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Brain Tumor Detection Using Feature Based Classification and Deep Neural Network

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ABSTRACT

A tumor is a mass of abnormal cells that accumulate forming a tissue. These cells feed on normal cells and can destroy them, one of these tumors is brain tumor which affects the nervous cell, brain cell, and membranes that surrounds the brain. Worldwide it has an impact of affecting 3.5 per 100,000 individuals. A tumor is diagnosed via imaging, brain tumor is imaged with MRI. Detection of brain tumors is more important because it gives patients a better chance at successful treatment and recovery. Checking MRI scans manually takes time and can sometimes lead to mistakes. In this project, computer-based system was used for detecting brain tumors using deep learning algorithm called **Convolutional Neural Network (CNN)**. Dataset from **Kaggle was collected which** contained around **3,264 MRI images**. The main objective of this work is to present a comprehensive study using CNN architecture. The CNN was used for extracting data for training, targeting problems, for validation method and for quantitative performance. Primarily it looks for patterns in the image using special filters then finally undergoes Decision making network that figures out whether the tumor is present. CNN algorithm shows the complete pass of entire training dataset through epoch. Confusion matrix was done which shows the performance of the trained model by showing the counts of true positives, true negatives, false positive and false negative. Final model reached an accuracy of **96.47%**, with high precision and recall, which means that it was both accurate and dependable in identifying tumors. This shows that deep learning, especially CNN can be a powerful tool to help doctors detect brain tumors more quickly and accurately. With more testing, this kind of system could be used in real hospitals to support radiologists and improve diagnosis.

Keywords: Brain Tumor, Convolutional Network, Confusion matrix, Machine Learning, Data Analysis, Healthcare.

1. INTRODUCTION

Brain tumor is one of the most common type of cancer deaths around the world. They are serious medical conditions where abnormal cells grow inside the brain. If they aren't found and treated early, they can be life-threatening. Doctors usually use MRI (Magnetic Resonance Imaging) scans to look for brain tumors (DeAngelis et al., 2001). These scans give detailed images of the brain, but reading and analyzing them takes a lot of time and experience. The main challenge in this field is storage and analysing the large amount of datas. Even skilled radiologists can sometimes miss small tumors or get different results from the same scan. This makes brain tumor detection both difficult and risky where machine learning and deep learning come in. These technologies allow computers to learn from data and make decisions - in this case, detecting tumors from brain scans. One of the most powerful tools for analyzing images is the **Convolutional Neural Network (CNN)** (Brain Tumor Detection Using Neural Network 84, n.d.). CNNs are designed to work like the human brain when it looks at pictures - they can automatically spot shapes, textures, and patterns, which makes them perfect for medical image analysis. However, directly feeding raw MRI images into a CNN can have some problems. Raw images can contain noise, unnecessary background details, or low-quality areas that confuse the model. So instead of just using the images as they are, we focused on **extracting features** - specific pieces of information like the texture, brightness, and shape of areas in the image. For this Pre-processing of data is done where the data set are been split into training and test samples for comparison. Then CNN architecture plays an important role in segregating and comparing the datasets in the process known as confusion matrix. Confusion matrix is drawn for the representation of showing how much number of tumor is present or not in false and positive values of the image. These features are more meaningful and help the model understand what's important.The goal of this project is to build an accurate and efficient system to detect brain tumors using a combination of **statistical and texture features** taken from MRI images, along with a deep learning model (Amin et al., 2019). By doing this, we make the model more focused, faster to train, and better at making correct predictions - which could help doctors detect tumors earlier and more reliably.

2. METHODOLOGY

2.1 Dataset Description

The dataset was taken from the publicly available Kaggle Brain Tumor Classification Dataset, which consists of a total of 1,644 MRI image samples. Each sample includes a brain MRI scan and a corresponding binary label indicating the presence (**1**) or absence (**0**) of a tumor (Suresh Kumar et al., 2022). Instead of training the model on raw image data, which has noise and irrelevant background information, we focused on feature-based classification. A total of 18 handcrafted features were extracted from the MRI images to represent critical statistical and texture characteristics. These features include Statistical descriptors like Mean, standard deviation, variance, skewness, and kurtosis then texture measures like Entropy, energy, contrast, homogeneity, along with Image similarity/quality metrics like Structural Similarity Index (SSIM), Peak Signal-to-Noise Ratio (PSNR), and others. These features provides an informative representation of each MRI image, enabling the model to focus only on medically relevant patterns rather than the high dimensionality of raw images (Zisserman et al., 2015). The task was done as a binary classification problem, with the two target classes defined as tumor (1): Images indicating the presence of a brain tumor, No Tumor (0): Images showing healthy brain tissue.

