Brain Tumor Classification Using Arconv in Convolutional Neural Network Approach

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Abstract

Brain tumor detection and classification from medical images is a critical task in medical diagnosis, as early and accurate identification can significantly improve patient treatment and survival rates. Manual analysis of brain Magnetic Resonance Imaging (MRI) scans by radiologists is time-consuming and may lead to human error. Therefore, automated systems based on deep learning have gained significant attention for improving diagnostic accuracy. In this study, a brain tumor classification framework based on an ArConv (Adaptive Residual Convolution) integrated Convolutional Neural Network (CNN) is proposed to enhance feature extraction and classification performance. The proposed model utilizes convolutional layers combined with the ArConv module to capture complex spatial features and improve the learning capability of the network. MRI images are first preprocessed through normalization and resizing to ensure consistency in the dataset. The processed images are then fed into the CNN architecture where ArConv layers adaptively learn important tumor-related features. The model is trained and evaluated on a publicly available brain MRI dataset containing different tumor classes. Experimental results demonstrate that the proposed ArConv-CNN model achieves improved classification accuracy, precision, recall, and F1-score compared with conventional CNN approaches. The findings indicate that integrating ArConv with CNN can effectively enhance feature representation and improve brain tumor classification performance, making it a promising approach for computer-aided medical diagnosis systems.

Keyword: Brain tumour, CNN, claddification, AI, Image Processing

Brain Tumor Classification, MRI Image Analysis, Deep Learning, Convolutional Neural Network, Adaptive Residual Convolution (ArConv), Medical Image Processing, Computer-Aided Diagnosis

Introductions

Brain tumors are one of the most critical neurological disorders that occur due to the abnormal and uncontrolled growth of cells in the brain. These tumors can be categorized as benign (non-cancerous) or malignant (cancerous), and both types can significantly affect brain functionality and the overall health of patients. Early detection and accurate classification of brain tumors are essential for determining appropriate treatment strategies such as surgery, radiation therapy, or chemotherapy. Among the various medical imaging techniques, Magnetic Resonance Imaging (MRI) is widely used for diagnosing brain tumors because it provides detailed and high-resolution images of brain tissues[1]. MRI scans allow physicians to analyze tumor size, location, and structure, which are important for effective treatment planning. However, the manual analysis of MRI images by radiologists can be a time-consuming and complex process, particularly when dealing with large volumes of medical data. In addition, human interpretation may sometimes lead to inconsistencies or diagnostic errors[2].

With the rapid advancement of artificial intelligence (AI) and machine learning technologies, automated medical image analysis has become an important area of research. In recent years, deep learning techniques have shown remarkable success in analyzing complex medical images and assisting healthcare professionals in disease diagnosis[3]. Among these techniques, Convolutional Neural Networks (CNNs) have gained significant popularity due to their powerful ability to automatically extract hierarchical features from images. CNNs consist of multiple layers such as convolutional layers, pooling layers, and fully connected layers that work together to learn meaningful patterns from image data. These networks have been widely applied in various medical imaging applications including tumor detection, disease classification, and image segmentation[4][5].

Despite the success of conventional CNN models in image classification tasks, they still face certain limitations when applied to medical imaging. Brain MRI images often contain complex textures, varying tumor shapes, and subtle differences between tumor and normal tissues[6]. Traditional CNN architectures may struggle to capture these complex spatial features effectively, which can affect classification accuracy. Furthermore, the loss of important information during convolution and pooling operations can reduce the model's ability to learn fine-grained details required for precise tumor classification[7].

To overcome these limitations, researchers have proposed advanced convolution techniques that enhance feature extraction and improve model performance. One such technique is Adaptive Residual Convolution (ArConv), which combines adaptive feature learning with residual connections to improve information flow within the neural network. The ArConv module helps the CNN model capture more discriminative features by dynamically adjusting convolutional operations and preserving important information during training. This approach enhances the model's ability to identify complex tumor patterns and improves overall classification performance[8].

