans[9]. Previous studies have demonstrated that combining multiple texture descriptors can significantly improve model performance, especially when dealing with grayscale, low-resolution, or low-contrast images. This implies that handcrafted texture features are still very robust and efficient, making them a viable alternative to the more complex and daunting machine learning based representations under certain conditions.

B. Radiomics-Based Feature Extraction

Radiomics provide a basis for extracting complex, quantitative features from medical images, with the goal of capturing meaningful information in a reproducible and interpretable manner[2][3]. With this technology texture descriptors like GLCM, LBP, and first-order statistical features are the foundational factors of the machine. Radiomics-based pipelines emphasize feature stability, scanner invariance, and interpretability, factors that are very important in clinical environments where transparency and consistency is needed the most.

Unlike deep learning approaches, radiomics workflows allow for selective inspection and selection of features, making it possible for domain experts to reason about which image characteristics contribute to a model's predictions[10]. Several studies have demonstrated that radiomics-based models can achieve competitive performance in medical

research, especially when reinforced with classical machine learning classifiers and feature selection strategies. This pushes the notion that handcrafted features are still used to this day.

C. Deep Learning Approaches

In recent years, Convolutional Neural Networks (CNNs) and transformer based architectures have dominated brain tumor classification tasks, achieving substantial and relatively positive results by learning hierarchical feature representation directly from the data. However, these models typically require large annotated datasets, high computational resources, and complex hyperparameter tuning processes[4][8]. This performance often comes with substantial computational requirements, extensive hyperparameter tuning, and reduced transparency in the decision-making process.

Above that, the reliance of deep learning models on large-scale datasets limit their usability in many real-world clinical settings, where labeled medical data is often low quality or doesn't exist. Although explainability techniques like saliency maps and activation visualizations have been proposed, these methods typically provide post-hoc insights rather than direct, semantically interpretable reasoning[7]. As a result, deep learning approaches may not be the best approach where data efficiency, reproducibility, and human understanding are the primary concern[8].

D. Previous Work in Brain Tumor Classification

Existing literature shows successful attempts at differentiating tumor types such as glioma, meningioma, and pituitary tumors using a variety of imaging techniques and classification strategies[4]. Many classical machine learning works focus on hand crafted features, feature selection techniques, and ensemble methods to improve predictive accuracy. Meanwhile, deep learning studies often rely on transfer learning or 3D CNNs to extract volumetric information from MRI sequences[5].

However, there are still gaps in studies focusing on low-resolution MRI classification using lightweight feature-based models, motivating the current project's emphasis on interpretability and computational efficiency[6]. These limitations motivate the present work, which emphasizes computational efficiency and interpretability while maintaining well structured classification performance.

III. Methodology

This section outlines the experimental framework used to classify brain tumor MRI slices. The pipeline consists of data acquisition, image preprocessing, texture feature extraction, and model training using hyperparameter optimization.

A. Dataset

The dataset used in this study is based on data from, "Brain Tumor MRI Dataset", sourced from the official Kaggle platform. Curated by Masoud Nickparvar, it is a dataset which is a combination of the following three datasets: figshare, SARTAJ dataset, Br35H. It contains 7023 images of human brain MRI images which are classified into 4 classes: glioma, meningioma, no tumor ,and pituitary. The no tumor class images were taken from the Br35H dataset. The SARTAJ dataset has a problem that the glioma class images are not categorized correctly, the curator realizes this from results of other people's work as well as the different models he trained, which is why he uses images from figshare instead for the glioma. The image in this dataset also comes in different sizes which will be resized later on.

TABLE. I. Data Distribution

	Training	**Testing**
Glioma	1321	300
Meningioma	1339	306
No Tumor	1595	405
Pituitary	1457	300

The distribution mentioned in Table I is the distribution from the dataset. The dataset already comes pre-distributed. It will be used for modelling. The image class is the target that will be used to predict the types or absence of a tumor. The images will be used to estimate whether it is a brain with what type of tumor or no tumor at all based on its features.

B. Data Preprocessing

A standardized preprocessing pipeline was applied to all images to ensure consistency and improve feature extraction quality. The transformations included:

1. **Resizing,** all images were resized to a uniform dimension of 244x244 pixels for better comparability.
2. **Grayscale conversion**, images were converted to grayscale to focus solely on intensity variations.
3. **Histogram equalization,** to enhance contrast and reveal subtle texture patterns.
4. **Denoising** using Gaussian filtering to reduce high-frequency noise artifacts.
5. **Sharpening** to emphasize edges and structural boundaries within tumor regions.
6. **Normalization** of intensity values to stabilize feature distribution.

This sequence produced cleaner and more standardized images, enabling more reliable extraction of texture descriptors.

C. Feature Extraction

The Gray Level Co-occurrence Matrix (GLCM) is a second-order statistical method that analyzes the spatial relationship between pixel intensities in a grayscale image. GLCM measures how often a pair of pixel values occurs at a specific distance and direction. Unlike first-order statistics that only consider individual pixel intensities, GLCM

captures textural information by considering the relationship between neighboring pixels.