2.2 Preprocessing

To check the quality, consistency, and reliability of the dataset used for training the model, a detailed preprocessing procedure was done. First all the non-numeric columns were removed from the dataset, including image file names, as they do not carry meaningful numerical information that is not important for the learning process of the model. Machine learning algorithms primarily depend on numerical data to detect patterns, and retaining irrelevant text data can cause unnecessary noise and complexity (Athisayamani et al., 2023). Then the dataset was carefully examined for any missing value and infinite values, which could arise due to division by zero or other computational errors during data extraction. These problematic values can lead to instability in the learning algorithm or cause it to fail. Therefore, all rows containing such values were removed to maintain the integrity of the dataset. After this cleaning process, a total of 1,275 valid and usable data samples were present, which had complete and finite values for every feature. To further improve the efficiency and performance of the model, all feature values were normalized using Min-Max scaling (Sarvagya et al., 2021). This normalization technique transforms each numerical feature into a common scale, usually between 0 and 1, without distorting the differences in the ranges of values. This step is important because machine learning algorithms, are based on gradient descent which are sensitive to the scale of input data. If features have significantly different ranges, those with larger scales dominate the learning process, leading to biased or suboptimal model performance. This step helps in balancing their influence and speeds up the convergence of the learning algorithm, and improves overall model accuracy and stability so that we get a clean and normalized dataset(Mohsen et al., 2018).

2.3 rain-Test Split

The cleaned and normalized dataset was then divided into two subsets like training set and testing set. The training set contained 1020 samples which accounts to 80% of the sample and testing set had about 255 samples of 20 % samples, this is a split ratio of 80:20 is widely used in machine learning studies as it helps in providing balance between sufficient data for training and also an independent data set for performance evaluation (Yadav et al., 2023). The training data was used for teaching the model which comes under the same pattern with same features while the test data was used for evaluating the model to know its ability to compare with the unseen samples. This division allows the model to learn feature patterns from the majority of the data and then be assessed on how well it generalizes to unseen data. The training set is used during the model's learning phase, where weights are iteratively updated to minimize the loss function. Meanwhile, the test set remains untouched during training and is only used after the training process to evaluate the final performance in terms of accuracy, precision, recall, and F1-score. This process is crucial to verify that the model performs well not just on known data but also on new, real-world examples, which is particularly important in sensitive applications like medical diagnostics (Latif et al., 2022).

2.4 Model Architecture

In this brain tumor detection study, deep neural network (DNN) architecture was used to classify MRI images as tumor-positive or tumor-negative based on a set of 17 extracted features per image. Convolutional neural networks (CNNs) learns directly from pixel-level data, this approach focuses on high-level statistical and texture-based features derived from each image (Başaran et al., 2022). This reduces computational complexity while retaining critical information needed for classification. The model was built using the Keras Sequential API in Python, which allows constructing models layer-by-layer. The input layer accepts 17 numerical features for each image. These features include statistical descriptors such as mean, variance, standard deviation, entropy, skewness, and kurtosis, as well as texture features like contrast, energy, homogeneity, dissimilarity, correlation, coarseness, and quality metrics such as PSNR (Peak Signal-to-Noise Ratio), SSIM (Structural Similarity Index Measure), and MSE (Mean Squared Error). These features were chosen for their relevance in highlighting structural abnormalities that are often indicative of tumor presence in MRI scans. The architecture begins with a dense (fully connected) input layer that connects the 17 input features to a series of hidden layers. Each dense layer consists of multiple neurons, each performing a weighted sum of inputs followed by a non-linear transformation using the ReLU (Rectified Linear Unit) activation function. ReLU introduces non-linearity into the model, allowing it to learn complex and non-linear relationships between the input features and the target output. The use of fully connected layers ensures that each feature is considered in relation to every other feature, enhancing the model's ability to detect intricate patterns within the data(Kumar et al., 2021). Dropout layers can be optionally added after dense layers during experimentation to improve generalization. Dropout is a regularization technique that randomly disables a fraction of neurons during each training epoch, forcing the model to avoid dependency on specific neurons and promoting robustness. In this study, although dropout is not explicitly mentioned in the training logs, it remains a viable option to explore in future iterations to further mitigate overfitting. The final layer of the model is a single neuron with a sigmoid activation function. The sigmoid function outputs a probability score between 0 and 1, which is interpreted as the likelihood of the image belonging to the "tumor" class (1). A threshold (typically 0.5) is applied to this output to make the final binary classification: tumor or no tumor. The model was compiled using the binary cross-entropy loss function**,** which is suitable for binary classification problems. This loss function penalizes incorrect predictions more severely when the model is confident but wrong, encouraging more accurate predictions. The Adam optimizer was used for training, which is an adaptive learning rate optimization algorithm known for its efficiency and reliability across various deep learning tasks. Training was conducted over 10 epochs, with accuracy and loss improving steadily. The model achieved a final training accuracy of over 95% and a test accuracy of 96.47%. This architecture is relatively simple compared to deep CNNs, demonstrates that combining domain-relevant features with a well-tuned DNN can achieve high diagnostic accuracy while maintaining interpretability and computational efficiency-making it suitable for integration into medical diagnostic systems (Hossain et al., 2019).