Literature review

Brain tumor classification using medical imaging has gained significant attention in recent years due to the growing demand for accurate and automated diagnostic systems. Magnetic Resonance Imaging (MRI) is widely used for brain tumor detection because it provides detailed information about brain tissues and tumor structures. However, manual interpretation of MRI images by radiologists is time-consuming and prone to errors, which has motivated researchers to develop automated classification systems using machine learning and deep learning techniques.

Early studies focused on traditional machine learning methods such as Support Vector Machine (SVM), K-Nearest Neighbors (KNN), and Decision Trees for tumor classification. These approaches relied heavily on manual feature extraction techniques such as texture, shape, and intensity features from MRI images. Although these methods achieved moderate accuracy, their performance was limited due to the complexity and variability of tumor structures in medical images[9].

With the advancement of deep learning, Convolutional Neural Networks (CNNs) have become the most widely used models for brain tumor classification. CNNs automatically learn hierarchical features from images and eliminate the need for manual feature extraction. Several studies have demonstrated the effectiveness of CNN architectures such as AlexNet, VGG, GoogLeNet, and ResNet for classifying MRI brain images. These deep learning models have significantly improved classification accuracy and robustness compared to traditional machine learning techniques[10].

For example, Khan et al. proposed a CNN-based framework combined with image processing and data augmentation techniques for brain tumor classification. Their model compared different pre-trained architectures such as VGG-16, ResNet-50, and Inception-V3, achieving high classification accuracy on MRI datasets. The results demonstrated that CNN models can effectively capture complex patterns in medical images and improve diagnostic performance.

Recent studies have also explored hybrid and transfer learning approaches to enhance classification performance[10]. For instance, researchers integrated pre-trained CNN models such as DenseNet, EfficientNet, and InceptionResNet with machine learning classifiers like Support Vector Machine (SVM) and Multi-Layer Perceptron (MLP). These hybrid frameworks improved feature extraction and achieved accuracy levels close to 100% on benchmark datasets.

Other researchers have investigated ensemble and hybrid deep learning methods for brain tumor detection. In a recent study, an ensemble CNN architecture combined with models such as MobileNetV2, Vision Transformer, and VGG16 was used to classify MRI images into multiple tumor types, including glioma, meningioma, and pituitary tumors.

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The proposed method achieved classification accuracy above 96%, demonstrating the effectiveness of deep learning in medical image analysis[13][14].

More advanced research has focused on improving CNN architectures through attention mechanisms, hybrid models, and explainable AI techniques. For example, CNN-based tumor classification models integrated with explainability tools such as LIME or Grad-CAM help identify important regions of MRI images responsible for classification decisions. These approaches improve model transparency and increase trust in AI-based medical diagnosis systems[12].

Despite these advancements, challenges still exist in brain tumor classification, including limited training datasets, variations in MRI image quality, and difficulty in extracting fine-grained tumor features. Therefore, researchers are exploring improved convolutional operations and adaptive feature extraction techniques to enhance CNN performance. Approaches such as adaptive convolution and residual learning help preserve important information during training and improve classification accuracy[15].

Medhology

The proposed methodology focuses on developing an efficient deep learning framework based on an Accelerated Reused Convolutional Network (ArConvNet) for disease classification using medical images. The methodology consists of several key stages including image preprocessing, data augmentation, ArConv layer design, model architecture construction, and model training and evaluation.

About dataset

The dataset used in this study consists of brain MRI images categorized into four classes: pituitary tumor (1457 images), meningioma tumor (1329 images), glioma tumor (1147 images), and no-tumor (1067 images), dataset taken from kaggle. It is designed for multi-class classification and computer-aided diagnosis of brain abnormalities. The dataset shows slight class imbalance, which may affect model learning and requires preprocessing techniques such as normalization, resizing, and data augmentation. MRI images provide clear soft-tissue contrast, helping in accurate tumor feature extraction. This dataset is suitable for training deep learning models and evaluating performance using metrics such as accuracy, precision, recall, and F1-score.

