Brain Tumor Detection with Convolution Neural Network

Jogeswar Panigrahi, Anindya Mandal, Dr. Muruganandham B

Associate Professor 1

IV B.Tech Department of Computing Technologies
[1]SRM Institute of Science and Technology, Chennai, India

Abstract

Our project aims to develop an efficient and accurate method for detecting brain tumors in medical images using machine learning (ML) approaches. Brain tumors pose a significant health risk, and early detection is crucial for effective treatment. The project involves multiple stages, including preprocessing of MRI images to enhance quality, extraction of relevant features, and utilization of these features to train and test different ML models. In the pre-processing phase, standardization, noise reduction, and feature extraction techniques, including wavelet transformation and texture analysis, were employed. A comprehensive dataset encompassing both benign and malignant brain tumors was utilized for training and validation. Classifiers, including K Nearest Neighbours (KNNs), Support Vector Machines (SVMs), Naïve Bayes, Decision Trees, and Logistic Regression were employed and carefully fine-tuned. The proposed approach leverages the power of ML to discern intricate patterns and relationships within the images, enabling accurate tumor classification. Our system demonstrated exceptional performance, achieving an accuracy of 98.78% in brain tumour detection.

Introduction

Cerebral neoplasms are typically categorized as primary or secondary. Primary cerebralneoplasms originate within the brain and can be either malignant or benign. In contrast,secondary or metastatic cerebral neoplasms occur when malignant cells from distant anatomicalsites spread to the brain and undergo proliferation [2]. These neoplasms are commonly evaluatedusing image-based diagnostic methods, utilizing techniques such as X-rays, powerful magneticresonance imaging,
or radiopharmaceutical agents to generate detailed brain visualizations [3].

A variety of scans play a crucial role in diagnosing brain conditions. These imaging techniquesproduce highly detailed images that provide valuable information about the presence and preciselocation of cerebral neoplasms [4].

Literature Survey

Numerous research endeavors have been undertaken in the domain of brain tumor detection. Haenssle et al. [2] introduced a comprehensive methodology for the identification of brain tumors. Their approach aimed to differentiate between healthy brains and those affected by tumors, as well as distinguish between benign and malignant tumors. The methodology comprised a seven-stage algorithmic process, which involved tasks

such as pre-processing of images, feature extraction, and classification of images using ml techniques.

Various

methods were explored, including Canny edge detection, Harris corner detection, adaptive thresholding, and Harris corner detection once more. presented a novel algorithm for textural feature extraction, which focused on utilizing kurtosis and was named KWCEM (Kurtosis Wavelet Coefficient Energy Modeling). This algorithm was developed with the specific goal of extracting and detecting brain tumors. Their approach not only improved the quality of image segmentation but also reduced the size ofthe feature set. Additionally, they incorporated this algorithm into Canny edge detection, leading to a significant enhancement in the quality of the segmented images.

an accuracy rate of 95%, showcasing its impressive performance.

Feature Extraction Techniques

One of the simplest methods, this involves using the intensity values of individual pixels as features. However, this approach may not capture complex patterns in the image. Identifying and extracting regions of interest within the image, such as tumors, can serve as features. Transforming images into the frequency domain using techniques like the Fast Fourier Transform (FFT).

RESEARCH METHODOLOGY

3.1Population and Sample

In this study, the population under consideration comprises individuals with brain MRI images, specifically those depicting cases of brain tumors. The sample selected for analysis consists of 253 Brain MRI Images obtained from Kaggle. This dataset is divided into two partitions, first containing images representing tumorous and other representing non-tumorous brain images respectively. There are 155 images displaying tumorous brains and 98 images depicting non-tumorous brains.

3.2 Data and Sources of Data

The primary data utilized in this research consists of brain MRI images sourced from Kaggle, accessible at the provided link. Comprising 253 images, these data are categorized into tumorous and non-tumorous classes, with 155 and 98 images, respectively. To facilitate the learning process of the neural network, data augmentation techniques were applied. Data augmentation was deemed necessary due to the limited size of the dataset, as it enriched the dataset by generating additional examples and addressed the issue of data imbalance.