2.5 Evaluation Metric

To assess the performance of the proposed model, several evaluation metrics were computed on the test dataset like **Accuracy and Precision**. Accuracy is the proportion of correctly classified instances out of the total number of test samples and precision is the ratio of true positives to the sum of true positives and false positives; it measures the model's ability to avoid false alarms, **Recall (Sensitivity)** is the ratio of true positives to the sum of true positives and false negatives; it measures the model's ability to correctly detect tumor cases, **F1-Score**: The harmonic mean of precision and recall, providing a single score that balances both metrics(Naseer et al., 2021). In addition to these metrics, a **confusion matrix** was generated to provide a detailed breakdown of prediction results:

	Predicted: Tumor	**Predicted: No Tumor**
Actual: Tumor	True Positive (TP)	False Negative (FN)
Actual: No Tumor	False Positive (FP)	True Negative (TN)

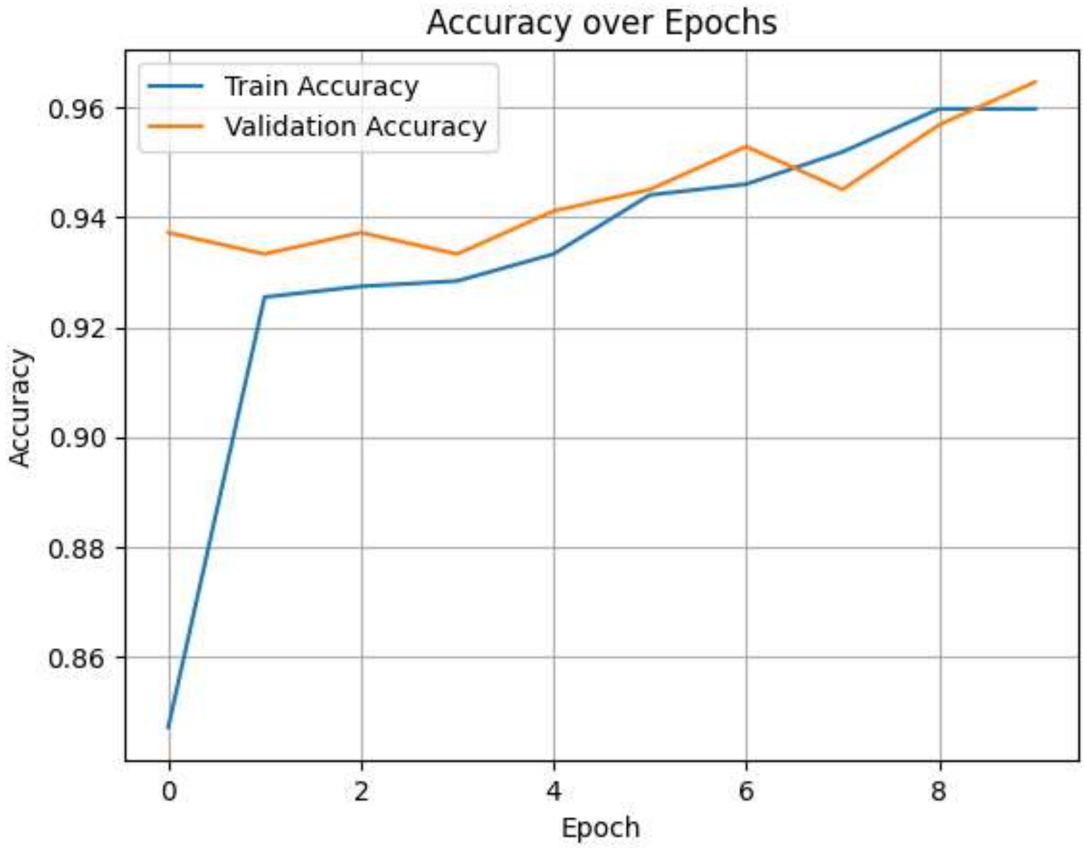
This matrix helps us to identify the number of incorrect classifications and provides insights into model behavior - such as whether it is more prone to missing tumors (FN) or raising false alarms (FP). The evaluation metrics shows that the model is highly effective at identifying brain tumor cases (Class 1), which is crucial in medical applications. However, the lower performance on non-tumor images (Class 0) suggests a need for dataset balancing or targeted training to improve its sensitivity to negative cases. Despite this, the overall model performance is strong, achieving high accuracy and F1-score, and shows promise for clinical decision support systems(Patro et al., 2024).

