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Brain tumor prediction and analysis based on simple CNN

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Abstract. The field of brain tumor prediction aims to detect potentially malignant tumors before overt symptoms appear. Early tumor detection can help tailor treatment pathways. To this end, this paper introduces a convolutional neural network (CNN) to construct a simple CNN analysis model. Subtle architectural changes to typical CNN designs are aimed at navigating and solving complex problems unique to medical imaging. Specifically, first, a preprocessing stage converts raw Magnetic Resonance Imaging (MRI) scans into analyzable data. This enables the model to delve into complex patterns in each image. Second, build a simple CNN model and evaluate it. Additionally, comparisons are made with established benchmarks set by traditional CNN architectures. The study further utilizes many available annotated datasets to develop a data augmentation paradigm that improves model resilience and generalizability. At the same time, the study deploys rigorous protocols to address and contain the ubiquitous overfitting threat, thereby enhancing the general applicability of the solution across a variety of healthcare settings. Empirical evaluations shed light on the significant superiority of the proposed simple CNN, especially in specific imaging environments and data structures. At the heart of this research is not only to expand technological horizons but also to reimagine clinical diagnostics to improve the standard of patient care.

Keywords: Brain Tumor Prediction, Convolutional Neural Network, Simple CNN, MRI Scans.

1. Introduction

The realm of tumor prediction underscores the importance of early detection and intervention. With the transformative potential of machine learning, particularly the The medical field is experiencing a transformative shift in diagnostics due to the Convolutional Neural Network (CNN), an artificial neural network specifically designed for video and image data [1]. Grounded in CNNs' ability to emulate intricate patterns akin to animal visual cortices, and bolstered by the surge in digital health data [2], their significance in tumor prediction has skyrocketed. CNNs process input images, extract features, and classify output images after learning [3]. They dominate AI medical image analyses, diagnosing diseases ranging from breast cancer to Alzheimer’s and brain tumors [4][5]. Leveraging such advanced technology, the medical domain is on the brink of unmatched precision in early tumor detection, offering not only better prognoses but also personalized treatment paths.

Medical images play a pivotal role in patient follow-up, ensuring successful therapy and forming a cornerstone of diagnosis and treatment processes [6]. Most medical experts, particularly radiologists, analyze these images. However, their evaluations can be affected by personal biases, differing opinions among colleagues, exhaustion, and time constraints. This often results in missed findings, delays, and a lack of quantification [7]. Though radiologists' expertise is unparalleled, their training is timeconsuming and expensive, leading some healthcare systems to consider cost-effective outsourcing. Amid these constraints, and with concerns of delayed or incorrect diagnoses, there's a pressing need for a more efficient, technology-driven approach. Integrating advanced solutions like CNNs might offer a proactive and streamlined diagnostic process, potentially setting a new benchmark in patient care.

Tracing the trajectory of image analysis reveals a rich tapestry of innovations, commencing with groundbreaking works like the recognition [8] and subsequently, the pioneering LeNet architecture [9]. Yet, the real turning point, the moment that redefined the contours of the domain, was the unveiling of advanced CNN frameworks, a prime example being the model introduced by Krizhevsky et al. in 2012 [10]. Krizhevsky and his team pioneered key principles that are foundational in today's CNNs, encompassing the incorporation of Rectified Linear Unit (RELU) functions, data augmentation, and dropout techniques. Delving into the annals of medical image analysis, the 1970s marked the dawn of the symbolic AI paradigm, spurring the genesis of rule-infused expert systems, with Shortliffe's MYCIN system [11] being a notable early foray. As the AI landscape matured, heuristic-based strategies gave way to manual feature extraction, which gradually transitioned to supervised learning. The crescendo in the discourse surrounding CNNs in the period from 2015 to 2017 further solidified their position in the vanguard of medical image analysis [12].