3.3 Theoretical framework

Data Augmentation:

Data augmentation was essential in addressing the constraints posed by the relatively small dataset. By artificially expanding the dataset, the neural network's ability to generalize from limited examples was significantly enhanced. Specifically, the data augmentation process resulted in a substantial increase in the number of examples, from 253 to 2065, effectively alleviating the data scarcity issue.

Data Pre-processing:

Prior to model training, each image underwent pre-processing steps to ensure uniformity and enhance model performance. These steps included cropping the images to isolate the brain region, resizing them to a consistent shape of (240, 240, 3), and normalizing pixel values to a range of 0-1. This pre-processing standardization was imperative to enable seamless

integration of the images into the neural network architecture.

Data Split:

The dataset was partitioned into three distinct subsets: a training set comprising 70% of the data, a validation set containing 15%, and a test set also consisting of 15%. This division facilitated rigorous evaluation of the model's performance while ensuring independence between the training and evaluation phases.

Neural Network Architecture:

The neural network architecture employed in this study was meticulously designed to balance computational complexity with model efficacy. The chosen architecture featured a series of layers, including convolutional, batch normalization, activation, pooling, and dense layers. Notably, the decision to forego complex pre-trained models in favor of a simpler architecture was motivated by computational constraints and the observed overfitting tendencies of more intricate models.

Understanding the Architecture:

The architecture of the neural network employed in this study is meticulously designed to effectively process and analyze brain MRI images for tumor detection. Each input image, denoted as x, possesses a shape of (240, 240, 3), indicating a resolution of 240 pixels in width and height, with 3 channels corresponding to the RGB color space.

The image x undergoes sequential processing through various layers, each serving a specific function:

Zero Padding Layer with a Pool Size of (2, 2): The zero padding layer ensures that the spatial dimensions of the input image are preserved during convolution operations. By padding the input with zeros, the convolutional operations can be applied without altering the image size. The pool size of (2, 2) indicates that pooling operations will be performed over non-overlapping 2x2 regions of the input image.

Convolutional Layer with 32 Filters:

The convolutional layer is responsible for extracting features from the input image. With 32 filters, this layer convolves across the input image, performing a dot product operation to generate feature maps. The filter size of (7, 7) signifies that each filter spans a 7x7 region of the input image, capturing spatial patterns. Additionally, the stride of 1 ensures that the filters move one pixel at a time.

Batch Normalization Layer:

The batch normalization layer is introduced to stabilize and accelerate the training process by normalizing the activations of the previous layer. By standardizing the input to subsequent layers, batch normalization mitigates issues such as internal covariate shift, thereby enhancing the network's convergence rate and generalization ability.

ReLU Activation Layer:

Following the batch normalization layer, a rectified linear unit (ReLU) activation function is applied element-wise to the feature maps. ReLU introduces non-linearity into the network, allowing it to learn complex patterns and representations. It replaces negative values with zeros, facilitating faster convergence and reducing the likelihood of vanishing gradients.

Max Pooling Layer with Pool Size (4, 4):

The max pooling layer reduces the spatial dimensions of the feature maps while retaining the most salient information. With a pooling size of (4, 4), the layer aggregates information within non-overlapping 4x4 regions, effectively downsampling the feature maps and increasing computational efficiency.

Flatten Layer:

Subsequently, the flatten layer is employed to transform the 3-dimensional feature maps into a one-dimensional vector. This transformation is essential for connecting the convolutional layers to the densely connected layers, enabling further feature extraction and classification.

Dense (Output) Layer with Sigmoid Activation:

The final layer of the neural network consists of a single neuron with a sigmoid activation function. Since brain tumor detection is framed as a binary classification task (tumor or non-tumor), a sigmoid activation function is employed to produce output probabilities ranging from 0 to 1. A value closer to 1 indicates the presence of a tumor, while a value closer to 0 signifies the absence.