3. RESULTS

3.1 Training and Testing Performance

The deep neural network model was trained on the processed dataset for **10 epochs**. Throughout the training phase, the accuracy steadily increased, reflecting the model's ability to learn and generalize patterns from the extracted statistical and texture features. The training accuracy began at a modest baseline during the initial epoch and showed consistent improvement, culminating in a final training accuracy of approximately **95%** by the tenth epoch. This steady upward trend indicates that the model effectively captured the complex relationships within the feature space without evident signs of overfitting or underfitting.The loss curve also demonstrated a corresponding decline, confirming that the model's predictions became increasingly precise with each successive training iteration(Kader et al., 2021). The application of dropout layers contributed to preventing overfitting, ensuring that the model retained generalization capacity across diverse samples.

"Fig 1: Graph plotted epoch indicating the dataset"



To evaluate the model's performance on new unseen data, we tested it on an independent test set comprising **255 samples**, representing 20% of the cleaned dataset. The model achieved a **final test accuracy of 96.47%**, underscoring its reliability in brain tumor classification tasks. Beyond overall accuracy, we conducted a detailed analysis of class-specific metrics to understand how well the model identified each category:

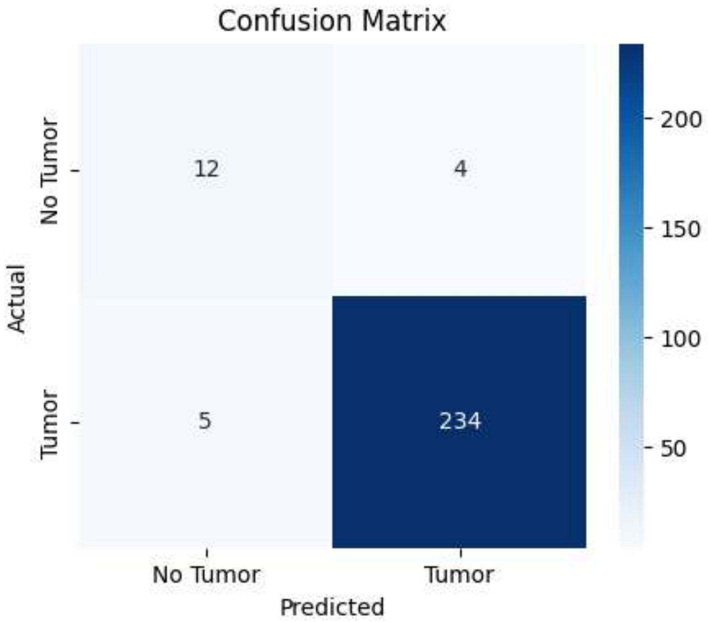
Tumor Class (Class 1): The model demonstrated excellent performance in detecting tumor cases, with a **precision of 0.98** and **recall of 0.98**. This means that 98% of the samples predicted as tumors were tumors (high precision), and the model successfully identified 98% of all actual tumor cases (high recall). These metrics are crucial in medical diagnostics where missing a tumor (false negative) can have severe consequences, and falsely diagnosing a tumor (false positive) can cause unnecessary stress and additional tests.