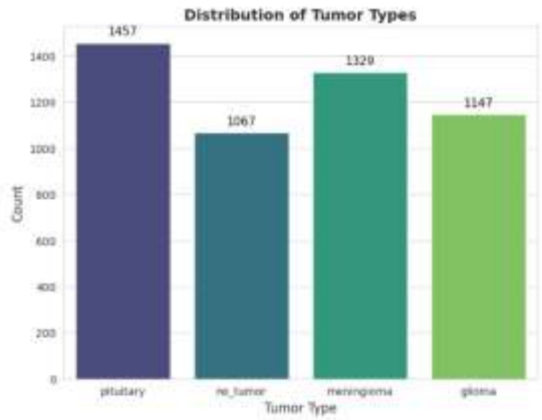

Fig. 1 Distribution of tumour types

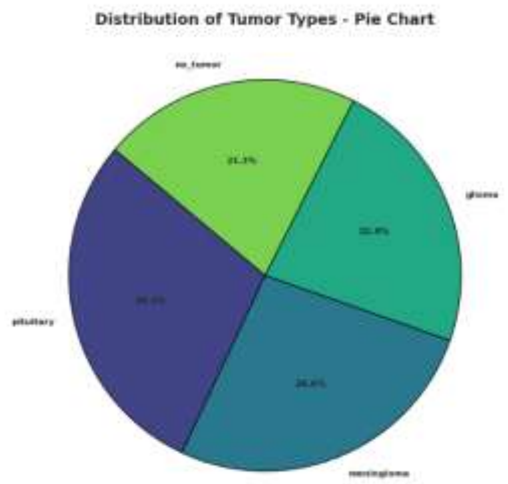

Fig2: Distribution of tumor types-Pie Chart

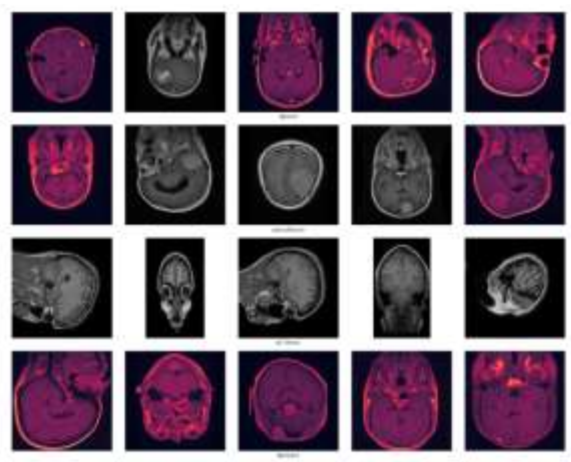

Fig3: image as a data set five five from each class

Image Preprocessing

Image preprocessing is performed to remove unnecessary regions from the input images. Since fundus images captured using DSLR cameras contain large black areas around the retina, an adaptive thresholding technique is applied to separate the important retinal region from the background. After generating a binary mask, the geometric boundaries of the eye are detected and the original image is cropped accordingly. This process helps eliminate noise and ensures that the model focuses only on relevant features present in the retinal region.

Data Augmentation

To improve the learning capability of the deep neural network, data augmentation techniques are applied to increase dataset diversity. Various transformations such as image rotation, brightness adjustment, contrast modification, color transformation, and zooming are used to generate additional training samples. Additionally, the study introduces a method of image integration, where two images are combined by averaging their corresponding pixel values. This technique produces new images that contain features from multiple diseases, enabling the model to learn more generalized disease patterns.

ArConv layer design

The core component of the proposed model is the Accelerated Reused Convolution (ArConv) layer, which is designed to reduce computational complexity while maintaining feature extraction capability. Instead of using standard two-dimensional convolution, the ArConv layer applies one-dimensional depthwise convolution sequentially across rows and columns. First, a depthwise convolution is applied along one spatial dimension, then the output is transposed and the same convolution is applied along the other dimension. This approach captures spatial relationships while reducing the number of parameters by approximately 66% compared to conventional convolution layers.

