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Diagnostic in Neuroimaging: A Comparative Study of Deep Learning and Traditional Approaches

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Abstract—In the realm of medical diagnostics, precise classifcation of brain tumors is pivotal. This study conducts a comprehensive comparative analysis of a Convolutional Neural Network (CNN) against traditional machine learning models, Logistic Regression (LR) and Support Vector Machines (SVM) on a dataset of MRI scans for multi-class brain tumor classifcation. The CNN, tailored for image recognition, is evaluated alongside LR and SVM, which have established benchmarks in classifcation tasks. The investigation reveals that the traditional models hold their ground in terms of precision and interpretability, with the SVM, in particular, achieving remarkable accuracy. However, the CNN distinguishes itself by demonstrating superior performance and high confdence in its predictions, highlighting the advantages of deep learning for complex pattern recognition in neuroimaging. These insights signify a substantial stride towards integrating advanced automated methods into diagnostic processes, promising enhanced accuracy and effcacy in healthcare diagnostics.

Index Terms—CNN, SVM, LR, Brain Tumor Classifcation, MRI, Machine Learning.

I. INTRODUCTION

Brain tumors present a formidable challenge in neurology, with their diagnosis and classifcation being critical for effective treatment planning. Advances in machine learning (ML) and deep learning (DL) have ushered in new frontiers in medical imaging, providing tools that could potentially surpass traditional methods in accuracy and efficiency [\[1\]](#page-6-0). Convolutional Neural Networks (CNNs), in particular, have gained attention for their ability to learn complex patterns in imaging data, thus showing great promise in the automatic detection and classifcation of tumor images [\[2\]](#page-6-1).

This study employs CNNs for the task of classifying MRI scans into various tumor categories and compares their performance to traditional ML models, Logistic Regression (LR) and Support Vector Machines (SVM). Both LR and SVM have been stalwarts in the domain of medical diagnostics due to their interpretability and statistical foundations [\[3\]](#page-6-2). However, their dependency on manual feature extraction is a limitation that CNNs aim to overcome with their hierarchical feature learning capabilities [\[4\]](#page-6-3).

Through this comparative analysis on a dataset of 3,264 brain MRI images, we explore the hypothesis that CNNs can achieve superior multi-class classifcation accuracy over LR and SVM. This study contributes to the ongoing discussion on the integration of ML and DL in enhancing diagnostic processes, with a focus on improving outcomes for patients with brain tumors [\[5\]](#page-6-4).

II. RELATED WORK

Recent advancements in neuroimaging have facilitated the development of machine learning algorithms capable of classifying brain tumors with signifcant accuracy. [\[6\]](#page-6-5) explored the efficacy of Convolutional Neural Networks (CNNs) in differentiating between malignant and benign tumors, illustrating promising results that pave the way for automated diagnostic systems [\[6\]](#page-6-5). Similarly, Smith and colleagues (2022) employed Support Vector Machines (SVM) to analyze MRI scans, achieving noteworthy precision, especially in cases of glioma and meningioma classifcation [\[7\]](#page-6-6).

Moreover, hybrid approaches combining traditional algorithms with deep learning techniques have shown improvement in generalization capabilities. For instance, Lee et al. (2023) integrated feature extraction methods with neural networks to enhance the interpretability and diagnostic power of their models [\[8\]](#page-6-7). These studies collectively underscore the potential of machine learning in revolutionizing brain tumor diagnostics, substantiating the research presented in this paper.

III. DATA DESCRIPTION

The dataset for this study is derived from anonymized brain MRI scans used to train models for diagnosing brain tumors. It comprises MRI scans categorized into various tumor types, along with scans identifed as having no tumors.

Attribute	Detail		
Total Instances	3,264 (2,870 Training, 394 Testing)		
Features per Instance	Image data, variable dimensions		
Missing Value	None		
Tumor Type	Glioma, Meningioma, No Tumor, Pituitary		
Image Types Represented	MRI scans		
Image Format	DICOM		

TABLE I: MRI Brain Tumor Dataset

The dataset is rigorously curated to ensure each scan is correctly annotated with its corresponding tumor type, facilitating precise training and validation of the diagnostic models. The images are stored in DICOM format, which is the standard for medical imaging and includes metadata essential for accurate diagnostics.

IV. METHODOLOGY

This study used a layered approach in model design and implementation, ensuring each model was optimized for the neuroimaging dataset. The following subsections detail the architecture and training processes for both the deep learning and traditional models.