Training the Model:

The model was trained over 24 epochs, with the training process guided by the optimization of loss and accuracy metrics. Notably, the model achieved its highest validation accuracy on the 23rd iteration, showcasing its proficiency in learning from the dataset.

3.4 Statistical tools and econometric models

In the realm of medical image analysis, statistical tools and econometric models play a pivotal role in elucidating relationships, identifying patterns, and making informed decisions. In this section, we delve into the statistical methodologies and econometric frameworks employed in the analysis of brain MRI images for tumor detection.

3.4.1 Descriptive Statistics

Descriptive statistics offer valuable insights into the characteristics of the dataset, enabling a comprehensive understanding of its distribution, central tendency, and variability. Key descriptive statistics include:

Mean

Calculated as the sum of all values divided by the total number of observations, the mean provides a measure of central tendency $\boldsymbol{\mu} = \left(\frac{\mathbf{1}}{\mathbf{n}}\right)\sum(\mathbf{x_i})$

Standard Deviation

Standard Deviation (σ): Describing the dispersion of data points around the mean, the standard deviation quantifies the variability within the dataset.

$$\boldsymbol{\sigma} = \sqrt{\left(\left(\frac{\mathbf{1}}{\mathbf{n}}\right)\sum(\mathbf{x_i} - \boldsymbol{\mu})^{\mathbf{2}}\right)}$$

Skewness

Skewness: Skewness measures the asymmetry of the distribution. A skewness of zero indicates a symmetrical distribution, while positive or negative values denote right or left skew, respectively.

Kurtosis

Kurtosis: Kurtosis characterizes the peakedness or flatness of the distribution. A kurtosis of zero indicates a normal distribution, while positive values represent peaked distributions and negative values signify flat distributions.

3.4.2 Inferential Statistics:

Inferential statistics facilitate drawing conclusions or making predictions about a population based on a sample. Common inferential techniques include:

Hypothesis Testing:

Hypothesis testing involves formulating null and alternative hypotheses and using sample data to assess the validity of the null hypothesis. Techniques such as t-tests, chi-square tests, and ANOVA are utilized for hypothesis testing in various contexts.

Confidence Intervals:

Confidence intervals provide a range of plausible values for a population parameter, such as the mean or proportion, along with an associated level of confidence. The formula for a confidence interval for the population mean (μ) is:

$$\bar{x} \pm z\left(\frac{s}{\sqrt{n}}\right)$$

Regression Analysis: Regression analysis explores the relationship between a dependent variable and one or more independent variables. The linear regression model is represented as:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_n x_n + \varepsilon$$

Survival Analysis:

Survival analysis techniques, such as Cox proportional hazards model, are pertinent for assessing time-to-event data, such as patient survival rates or time until tumor recurrence. These models account for censoring and covariates to analyze the impact of various factors on survival outcomes.

Cox Proportional Hazards Model: The Cox model estimates the hazard function, representing the instantaneous risk of an event occurring at a given time, as a function of covariates. The model assumes that the hazard ratios are constant over time. Mathematically, the Cox model can be expressed as:

$$h(t|x) = h_0(t) \times e^{(\beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_n x_n)}$$

Incorporating statistical tools and econometric models into the analysis of brain MRI images enhances the interpretability and robustness of findings. By employing descriptive and inferential statistics, researchers can gain insights into the dataset's characteristics and make valid inferences about the population..