The main objective of this research is to provide insight into the adaptation and performance of CNNs in the complex field of medical imaging. First, a preprocessing model is utilized to carefully fine-tune the model for different imaging techniques to ensure that a large amount of data extracted from these methods can be used for CNN-based discriminative inspection. Based on this, a Simple CNN model is proposed. Subtle architectural changes to typical CNN designs seek to navigate and solve the intricacies unique to medical imaging. Naturally, the Simple CNN model is evaluated exhaustively and compared to the established benchmarks set by the conventional CNN structure. The study further utilizes many available annotated datasets to develop data enhancement paradigms, thereby increasing the resilience and generality of the model. At the same time, the research deploys rigorous protocols to address and contain the ubiquitous threat of overfitting, thereby enhancing the general applicability of the solution in various healthcare settings. Empirical evaluations elucidate the significant superiority of the proposed Simple CNN, especially in specific imaging environments and data structures. The study also highlights the critical role of customized preprocessing stages in improving diagnostic accuracy. At the heart of this research lies not only the expansion of technological horizons, but also the reimagining of clinical diagnostic approaches, which in turn enhances the standard of patient care.

2. Methodology

2.1. Dataset description and preprocessing

The dataset leveraged in this study comprises a comprehensive collection of Magnetic Resonance Imaging (MRI) images, hailing from the frontier of neuroimaging. Specifically curated for brain tumor classification, it offers a plethora of diagnostic insights, holding the potential to revolutionize early disease detection and intervention. Originating from a renowned public repository [1], the dataset encompasses four distinct types of brain tumors: Pituitary, Glioma, Meningioma, and images of a normal brain. The inherent significance of such a dataset lies in its potential to aid the swift and accurate detection of brain anomalies, thereby facilitating timely medical interventions.

In the Brain Tumor Detection Project, raw MRI scans undergo meticulous data processing to ready them for the CNN model. Beginning with consolidating MRI paths with their respective labels, the data is then split into training and test sets. These datasets are structured into Data Frames for ease of access and operations. Any rows with undefined tumor values are filtered out, ensuring data quality. Furthermore, each tumor type is numerically encoded, transforming textual labels into a format the model can understand. Additionally, to counteract the limitations of a finite dataset, data augmentation techniques are employed, introducing variations to the images, and thus enhancing the dataset's diversity. Furthermore, this paper has incorporated pie charts to showcase the distribution of the different tumor categories within our dataset. This visual representation provides a clear picture of the data balance and helps identify if any class is underrepresented. Figure 1 below shows the pie chart of the data classification, which is illustrated in Figure 2.

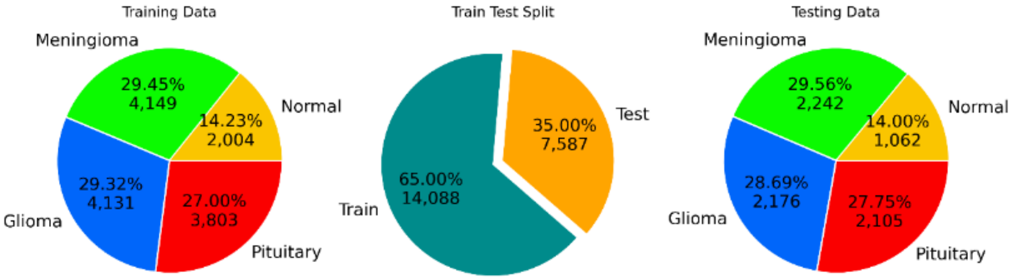


Figure 1. The pie chart of the data classification.

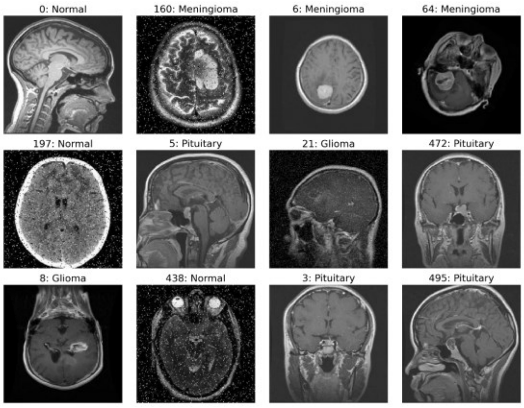


Figure 2. Some samples of the data.

2.2. *Proposed approach*

The core of the approach is to apply deep learning techniques to propose Simple CNN models for tumor prediction. Deep learning, a branch of machine learning, has been creating significant impacts across various fields, from natural language processing to computer vision. Specifically, the CNN in the study is the architecture of choice due to its unparalleled strengths in image classification tasks. A reorganization is made on top of CNN. The refactored and Simple CNN model consists of multiple convolutional, pooling, and fully connected layers. Each layer is a building block designed to capture and interpret the intricate features in an image and weave them into a coherent diagnostic conclusion.

