INTRODUCTION

Gliomas are the most common type of primary brain tumor accounting for 40% of all CNS tumors and 80% of malignant brain tumors [1].

Manual segmentation of Gliomas from MRI is time-consuming and subjected to high inter-and intra-observer variation [2].

Convolutional Neural Networks (CNNs) have been shown to perform impressively on brain tumor segmentation but require a large amount of training data [2, 3, 4].

Which is a time-consuming and costly task involving the precious time and effort of radiologists. Other difficulties lie in obtaining diverse annotated training data that covers the entire spectrum of potential situations along with consistent MRI modalities for each training sample.

Recently Lifelong Learning (LL) [5] proposed a feasible solution using sequential knowledge acquisition through continual learning from the new set of training data, along with enhancing the existing knowledge gained from the previous training.

Although it appears like an easy-to-implement solution, significant difficulty involves due to catastrophic forgetting, which occurs when a network’s parameters are changed during adaptation to the new set of training data.

In this paper, we consider one of the possible practical scenarios, i.e., non-uniform MRI modalities in training samples.

Fig. 1 illustrates the LL training performance of a U-Net [6] based segmentation network for Glioma segmentation in three different settings. Lifelong training with small or large batches of alternate modalities leads to “catastrophic forgetting”.

Methods

The purpose of dynamic convolution is to learn a set of kernel coefficients or weights to convert the fixed kernels into a dynamic one. Fig. 2(a) depicts the general architecture of dynamic convolution [7, 8]. It predicts the kernel coefficients using a trainable attention coefficient prediction module. Then, the fixed convolution kernels are multiplied by the dynamic weights to form a set of dynamic convolution kernels based on the training batch.

The purpose of the ACP module is to predict coefficients or weight values for each fixed convolution kernel in the convolution layer to convert them into dynamic convolution kernels based on the input as shown in Fig. 2(b).

To produce dynamic Convolution Kernels of size k×k×C output, the dynamic convolution kernel generation layer uses k×k×C fixed convolution kernels (based on the number of response maps generated from the previous layer) and corresponding attention weight vector of size 1×1×C input generated by the ACP module as follows.

RESULTS

We have collected T2 and Flair MRI volumes from 130 Glioma patients (pre-operative multi-institutional scans) from The Cancer Imaging Archive (TCIA) Glioblastoma Multiforme (TCGA-GBM) data collection [2, 3].

For model training, we randomly selected 110 patients and used 55 patients with only T2 volume and the remaining 55 with Flair volume. The remaining 20 patients are used as the test set, among which 10 patients are used with T2 volume, and the remaining 10 are used with Flair volume for testing the models’ performance.

LL-based training approach is used to train the models. Streams of training data are coming in small or large batches consisting of alternate MRI modalities as being curated from hospitals.

CONCLUSIONS

Here we have presented a novel Dy-CNN-based segmentation network for Glioma segmentation and experimentally demonstrated its suitability in a lifelong sequential learning-based scenario with multi-modal MR images. Experimental results demonstrated the superiority of the Dy-CNN-based segmenting network in terms of learning through multi-modal MRI images and better convergence of lifelong learning-based training.

REFERENCES


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