A. Deep Learning: Convolutional Neural Network (CNN)

The CNN architecture was designed to handle threedimensional input data representing neuroimaging scans. The architecture is composed of several layers that transform the input image through a series of convolutional operations, non-linear activation functions, pooling operations, and fully connected layers, eventually leading to a classifcation output.

Input Layer:

• Input neuroimaging data is represented as $X \in$ $\mathbb{R}^{256 \times 256 \times 3}$, where 256x256 represents the spatial dimension and 3 represents the RGB color channels.

Convolutional Layers:

• The first convolutional layer applies 32 filters of size 3x3, resulting in feature maps which are then passed through a ReLU activation function defned as:

$$
O_1 = \text{ReLU}(X * F_1 + b_1)
$$

where $F_1 \in \mathbb{R}^{3 \times 3 \times 3 \times 32}$ and b_1 are the filters and bias terms respectively, and ∗ denotes the convolution operation.

• Each convolutional layer is followed by a 2x2 max pooling operation which reduces the spatial size by half. The operation can be represented as:

$$
P_k = \text{MaxPool}(O_k)
$$

Dense Layers

• Prior to the dense layers, the feature maps are fattened:

$$
F = \text{flatten}(P_{\text{last}})
$$

• A fully connected layer with 512 neurons applies a linear transformation followed by a ReLU activation:

$$
D_1 = \text{ReLU}(W_1 \cdot F + b_{\text{dense1}})
$$

• The fnal output layer uses a softmax activation function to derive the probabilities for the four classes:

$$
D_2 = \text{softmax}(W_2 \cdot D_1 + b_{\text{dense2}})
$$

where W_1 , W_2 , b_{dense1} , and b_{dense2} are the weights and biases for the dense layers.

Regularization

• Dropout is implemented as a regularization technique in between the dense layers to prevent overftting, described by:

$$
D_k' = \operatorname{Dropout}(D_k, p=0.5)
$$

Loss Function and Optimization

• The model uses Sparse Categorical Crossentropy as the loss function, essential for multi-class classifcation:

$$
L(y, \hat{y}) = -\sum_{i} y_i \log(\hat{y}_i)
$$

where y is the true label and \hat{y} is the predicted probability distribution across classes.

• Adam optimizer is employed for its adaptive learning rate capability, enhancing the convergence speed.

Visual Representation of CNN Architecture

Fig. 1: Initial CNN architecture with convolutional and max-pooling layers.

Fig. 2: Expanded CNN architecture including dense and dropout layers.

Figure 1 depicts the initial architecture, showcasing the convolutional layers (Conv) interspersed with max-pooling (MaxPool) operations. The depth of the bars corresponds to the number of flters, which increases with each subsequent convolutional layer, a design choice intended to capture more complex features in the latter stages of the network.

Figure 2 expands on this, including the fnal dense layers (Dense) and the dropout layers (Dropout) for regularization. The substantial width of the dense layer bars refects their greater number of neurons, emphasizing the transition from spatial feature extraction to classifcation. The dropout layers are visualized with reduced depth, symbolizing their role in selectively deactivating neurons to prevent overftting.

Fig. 3: Exploded view of the CNN showing the detailed layer structure.

Figure 3 provides an exploded view of the network, offering a clear visualization of each individual layer, color-coded to match Figures 1 and 2. This perspective aids in understanding the hierarchical nature of CNNs, where initial layers capture basic features like edges, and deeper layers synthesize these to detect more abstract concepts.

Fig. 4: Training and validation accuracy and loss curves for the CNN model.

The left plot illustrates the accuracy of the model during the training phase, with the blue line representing training accuracy and the orange line representing validation accuracy.

The right plot shows the model's loss over the training epochs, with the blue line indicating training loss and the orange line indicating validation loss. These plots are crucial for understanding the model's learning process and for ensuring that overftting is minimized.

As noted in Figure [4,](#page-3-0) the model's performance on the validation set closely tracks the performance on the training set, indicating good generalization. The minor fuctuations in the validation curves suggest that the model is learning new patterns from the data throughout the training process without overftting.

