Brain Tumour Classification using Convolutional Neural Network

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Abstract. In this extended abstract, we address the problem of classifying MRI images of different brain tumours to facilitate the development of an automated system for early brain cancer detection. In particular, we adapt the convolutional neural network based on the AlexNet architecture to develop a model that achieves a classification accuracy of 97.5% on average on a real-world dataset containing MRI images of healthy brains and three different kinds of tumours.

Keywords: MRI image classification \cdot Brain tumour \cdot Deep learning.

1 Introduction

Brain cancer is a life-threatening disease, and a fast and accurate diagnosis could be the difference between life and death. The diagnosis of brain cancer usually involves manual segmentation and classification of brain tumours by doctors. However, this is not always a fast process, especially in remote areas with a limited number of doctors. A solution to this problem is to create an automatic and accurate classification system that speeds up the process without human intervention and allows patients to be diagnosed faster and receive appropriate treatment more quickly. Automatic classification of a brain tumour is very challenging because it involves extracting high-level features from the Magnetic Resonance Imaging (MRI) images. Deep learning classification techniques are being used for decision-making support in medicine [4]. Such methods include Convolutional Neural Network (CNN) [3]. A CNN is a form of neural network that uses convolutions to learn image patterns and perform pattern analysis without requiring explicit feature extraction. One of the earliest CNN was the pioneering LeNet by Yann LeCun et al. [3], used for Optical Character Recognition (OCR). Following the success of the LeNet CNN in OCR, the method has been adapted for many other medical applications including, X-ray image classification [1]. This paper aims to build upon the success of CNN in medical image analysis by adapting a CNN that is based on AlexNet architecture [2] for accurate classification of a brain tumour in MRI scans.



Fig. 1. Four samples of the MRI images used in this paper.

2 Methodology

2.1 Dataset Description and Preprocessing

The dataset used in this paper contains 7022 MRI images of the human brains, categorised into four types of tumour groups: Glioma, Meningioma, Pituitary, and No Tumour (healthy). To prepare the MRI images for our modelling process, we cropped out parts of the images that are not informative and centred images to maintain an aspect ratio of 1:1. We resize the centred images to 224x224 to allow for a consistent input data size for the classification model. Because classical CNN requires large training data to generate a good model, we augmented the image set by duplicating it four times. For each image in the image set, we rotated it at an angle of 45, 90, -45, and -90 degrees, respectively. The duplicated images were then merged with the original image set. We split the image set into training and evaluation set on a ratio of 80:20, respectively. Figure 1 shows samples of the training set.

2.2 Classifier Modelling

The CNN developed in this paper is inspired by the AlexNet-like network [2]. In our design however, we modified the input layer to accept gray-scale images instead of the intended RGB images. Because of the low spatial resolution of the MRI images, a relatively high number of convolutional layers is required for distinguishing the different brain tumours. Thus, we used the same number of convolutional layers as in [2]. Figure 2 shows the proposed CNN model built for the classification task in this work. The CNN architecture is defined sequentially and is built layer by layer. The first layer is the input layer, which accepts the input image defined as a 224 x 224 matrix. The next layer is the first convolutional layer with 96 convolutional filters, a kernel size of 11x11, and a stride of 4. Batch normalisation and a ReLU activation function are added before a max-pooling layer of size 2x2 and stride of 2. The second convolutional layer has 256 convolutional filters, a kernel size of 5x5, and a stride set to 2. The batch normalisation and a ReLU activation function are added before the max-pooling layer. The third and fourth convolutional layers are identical, with both having 384 convolutional filters, a kernel size of 5x5, a stride of 1, batch normalisation,



Fig. 2. A diagram of the CNN network, showing the pipeline from input to output through the convolutional layer and the fully connected layer.

and a ReLU activation function. The fifth and last convolutional layer has a filter size of 256, a kernel size of 3x3, and a stride of 1, with batch normalisation, ReLU activation function, and max pooling. The outputs of the convolutional layer are flattened and provided as input to the fully connected layer. The fully connected layer begins with a dense layer with 4096 neurons, batch normalisation, and ReLU activation function, followed by a dropout that is set to 0.4. The second and third layers are identical to the first connected layer, except the third layer has 1000 neurons instead of 4096. The last layer is the output layer which consists of a dense with 4 neurons: one for each of the four categories of the brain tumour, a batch normalisation, and a soft-max activation function.

3 Experimentation and Preliminary Results

We implemented the proposed CNN model using Keras with Tensorflow; a collection of machine learning libraries for the Python programming language. We trained the CNN with a categorical cross-entropy loss function and the 'Adam' optimiser with a learning rate of 0.001. We used the dataset described in section 2.1 for the training and evaluating the model. Table 1 shows the results of two experiments performed. We performed the first experiment (a) using the CNN model trained with the augmented image data appended to the training data. We conducted the second experiment (b) with the CNN model developed without augmenting the training data. The CNN model trained in the first experiment performed better with a classification accuracy of 97.5% compared to that trained with only the original data that achieved 93.3% accuracy on the evaluation dataset. Figure 3 shows a confusion matrix of the true labels of the brain tumour compared to the predicted labels by the CNN model in Experiment (a). The CNN model correctly predicted all the test MRI images for the glioma, and obtained at least 97% accuracy for the other types of brain tumours. The preliminary results are encouraging and show the effectiveness of the proposed approach, nevertheless, there is a need for extensive simulations to further assess the quality of the results (both in terms of accuracy and computational cost).

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Experiment	Setup					Accuracy
(a)	Experiment using both original data and image augmentation					0.975
(b)	Experiment without using any image augmentation					0.933
True labels	No Tumor	99%	0%	1%	0%	
	Glioma	0%	100%	0%	0%	
	Meningioma	0%	2%	98%	0%	
	Pituitary	0%	1%	2%	97%	
		No Tumor	Glioma	Meningioma	Pituitary	
	Predicted labels					

Table 1. Classification accuracy for the two experiments conducted.

Fig. 3. A confusion matrix of the brain tumour classification results of experiment (a).

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