ArConv block architecture

In ArConv block architecture each block begins with a dense layer that expands the number of channels, followed by either a depthwise convolution layer (for down-sampling) or an ArConv layer (for feature extraction) depending on the stride value. After feature extraction, the channels are summarized using another dense layer and normalized using Batch Normalization. Residual connections are also included to improve information flow and prevent gradient degradation during training.

Initially, the input MRI images are provided to the network after undergoing standard preprocessing steps such as normalization and resizing. These preprocessing operations ensure that all images maintain uniform intensity distribution and spatial dimensions, thereby improving the stability and performance of the deep learning model during training.

After preprocessing, the input feature maps are passed through an expansion layer followed by a Rectified Linear Unit (ReLU) activation function. The expansion stage increases the number of feature channels, allowing the network to capture more detailed spatial information related to tumor structures. The expanded feature maps are then processed using a depthwise convolutional layer with stride 2, which performs efficient spatial filtering while simultaneously reducing the spatial resolution of the feature maps. This helps in lowering computational complexity without losing significant diagnostic information. A subsequent ReLU activation is applied to introduce non-linearity and enable the network to learn complex tumor patterns effectively.

Following this, a channel summarization operation is performed to refine and compress the extracted features into more meaningful representations. The summarized features are then normalized using batch normalization, which stabilizes the learning process, accelerates convergence, and reduces internal covariate shift. In parallel to this path, the expanded feature maps are also forwarded to the ArConv layer with stride 1. The ArConv module adaptively learns important tumor-related features by integrating residual learning principles with convolutional operations. This allows the network to focus on subtle variations in tumor boundaries and textures.

The output from the ArConv layer undergoes another sequence of ReLU activation, channel summarization, and batch normalization to enhance feature discriminability. An identity skip connection is then introduced, enabling the original input representation to be combined with the transformed feature maps using an addition layer. This residual connection helps in mitigating gradient vanishing problems and supports deeper network training by preserving essential low-level information.

Finally, the fused feature maps are directed toward the output layer for tumor classification. The overall architecture effectively combines depthwise convolution, adaptive residual learning, normalization techniques, and skip connections to build a robust and computationally efficient framework for accurate brain tumor classification from MRI images.

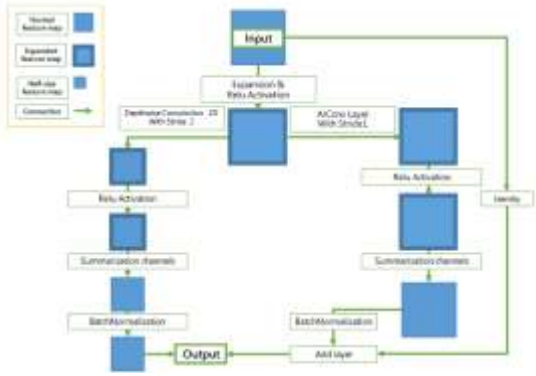

Fig4: Proposed model

Training and Validation

The training performance of the proposed model over multiple epochs using loss and accuracy curves. The training loss shows a consistent decreasing trend from a higher initial value to a very low level, indicating effective learning and convergence of the model. Simultaneously, the training accuracy steadily increases and stabilizes at a high value, demonstrating improved classification capability and overall robustness of the deep learning framework.

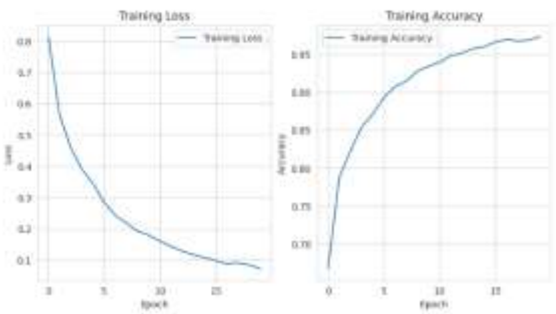

Fig5: training loss and accuracy graph

The confusion matrix shows strong classification performance with most samples correctly predicted along the diagonal. Glioma, meningioma, no-tumor, and pituitary classes achieve high accuracy, with minimal misclassifications. The pituitary class shows perfect prediction, indicating the model's effective feature learning and discrimination ability.