B. Traditional Models: Logistic Regression and Support Vector Machine (SVM)

Logistic Regression (Softmax Regression)

 $P(y^{(i)} = k|x^{(i)}; \theta)$ that a given feature vector $x^{(i)}$ belongs In addressing multi-class classifcation within our dataset, which consists of four distinct neuroimaging categories, we implement a Softmax Regression model. The probability to a class k is computed using the softmax function:

$$
P(y^{(i)} = k | x^{(i)}; \theta) = \frac{e^{\theta^{(k)T} x^{(i)}}}{\sum_{j=1}^{K} e^{\theta^{(j)T} x^{(i)}}}
$$

For the cost function $J(\theta)$, we use the categorical crossentropy loss and include a regularization term to reduce overftting:

$$
J(\theta) = -\frac{1}{m} \sum_{i=1}^{m} \sum_{k=1}^{K} 1\{y^{(i)} = k\} \log(h_{\theta}^{(k)}(x^{(i)})) + \frac{\lambda}{2m} \sum_{k=1}^{K} ||\theta^{(k)}||
$$

Here, K represents the total number of classes, m denotes the number of training instances, $1\{\}$ is the indicator function, Fig. 5: Distribution of image count across four tumor cate-
gories in the dataset. and λ signifies the regularization parameter.

Support Vector Machine (SVM)

For SVM classifcation in a multi-class setting, we adopt a One-vs-One (OvO) strategy as implemented by default in Scikit-learn's SVC method. In this strategy, a binary SVM classifer is trained for each pair of classes from the total K classes, resulting in $\frac{K(K-1)}{2}$ classifiers. Each classifier decides between two classes, and the fnal classifcation of new instances is determined by a majority voting system among all classifers.

The decision function for these classifers is defned as:

$$
f_{jk}(x) = sign(\sum_{i=1}^{n} y_i \alpha_i K(x, x_i) + b)
$$

where $K(x, x_i) = \exp(-\gamma ||x - x_i||^2)$ is the Radial Basis Function (RBF) kernel, enabling complex decision boundaries by mapping input features into higher-dimensional space. The parameters α_i are the dual coefficients, n is the number of support vectors, and b is the bias term.

Training

Our models are trained on a normalized dataset to ensure pixel value consistency, critical for maintaining uniformity in feature scaling. The model parameters are optimized to minimize respective cost functions through methods like grid search, coupled with cross-validation to determine the best parameter settings. The performance of our models is then evaluated using a comprehensive set of metrics including accuracy, precision, recall, and F1-score, which are essential for assessing the ability of the models to accurately identify each of the four neuroimaging categories.

V. EXPLORATORY DATA ANALYSIS

Exploratory Data Analysis (EDA) is a foundational step in our study to understand the distribution and characteristics of the neuroimaging data. Through visual and quantitative methods, we aim to identify patterns, spot anomalies, and test hypotheses which could inform subsequent stages of the analysis, particularly the design and training of our classifcation models.

A. Image Count per Category

Figure [5](#page-3-1) illustrates the distribution of images across four distinct tumor categories: no tumor, meningioma tumor, glioma tumor, and pituitary tumor. It is evident from the bar chart that our dataset is fairly balanced, which is benefcial for training classifcation models as it mitigates the risk of developing a bias toward a more represented class.

B. Sample Neuroimaging

Fig. 6: Sample MRI scans for glioma and meningioma tumor categories.

Figure [6](#page-4-0) displays representative MRI scans from the glioma and meningioma tumor categories. These images highlight the variability in tumor size, shape, and location, challenging the model to learn robust features that can generalize well across different cases.

Fig. 7: Variations in MRI scan presentations for glioma and meningioma tumors, showcasing diverse angles and crosssections.

In Figure [7,](#page-4-1) we delve deeper into the variations within the glioma and meningioma categories. The scans are presented in various angles and cross-sections, providing an in-depth view of the complexities involved in diagnosing and classifying these tumors.

The EDA phase of this study underscores the complexity and diversity of the neuroimaging data, setting the stage for the application of advanced machine learning techniques that are capable of capturing the intricate patterns necessary for accurate diagnosis.

VI. RESULTS

A. Convolutional Neural Network Evaluation

We evaluated the performance of our Convolutional Neural Network (CNN) on the two sets (Training and Testing).

1) Model Predictions and Confdence on Test Dataset: The CNN demonstrated high confdence in its predictions on the test dataset, as visualized in Figure [8.](#page-4-2)

Fig. 8: Predictions by the CNN on the test dataset, showing actual labels, predicted labels, and confdence percentages.

Each MRI scan from the test dataset was fed into the trained model, which then predicted the category along with a confdence score. The model's high accuracy and confdence levels often above 90% emphasize its capability to accurately classify neuroimaging data.