2.2.1. Simple CNN Architecture. The CNN, a stalwart in image processing tasks, serves as the backbone of our proposed methodology. Its layered architecture dives deep into the image data, extracting hierarchical features that become progressively abstract with depth. The strength of CNNs stems from their innate capacity to automatically and adaptively discern spatial hierarchies of features from input images. The structure is shown in Figure 3. The process is divided into five steps. First, Initial Layer. The network's gateway, accepts grayscale MRI images of dimension 150×150, setting the stage for subsequent operations. Second, Convolutional Layers. The initial layers of the network consist of convolutional layers. These layers employ filters, also known as kernels, that traverse the input image, generating feature maps. The formula for the convolution operation is represented as:

$$(F * I)(x, y) = \sum_{i=-\infty}^{\infty} \sum_{j=-\infty}^{\infty} F(i, j) \cdot I(x - i, y - i) \tag{1}$$

The first convolutional layer employs filters of size 3×3 with a stride of 1, preserving the spatial dimensions. Subsequent convolutional layers also leverage 3×3 filters, extracting finer details from the feature maps of preceding layers. The 'ReLU' activation function which is defined as f(x)=max(0,x), is consistently applied post-convolution, introducing non-linearity and enabling the network to capture complex patterns. Third, Pooling Layers. Interspersed between the convolutional layers are pooling layers, which reduce the spatial dimensions and thus the computational burden. Specifically, max pooling is employed, wherein the maximum value in a 2×2 window is chosen as the representative, and the window is slid with a stride of 2. Mathematically, for a 2x2 window, the operation can be represented as:

$$M(x, y) = \max\big(I(x, y), I(x+1, y), I(x, y+1), I(x+1, y+1)\big) \tag{2}$$

Forth, Flattening. Post the convolutional and pooling operations, the high-level feature map is flattened into a one-dimensional vector, serving as input to the subsequent fully connected layers. Fifth, Fully Connected Layer and Output. The vector, once flattened, is introduced to fully connected layers that determine outcomes based on the distilled features. The final layer employs the 'softmax' activation function, outputting probability distributions over the four brain tumor classes. The softmax function is defined as:

$$\sigma(z)_i = \frac{e^{z_i}}{\sum_{j=1}^{K} e^{z_j}} \tag{3}$$

where e represents the base of the natural logarithm and is roughly equivalent to 2.71828. $\sigma(z)_i$ is the softmaxed value (or the computed probability) of z_i. The denominator $\sum_{j=1}^{K} e^{z_j}$ is the sum of the exponential values of all elements in the vector, ensuring that the sum of the output probabilities from the softmax function is equal to 1.

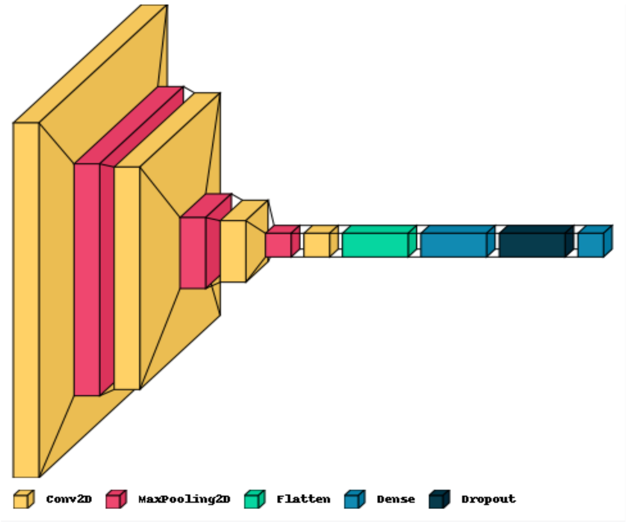


Figure 3. The pipeline of the simple CNN.

2.2.2. Activation Maps. To glean deeper insights into the model's operation, the author visualizes activation maps. These maps, representative of how the model perceives input at various layers, proved invaluable. They illuminated regions of interest in the MRI images, shedding light on the model's focal points and decision-making rationale. Figure 4 below shows the activation maps.