In this study, the GLCM is computed using the following parameters:

- Distance (d) = 1 pixel
- Angle (θ) = 0° (horizontal direction)
- Gray levels = 256
- Symmetric matrix = enabled
- Normalized matrix = enabled

The GLCM is generated by counting the frequency of occurrence of pixel pairs (i,j) separated by the specified distance and angle. The resulting matrix is normalized so that the sum of all elements equals one, allowing it to be interpreted as a probability distribution. From the normalized GLCM, four statistical texture features are extracted. There are Contrast, Energy, Homogeneity, and Correlation.

Local Binary Pattern (LBP) is a texture descriptor that characterizes local spatial patterns by comparing each pixel with its neighboring pixels. LBP is widely used due to its simplicity, computational efficiency, and robustness to illumination changes.

In this study, LBP is computed using the following parameters:

- Radius (R) = 1
- Number of neighbors (P) = 8
- Method = uniform

For each pixel, the grayscale value of the center pixel is compared with its surrounding neighbors. If the neighbor's value is greater than or equal to the center pixel, a value of 1 is assigned; otherwise, a value of 0 is assigned. These binary values are concatenated to form a binary pattern. The uniform LBP method groups patterns with at most two bitwise transitions, reducing feature dimensionality and improving robustness.

After computing the LBP image, a histogram of LBP values is constructed to represent the distribution of local texture patterns. For uniform LBP with 8 neighbors, the histogram consists of 10 bins, each corresponding to a specific uniform pattern. The histogram is normalized so that the sum of all bins equals one, ensuring scale invariance. Thus, ten LBP features are extracted for each image.

The final feature vector is formed by concatenating the GLCM and LBP features:

- GLCM features: 4
- LBP features: 10

Therefore, each image is represented by a 14-dimensional feature vector, which combines global texture characteristics (GLCM) and local texture patterns (LBP). Before classification, feature scaling is applied using standardization. Each feature is transformed to have zero mean and unit variance. This step is particularly important for distance-based and optimization-based classifiers to ensure that all features contribute equally to the learning process.

D. Model Training and Hyperparameter Tuning

Two groups of handcrafted features being GLCM and LBP were extracted from the preprocessed images. GLCM properties were computed using quantized gray levels and multiple directional offsets, while LBP histograms were generated with similar patterns to reduce redundancies. The combined feature sets were standardized using z-score normalization before being fed to each model.

Three Machine Learning models were evaluated:

1. Support Vector Machine (SVM).
2. Random Forest
3. XGBoost

To maximize performance, we employed GridSearchCV to exhaustively search for the optimal hyperparameters.

- Random Forest
  - Search Space:
    n_estimators [100, 200, 300],
    max_depth [10, 20, 30, None],
    min_samples_split [2, 5, 10].
  - Best Parameters:
    'max_depth': None,
    'min_samples_split': 5,
    'n_estimators': 200

- Support Vector Machine (SVM)
  - Search Space:
    C [0.1, 1, 10, 100, 1000],
    gamma [1, 0.1, 0.01, 0.001, 0.0001],
    kernel ['rbf'].
  - Best Parameters:
    'C': 10,
    'gamma': 1,
    'kernel': 'rbf'

- XGBoost
  - Search Space:
    n_estimators [100, 200, 300],
    learning_rate [0.01-0.5],
    max_depth [3, 5, 7],
    subsample [0.7-0.9],
    gamma [0-0.5].
  - Best Parameters:
    'gamma': 0,
    'learning_rate': 0.1,
    'max_depth': 7,
    'n_estimators': 300,
    'subsample': 0.7

E. Model Evaluation

Model performance was assessed using a held-out test set. The evaluation metrics included:

1. Accuracy
2. Precision
3. Recall
4. F1-Score

These metrics were chosen to identify class imbalance and to measure the model's ability to generalize across all tumor categories. Confusion matrices and classification reports were also analyzed to identify misclassification trends and strengths of each model.

IV. Results and Discussions

The experimental results indicate that SVM achieved the highest overall performance, outperforming Random Forest and XGBoost across most metrics. SVM obtained an outstanding accuracy of 90%, precision of 90%, recall of 90%, and Macro F1-Score of 89%. This suggests that the RBF kernel effectively captured the nonlinear relationships present in the texture descriptors.