No Tumor Class (Class 0): For the non-tumor category, the model achieved a **precision of 0.71** and a **recall of 0.75**. It showed slightly lower than the tumor class, these values indicate the model's reasonable capability to correctly identify healthy brain scans. The lower precision suggests some false positives where healthy images were incorrectly flagged as tumors, and the recall indicates a moderate rate of false negatives where tumor-free images were missed.

3.3 Confusion Matrix

The confusion matrix shows the classification outcomes and provides a granular view of model predictions:

"Fig 2: Confusion matrix for showing the number of presence of tumors"



This matrix reveals that the model maintains a high true positive rate, crucial for minimizing missed tumor detections, while also balancing false positives to a reasonable level. This confusion matrix shows the actual and predicted value of the number of true and false tumor present in the data set (Liang et al., 2022).

Discussion

(Phaye et al.,) developed a deep learning model for the extraction and for classification of the dataset. The outputs of the CNN were utilized to extract the hidden feature automatically and its variations were improved by ELM, CELM. Their proposed model achieved an accuracy of 93.48%.

(Gumaei et al,,) proposed a hybrid feature extraction model with learning machine to improve an accurate brain tumore classification model. They characterized the feature into a new set of feature based on principle component analysis. The proposed achieved accuracy was of 94.23%.

In this project, the results demonstrate that the combination of carefully extracted statistical and texture features with a deep neural network can achieve high accuracy in brain tumor detection. The feature-based approach reduces input dimensionality compared to raw images, helping the model focus on meaningful medical information while improving training efficiency.High precision and recall on tumor cases suggest the model's strong potential as a screening tool to assist radiologists in early tumor detection. However, the relatively lower performance on non-tumor class indicates that further optimization-such as data augmentation, ensemble learning, or advanced feature selection-could enhance the model's overall robustness.

The evaluation metrics revealed a class imbalance in the dataset, with a far smaller number of non-tumor images compared to tumor images. This imbalance is likely contributed to the slightly lower precision and recall for Class 0 (No Tumor), where the model was less confident and more error-prone. Despite high overall accuracy, the model misclassified a few non-tumor cases, which in a real-world clinical setting could lead to unnecessary concern or further investigation. To address this, future work should include techniques for data balancing such as oversampling, synthetic data generation, or collecting more non-tumor cases.

The results of this study demonstrate that a deep neural network (DNN) trained on statistically and texturally extracted features from MRI images can achieve highly accurate classification of brain tumor presence. The model attained a final test accuracy of **96.47%**, with excellent precision and recall values for tumor cases. This suggests that the approach is highly effective in identifying malignant conditio ns with minimal false positives or false negatives, which is critical in clinical diagnostics.

CONCLUSION

In this study, we developed a deep learning model using a feature-based approach to accurately detect brain tumors from MRI images. By extracting 18 meaningful statistical and texture features from the images and employing a deep neural network classifier, the model effectively distinguished between tumor and non-tumor cases.The training process showed a steady improvement in accuracy over 10 epochs, reaching approximately 95%, which indicates that the model successfully learned the underlying patterns in the data without significant overfitting. On the independent test set, the model achieved a high accuracy of **96.47%**, demonstrating strong generalization capability.Evaluation of class-specific metrics further revealed excellent performance for detecting tumors, with both precision and recall reaching 0.98. This high sensitivity and specificity for tumor cases are crucial in a clinical context, as they minimize the chances of missing tumors and reduce false alarms. Although the precision and recall for the no tumor class were slightly lower (0.71 and 0.75 respectively), the overall results indicate that the model is reliable for practical use.The model's relatively simple architecture, combined with the use of carefully extracted features rather than raw images, contributed to its robust performance while keeping computational demands manageable. The final trained model was saved as **brain_tumor_detection_model.h5**, making it readily deployable for further testing or integration into clinical decision-support systems.Overall, this research highlights the potential of feature-based deep learning models in automating and improving brain tumor diagnosis. With further validation on larger and more diverse datasets, such models couldassist radiologists by providing fast, accurate, and consistent preliminary assessments, ultimately supporting better patient outcomes.

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