2) Quantitative Performance Metrics: The classifcation report for the test dataset is summarized in Table [II.](#page-4-3)

Class	Precision	Recall	F1-score
Glioma Tumor	0.91	0.95	0.93
Meningioma Tumor	0.93	0.91	0.92
No Tumor	0.95	1.00	0.98
Pituitary Tumor	0.99	0.94	0.96
Accuracy		0.94	
Macro Avg	0.95	0.95	0.95
Weighted Avg	0.95	0.94	0.94

TABLE II: Classifcation report.

The model attained high accuracy confirming the efficacy of the CNN architecture and training methodology employed in our study.

B. Traditional Machine Learning Models

The traditional machine learning models employed in our study, Support Vector Machine (SVM) and Logistic Regression, provide a benchmark against our deep learning approach.

These models are used for multiclass classifcation to identify four distinct tumor types in the neuroimaging dataset.

1) SVM Model Performance: The SVM model underwent rigorous training and subsequent evaluation to ascertain its classifcation effcacy across the extended range of tumor categories. Figure [9](#page-5-0) presents the confusion matrix for the SVM model, delineating the correct and incorrect predictions for each class.

Fig. 9: Confusion matrix for the SVM model, illustrating the distribution of predicted classes in comparison to the actual classes.

The SVM model displayed commendable precision and recall across all tumor types, achieving an overall accuracy of 86% on the test set. The model was particularly effective in distinguishing pituitary tumors with a precision and recall of 94% and 98%, respectively.

2) Logistic Regression Model Performance: In parallel, the Logistic Regression model was also evaluated for its multiclass classifcation performance. Figure [10](#page-5-1) showcases the corresponding confusion matrix.

Fig. 10: Confusion matrix for the Logistic Regression model, indicating predictive accuracy across classes.

The Logistic Regression model demonstrated a profciency akin to the SVM model, with overall accuracy reaching 79%. This model's precision and recall for pituitary tumors were notably high at 90% and 96%, respectively.

3) Quantitative Evaluation: The expanded quantitative evaluation for both models is captured in Table [III,](#page-5-2) which includes precision, recall, and F1-scores that refect the multiclass classifcation.

C. Discussion

This study's analysis reveals that traditional machine learning models like SVM and Logistic Regression are not only viable but also formidable contenders in medical image classifcation tasks. The SVM model, in particular, displayed notable precision and recall across various tumor types, indicating its robustness in a multiclass setting. The results affrm the value of these models in clinical scenarios, especially for initial screenings where speed and reliability are paramount.

The performance of the Logistic Regression model, while slightly less impressive than SVM, still demonstrates its relevance in the medical diagnostics feld. It offers a simpler, more interpretable alternative that retains a commendable level of accuracy, which is crucial for clinical decision-making.

Signifcantly, the CNN model stands out with its exceptional accuracy, reinforcing the transformative impact of deep learning in neuroimaging diagnostics. The CNN's ability to discern nuanced patterns within complex data positions it as an advanced tool that could potentially redefne diagnostic practices.

Our study's fndings advocate for a synergistic approach where traditional models can be deployed for their speed and interpretability, while deep learning models can be reserved for their higher accuracy and confdence levels. This combination could lead to more robust, accurate diagnostic processes, enabling better patient outcomes in neurology.

VII. CONCLUSION

The exploration into the classifcation capabilities of traditional models and a Convolutional Neural Network (CNN) for neuroimaging diagnostics has yielded illuminating results. The SVM and Logistic Regression models, with their commendable performance metrics, have proven to be robust and reliable for multiclass classifcation, particularly effective for identifying pituitary tumors. Meanwhile, the CNN has demonstrated superior accuracy, with a striking 94% on the test set, showcasing its advanced pattern recognition ability in image-based diagnostics. The integration of the CNN, alongside traditional models, could enhance the precision and reliability of brain tumor diagnostics. This study underscores the signifcant potential for combining the interpretability of traditional models with the advanced capabilities of CNNs in creating a comprehensive diagnostic framework.

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APPENDIX A

CODE

Link to code [:Diagnostic in Neuroimaging: A Comparative](https://amissana21.github.io/Diagnostic-in-Neuroimaging/Diagnostic%20in%20Neuroimaging_A%20Comparative%20Study%20of%20Deep%20Learning%20and%20Traditional%20Approaches%20(1)) [Study of Deep Learning and Traditional Approaches.](https://amissana21.github.io/Diagnostic-in-Neuroimaging/Diagnostic%20in%20Neuroimaging_A%20Comparative%20Study%20of%20Deep%20Learning%20and%20Traditional%20Approaches%20(1))