SVM Metrics

```
Accuracy SVM Tuned: 0.9000762776506483
Recall SVM Tuned: 0.8918046477850399
Precision SVM Tuned: 0.8983875869476236
F1 SVM Tuned: 0.8917303228517206
```

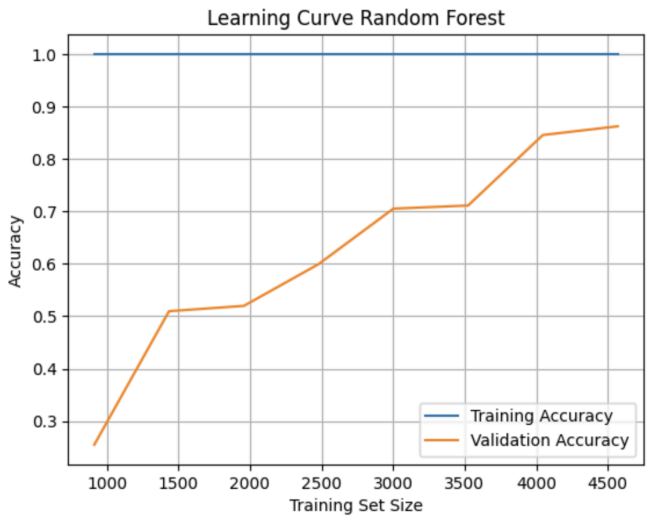
XGBoost Metrics

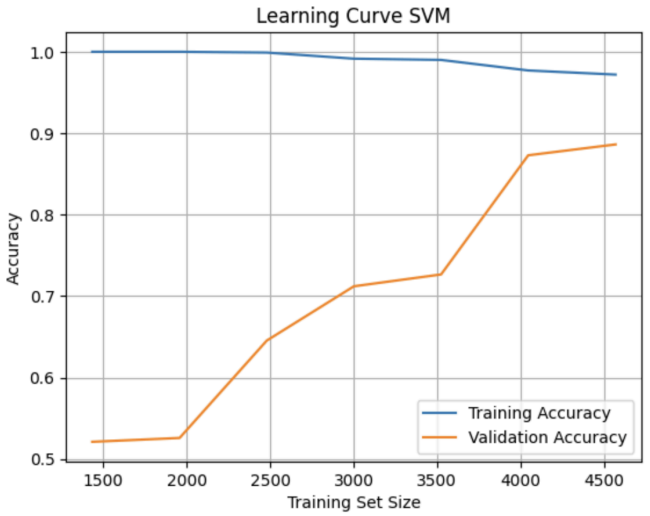
```
Accuracy XGBoost Tuned: 0.8977879481311976
Recall XGBoost Tuned: 0.889720406681191
Precision XGBoost Tuned: 0.8962506085036279
F1 XGBoost Tuned: 0.8891561881340004
```

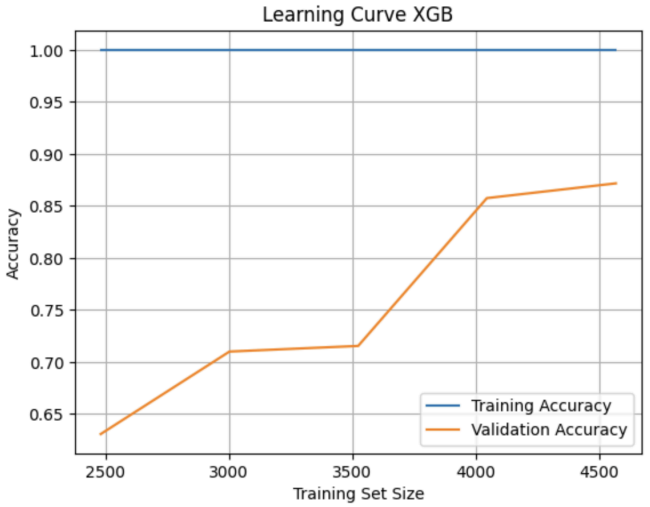
Random Forest Metrics

```
Accuracy Random Forest Tuned: 0.8863463005339436
Recall Random Forest Tuned: 0.8777342047930283
Precision Random Forest Tuned: 0.8831270836078489
F1 Random Forest Tuned: 0.8768868310870018
```

In contrast, Random Forest and XGBoost, while still performing very well, appeared less capable of modeling the fine-grained texture variations inherent in low-resolution MRI images. The confusion matrices revealed that misclassifications primarily occurred between structurally similar tumor types, such as glioma, and meningioma, consistent with observations from prior literature.







These graphs show the accuracy of the models.

These findings demonstrate that lightweight, feature-based models can remain competitive in environments with limited data and without reliance on deep learning architectures. The results highlight the importance of strong preprocessing and carefully engineered features in classical computer vision pipelines.

V. Conclusion

This project successfully developed a complete texture-based classification system for brain tumor MRI images through machine learning advancements. The combination of GLCM and LBP descriptors, when paired with effective preprocessing and feature scaling, produced strong discriminative performance. Among the evaluated models, SVM demonstrated superior classification capability, confirming its suitability for tasks requiring nonlinear boundary modeling.

Future improvements may include an expansion to the dataset, including multi-slice volumetric information, or experimenting with hybrid deep learning + hand crafted feature architectures to further enhance accuracy. Additional exploration into interpretability tools, such as saliency mapping or feature attribution techniques, may also support clinical applicability

Author's Contribution

All authors contributed to the project through data prep, preprocessing design, feature engineering, modeling, evaluation, and documentation. Collaborative effort ensured methodological success and reproducibility through the project cycle.

Availability Data and Materials

The Brain Tumor MRI dataset used in this study is publicly available on https://www.kaggle.com/datasets /masoudnickparvar/brain-tumor-mri-dataset.

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