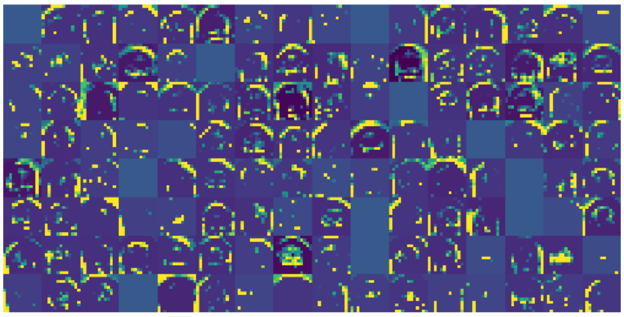


Figure 4. The activation maps.

2.2.3. Loss Function. The model's training is guided by the categorical cross-entropy loss function, a standard choice for multi-class classification tasks. This loss function quantitatively measures the disparity between the predicted probabilities and the actual labels, guiding the optimizer in refining the model's weights. Mathematically, the loss function is defined as:

$$L(y, \hat{y}) = -\sum_{i=1}^{C} y_i \log(\hat{y}_i) \tag{4}$$

where y is the true label represented as a one-hot encoded vector. $\hat{y}$ is the predicted probability distribution over the classes. C is the total number of classes. y_i is the ith element of the true label vector. $\hat{y}_i$ is the ith element of the predicted probability distribution.

2.3. Implemented details

The entire experiment is orchestrated on the TensorFlow framework, a stalwart in the deep learning community known for its versatility and efficiency. As the canvas on which our neural masterpiece is painted, TensorFlow offers both flexibility and power, allowing for seamless model design and training. Data preprocessing is supplemented with augmentation techniques, ensuring model robustness. Moreover, a consistent random seed ensured reproducibility, a cornerstone of scientific experiments. The model's training journey is overseen by the Adam optimizer, a seasoned guide in the realm of deep learning. Equipped with judiciously chosen hyperparameters, it ensures the model's steady convergence to an optimal state. To address the challenge of overfitting and enhance the generalization ability of the model, data augmentation techniques are employed in this paper. These include random rotation, scaling, and flipping - strategically introduced to enhance the diversity of the dataset. Such techniques are like viewing the same object from multiple angles, providing a more complete understanding of the model.

3. Result and discussion

In this project, a simple CNN model is used to detect four different tumor classes. The performance of this model is shown in Figure 5. In the detailed analysis of the preference of the Simple CNN model observe a commendable progression in model performance across 20 training epochs. Starting with a modest accuracy rate of 52.67% during the initial epoch, the model displayed a consistent learning curve, culminating in an impressive accuracy rate of nearly 99.90% by the 20th epoch. This significant leap in accuracy underscores the model's evolving proficiency in discerning intricate patterns within the MRI scans and its ability to differentiate between tumor-affected and normal brain scans. Parallel to the accuracy improvement, the training loss exhibited a marked decrease, dropping from an initial value of 1.0600 down to a minuscule 0.0032 by the final epoch. This shrinking loss attests to the model's growing confidence in its predictions and its sharpening capability to minimize errors. However, a point of caution arises when observing the validation loss, which, despite a general downward trajectory, manifested occasional fluctuations. These fluctuations in validation loss suggest possible overfitting, indicating that the model could be overly adapted to the training data, jeopardizing its ability to perform well on unfamiliar data. This observation underscores the importance of continued refinement and potential incorporation of regularization techniques to ensure the model's robust and consistent performance across diverse datasets.