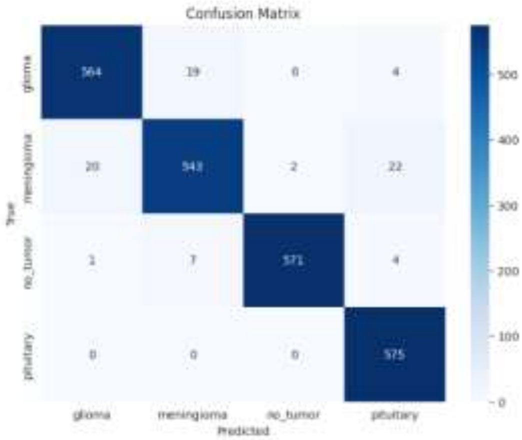

Fig6: Confusion matrix

Result and discussion

Table 1. Comparison table

Class	Precision	Recall	F1-Score
glioma	0.96	0.96	0.96
meningioma	0.95	0.93	0.94
no_tumor	1.00	0.98	0.99
pituitary	0.95	1.00	0.97
macro avg	0.97	0.97	0.97
weighted avg	0.97	0.97	0.97

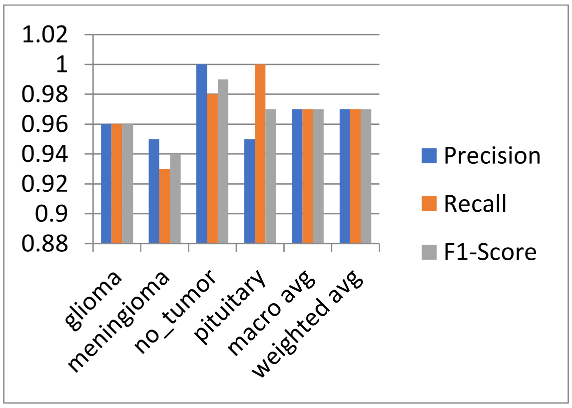

Fig7: Result comparison in chart

The performance metrics presented in the table demonstrate the effectiveness and robustness of the proposed deep learning model in classifying different types of brain tumors using MRI images. The evaluation is based on three important measures: precision, recall, and F1-score, which collectively assess the model's accuracy, sensitivity, and overall balance in prediction.

For the glioma class, the model achieved a precision of 0.96, recall of 0.96, and F1-score of 0.96. These values indicate that the model can accurately detect glioma tumors with a well-balanced trade-off between false positive and false negative predictions, reflecting reliable classification capability.

For the meningioma class, the precision value is 0.95, while recall is slightly lower at 0.93, resulting in an F1-score of 0.94. This suggests that although the model performs strongly in identifying meningioma tumors, a small number of samples may have been misclassified. Such variations can occur due to similarities in tumor appearance, intensity, or structural patterns in MRI images. Despite this, the model still maintains high performance for this class.

The no-tumor class shows excellent results with a precision of 1.00, recall of 0.98, and F1-score of 0.99. This indicates that the model is highly effective in distinguishing normal brain images from tumor-affected images, with almost no incorrect predictions. Accurate identification of healthy cases is crucial in medical diagnosis, as it helps avoid unnecessary clinical procedures.

Similarly, the pituitary tumor class achieved a precision of 0.95 and a perfect recall of 1.00, resulting in an F1-score of 0.97. This shows that all pituitary tumor samples were correctly detected by the model, demonstrating strong sensitivity toward this tumor category.

Conclusion

This study presented an effective deep learning framework for brain tumor detection and classification using an Adaptive Residual Convolution (ArConv) integrated CNN architecture. The proposed model successfully enhanced feature extraction capability by combining expansion layers, depthwise convolution, residual learning, and batch normalization. Experimental results demonstrated a consistent reduction in training loss and a significant improvement in classification accuracy, indicating stable learning and efficient convergence. The confusion matrix analysis further confirmed that the model achieved high prediction performance across all tumor classes, with minimal misclassification and excellent discrimination of pituitary tumors.

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