Classification of Brain Tumors Using Deep Features Extracted Using CNN

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Abstract. Deep learning play a major role in medical automation, Convolutional Neural Networks (CNN) is an important machine learning technique for medical image segmentation and classification. In this work, we propose a novel approach that uses CNN_S for classifying brain tumors in to normal and three different types. The tumor is initially segmented from the MRI images using an enhanced ICA mixture mode model. From the segmented image deep features are extracted and classified. The results have been validated by measuring the performance of classifier on a data set available with Harvard Medical School.

Key words: CNN, ICA, Brain Tumor, CNN_S

1. Introduction
There has been an increase in the number of medical imaging techniques aligning with computer based classification and segmentation algorithms that are put under examination and accordingly validated by the researchers. Various clinical applications such as cancer tumor staging use these analytic methodologies [1]. Since the human classification of images to grade tumors is related to inter-reader variability depending on the visual features of lesions, these novel approaches play a vital role. Hence, the brain tumors that are capable of quantitatively assisting in more objective diagnosis are classified using an automated image analytic process. There are no pre-defined characteristics of a tumor and hence the lesions require an accurate differentiation from being a normal one to that being a cancerous tissue. This makes task of brain tumor image analysis a challenging one. The effort is, instead of genetic analysis of tissue it uses image analysis for cancer diagnosis [2].

The past few years a substantial improvement is recognized in the field of speech recognition, visual object recognition, object detection and many other domains such as drug discovery and genomics [3], owing to the deep learning techniques, especially Convolutional neural networks (CNN) [4]. Also, recently CNN has improved biomedical and biological image analysis applications such as mitosis cell detection from histological images [5, 6], carcinoma cancer detection from slide images [7, 8], neuronal membranes segmentation in electron microscopy images [9], skin disease or cancer
classification [10], immune cell detection for immunohistochemistry images [11], and segmentation of mass in mammograms [12, 13].

Figure 1. An overview of the classification modality

In this work classification of brain tumors in MRI images has been carried out using a classifier based on Convolutional Neural Networks (CNN). As a first stage the tumor region is segmented using an enhanced ICA mixture mode model [22]. From the segmented image deep features are extracted using CNN. From a single segmented region 8192 deep features are extracted and compared. The classifier performance is evaluated with help of Harvard Medical School AANLIB data set comprising 66 MRI images. The classification is effected for normal, Glioblastoma, Sarcoma and Bronchogenic carcinoma. The classifier performance has been validated using different performance parameters like accuracy, sensitivity, specificity etc...

2. Convolutional Neural Networks (CNN)

The combination of multiple linear and non-linear transformations of the input data forms deep learning architecture that are aimed at yielding more abstract – and ultimately more useful – representations. Since these methods have provided outstanding performance in different computer vision and pattern recognition tasks [14, 15], there has been an increase in their popularity. These deep learning architectures have evolved from multilayer neural networks that involve different design and training strategies to make them competitive. These strategies incorporate spatial invariance, hierarchical feature learning and scalability [15]. Another characteristic of this approach includes feature extracting that is a part of the learning process. This includes layers of deep learning architectures that help in finding an appropriate representation of input images in terms of multi-level visual feature maps that can be learnt [16].

The degree of freedom of models that operate on spatially correlated features can be reduced by the application of CNN which is a neural network architecture that uses extensive weight-sharing for the same[17].The three layers that are Convolution, max-pooling, and fully-connected forms the CNN network. One of the classic CNN arrangements includes alternating the Convolution and max-pooling layers which is then followed by fully-connected hidden layers. First, the Convolution of the input images is done by the Convolutionalal layer using a learned kernel. Every Convolutionalal layer posses same dimensionality as the input, however, each pixel is only activated by a region centred about that pixel (i.e., the kernel). Next, the max pooling layer performs an image down-sampling. Going by the empirical results, it is seen that this down sampling yields better performance when the maximum in each sub region is taken rather than averaging, in most of the cases [18]. Apart from “summarizing” each sub-region, the network acquires some degree of translational and rotational invariance through max-pooling. Finally, fully-connected layer is used to encode the position-dependent information and more global patterns.

The weight parameters are updated by the deep CNN in which stochastic gradient descent (SGD) is used for the same. The reason for choosing SGD over ordinary gradient descent algorithm is that the weight parameters are updated by estimating the gradient over the full training set in the latter while SGD proceeds comparatively faster than the ordinary gradient descent algorithm. This is due to the fact that SGD estimates the gradient by taking few examples or a mini-batch of the training set at a
time unlike the ordinary gradient decent where the entire training set is taken to estimate the gradient. However, choosing an appropriate learning rate and its related decreasing scheme can be difficult to achieve. Also, selecting an appropriate size for the mini-batch in SGD is also necessary.