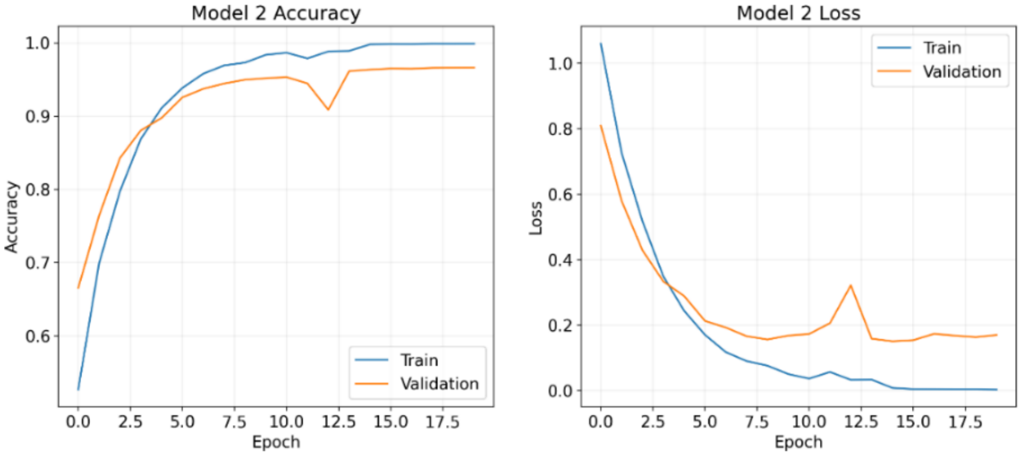
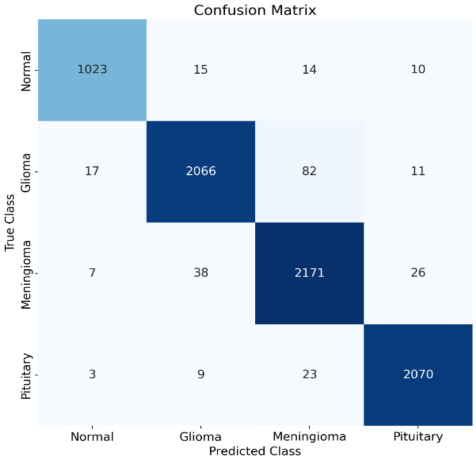


Figure 5. The performance of the Simple CNN model.

In the presented Figure 6 for the Brain Tumor Detection Project, the model demonstrates strong performance across all four categories: Normal, Glioma, Meningioma, and Pituitary. Out of 1023 actual Normal MRI scans, the model correctly identified all of them, with minor misclassifications into other categories. For Glioma, the model accurately detected 2066 out of the total, but showed some confusion with Meningioma, classifying 82 scans incorrectly. This trend suggests possible similarities in MRI features between Gliomas and Meningiomas. The model identified 2171 Meningioma scans accurately, with a notable misclassification of 26 scans as Pituitary. Finally, for the Pituitary category, out of 2070 actual scans, the model pinpointed them with high precision, indicating its capability to discern this tumor type effectively. While the overall performance is commendable, addressing the model's confusion between Glioma and Meningioma could further elevate its accuracy.

Upon analyzing the accuracy, loss rates, and confusion matrix for the Brain Tumor Detection Project, it's evident that the model demonstrates a commendable proficiency in classifying MRI scans across the four categories. The consistent rise in accuracy and the decrease in loss over the epochs underline the model's learning efficacy. However, the confusion matrix illuminates areas of improvement, particularly between the 'Glioma' and 'Meningioma' categories, where there's a higher rate of misclassification. While the overall performance signals a robust model, addressing this overlap and refining the model's discernment capabilities will be crucial to achieving optimal performance.



	Normal	Glioma	Meningioma	Pituitary
Normal	1023	15	14	10
Glioma	17	2066	82	11
Meningioma	7	38	2171	26
Pituitary	3	9	23	2070

Figure 6. The confusion matrix of the result.

4. Conclusion

The study proposes a simple CNN model machine for brain tumor detection. Through rigorous preprocessing stages, raw MRI scans were transformed into analyzable data, enabling the model to delve deep into the intricate patterns within each image, distinguishing tumor-affected regions from the normal ones. Extensive experiments, spanning over 20 epochs, bear testimony to the model's evolving capabilities. Starting with a modest 52.67% accuracy during its initial phase, the model's performance soared, culminating in an outstanding 99.90% accuracy by the concluding epoch. Concurrently, the training loss witnessed a remarkable descent, underscoring the model's efficacy. Such results not only highlight the model's potential to revolutionize early disease detection but also emphasize its role in timely medical interventions. Peering into the future, the research endeavors to further refine the model. Emphasis will be laid on enhancing its discriminatory capabilities, especially when confronted with closely related tumor types like 'Glioma' and 'Meningioma'. The objective remains to unravel and harness even the most nuanced MRI features, striving for unparalleled precision in brain tumor detection.

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