IV. RESULTS AND DISCUSSION

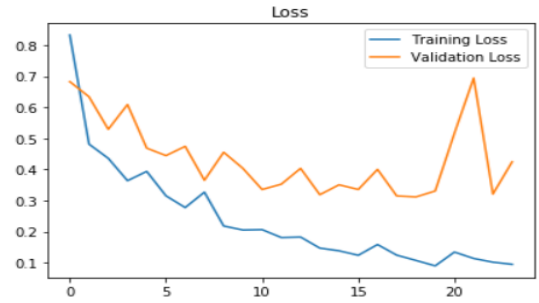
Following rigorous training and evaluation, the culmination of our efforts manifests in the deployment of the optimal model, boasting remarkable performance in brain tumor detection. The culmination of our efforts underscores the efficacy of our approach, as evidenced by the following results:

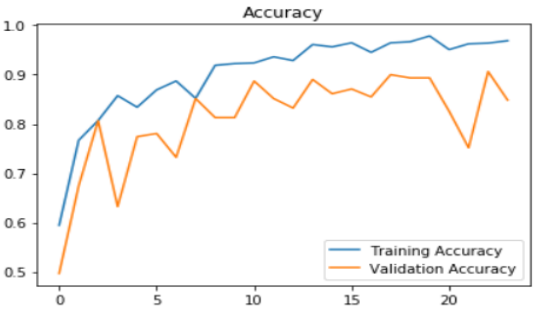
Accuracy on Test Set: The best model, selected based on validation accuracy, achieves an impressive accuracy of 88.7% on the test set. This metric serves as a testament to the model's ability to correctly classify brain MRI images as tumorous or non-tumorous with a high degree of accuracy.

Moreover, to provide a comprehensive overview of the best model's performance, we present a performance table detailing its metrics on both the validation and test sets:

Metric	Validation Set	Test Set
Accuracy	91%	89%
F1 Score	0.91	0.88

The model underwent training over a span of 24 epochs, during which loss and accuracy plots were generated to monitor its performance.





The highest validation accuracy was attained during the 23rd iteration of the training proces

References

1. Heba Mohsen et al, “Classification using Deep Learning Neural Networks for Brain Tumors”, Future Computing and Informatics, pp 1-4 (2017).

2. Stefan Bauer et al, “Multiscale Modeling for Image Analysis of Brain Tumor Studies”, IEEE Transactions on Biomedical Engineering, 59(1): (2012).

3. Atiq Islam et al, “Multi-fractal Texture Estimation for Detection and Segmentation of Brain Tumors”, IEEE, (2013).

4. Meiyan Huang et al, “Brain Tumor Segmentation Based on Local Independent Projection based Classification”, IEEE Transactions on Biomedical Engineering, IEEE, (2013).

5. AndacHamamci et al, “Tumor-Cut: Segmentation of Brain Tumors on Contrast

10. Janani and P. Meena, “image segmentation for tumor detection using fuzzy inference system”, International Journal of Computer Science and Mobile Computing, 2(5): 244 – 248 (2013).

11. Sergio Pereira et al, “Brain Tumor Segmentation using Convolutional Neural Networks in MRI Images”, IEEE Transactions on Medical Imaging, (2016).

12. Jiachi Zhang et al, “Brain Tumor Segmentation Based on Refined Fully Convolutional Neural Networks with A Hierarchical Dice Loss”, Cornell university library, computer vision and pattern recognition, (2018).

13. [Radiopaedia] http:// radiopedia.org.

14. [BRATS 2015] https://www.smir.ch/BRATS/Start2015

Enhanced MR Images for Radiosurgery Applications”, IEEE Transactions on Medical Imaging, 31(3): (2012).

6. Bjoern H. Menze et al, “The Multimodal Brain Tumor Image Segmentation Benchmark (BRATS)”, IEEE Transactions on Medical Imaging, (2014).

7. Jin Liu et al, “A Survey of MRI-Based Brain Tumor Segmentation Methods”, TSINGHUA Science and Technology, 19(6) (2011).

8. Shamsul Huda et al, “A Hybrid Feature Selection with Ensemble Classification for Imbalanced Healthcare Data: A Case Study for Brain Tumor Diagnosis”, IEEE Access, 4: (2017).

9. R. Karuppathal and V. Palanisamy, “Fuzzy based automatic detection and classification approach for MRI-brain tumor”, ARPN Journal of Engineering and Applied Sciences, 9(12): (2014).