Figure 2. Illustration of CNN

3. Methodology
Pre-trained CNN were used to extract deep features through transfer learning. Here, the pre-trained CNN model chosen was CNN_S [19] which contained five Convolutional layers and three fully connected layers. CNN_S had hyper parameters as follows: weight decay $5 \times 10^{-4}$, momentum 0.9, initial learning rate $10^{-5}$. The initial rate was down to one tenth, once the validation error stopped diminution. Next, linear transformation is used to normalize the gray values to range [0,255]. The features of the CNN model used are listed using Table 1.

Table 1. Features of the CNN model

| Network Parameter                  | Value     |
|-----------------------------------|-----------|
| Number of Convolutional Layers    | 5         |
| Number of fully connected Layers  | 3         |
| Weight Decay                      | $5 \times 10^{-4}$ |
| Momentum                          | 0.9       |
| Initial learning rate             | $10^{-5}$ |

The segmentation results are used to crop three tumor sub regions and then, resizing of the cropped region is done to $224 \times 224$ with biueic interpolation. These cropped images are used as model input. In order to make sure that only grayscale images enter the model, the G and B channels of CNN_S were turned off. In the final stage, the deep features are computed using forward propagation and extracted from fully-connected layer 6 and fully-connected layer 7.
4. Dataset
There are more than 120 types of brain tumors which differ in origin, location, size, characteristics of the tumor tissues, as defined by the World Health Organization (WHO) classification system [20, 21]. Out of these, we have considered three types of malignant tumors. The first one is Glioblastoma: primary malignant brain tumors classified as Grade IV and developed from star-shaped cells, called astrocytes that support nerve cells, which usually starts from cerebrum. Sarcoma tumor has a grade that varies from 1 to IV. This tumor arises in the connective tissues like blood vessels. The next one is Metastatic bronchogenic carcinoma, a secondary malignant brain tumor that spreads to the brain from bronchogenic carcinoma lung tumor. 66 human brain MRIs along with 22 normal and 44 abnormal images make up the data set. These include glioblastoma, sarcoma and metastatic bronchogenic carcinoma tumors collected from Harvard Medical School website (http://med.harvard.edu/AANLIB/) [20]. The brain MRIs were in axial plane, T2-weighted and 256 × 256 pixel. Figure 4 shows a sample of the data set.

**Figure 3. Illustration of deep feature extraction**

**Figure 4(a). Metastatic Bronchogenic Carcinoma**

**Figure 4(b). Sarcoma**

**Figure 4(c). Glioblastoma**

**Figure 4. Sample of data set**
5. Results And Conclusion

Two data sets were formed to validate the proposed classifier. These two data sets included a total of 40 images (20 images each) and were heterogeneous with both normal and abnormal images. The term ‘True positive’ is used to categorize correct classification of abnormality while ‘true negative’ is used to categorize correct classification of normal image. Similarly an incorrect classification of abnormality is classified as ‘False negative’ and incorrect classification of normality is categorized as ‘False positive’. The table 2.0 shows the performance of the proposed classifier.

| Data set | TP | FP | TN | FN |
|----------|----|----|----|----|
| DS-1     | 14 | 1  | 4  | 1  |
| Ds-2     | 15 | 0  | 5  | 0  |

The ability of the classifier is defined by the accuracy with which it discriminated between healthy and diseased states. The proposed classifier has an accuracy of 0.9 or 90% for data set DS1 while it is 1 or 100% for data set DS2. The sensitivity is another parameter which is used to define the classifier performance. It is nothing but the fraction of actual positives that have been correctly predicted. The sensitivity of the proposed classifier is 0.93(93%) and 1(100%) for dataset DS1 and dataset DS2 respectively.

The fraction of actual negatives that are correctly classified is identified by the specificity of the classifier. For the proposed classifier, the specificity is 0.80(80%) and 1(100%) for data set DS1 and DS2 respectively. The probability of the classifier that it will provide correct classification for images under test is quantified using positive predictive value (PPV) and negative predictive value (NPV) parameters. The portion from image data set which correctly classifies tumor as malignant is indicated by PPV while the NPV indicates the proportion of samples with negative results that resulted in correct classification of benign tumors.

MCC or Matthew’s correlation coefficient can be used to quantify the performance of classifier. MCC value of +1 represents perfect classification and 0 represents a very poor classification and –1 indicates a total disagreement between actual and observed classification. For data set DS1, MCC is 0.733 while that for DS2 is 1.

The performance of the proposed classifier in terms of the performance measures has been summarized using the Figure 5.
In this work a classifier based on CNN_S has been successfully implemented and validated. A total of forty images comprising both malignant and benign tumors have been considered for validation. The performance of the classification was quantified with the help of different measures like accuracy, sensitivity, specificity, PPV, NPV and MCC. The performance measure validates and demonstrates the suitability of the proposed classifier in identifying different types of brain tumors considered in this study.

6. References

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