FCNN For Brain Tissue Segmentation With The Aid of Label Fusion

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Abstract- *A stochastic model for characterizing tumor texture in brain MR images is proposed. The efficiency of the model is demonstrated in patient-independent brain tumor texture feature extraction and tumor segmentation in magnetic resonance images (MRIs). There are different tissues namely gray matter (GM), white matter (WG) are spread over the entire brain. It is difficult to segment individually when a brain image is considered. The boundaries are not well defined. The multi scale patch driven active contour methodology is proposed in this paper for automated brain MRI image segmentation into WG, GM, Brain tumor. Label-fusion aided deep-learning approach for automatically segmenting isointense infant brain images into white matter, gray matter and cerebrospinal fluid using T1- and T2-weighted magnetic resonance images. A key idea of our approach is to apply the fully convolutional neural network (FCNN) to individual brain regions determined by a traditional registration-based segmentation method instead of training a single model for the whole brain. This provides more refined segmentation results by capturing more region-specific features. Segmentation of brain tumors from magnetic resonance imaging (MRI) datasets is great important for earlier detection of tumors for treatment stages and find, which part of the brain is affected mainly.*

Keywords- MRI, Deep learning, Brain tumor, FCNN

I. INTRODUCTION

To replace the time-consuming and labor-intensive manual segmentation procedure for classifying images of infant brains into regions of white matter (WM), grey matter (GM) and cerebrospinal fluid (CSF), automated segmentation approaches have been extensively studied. Different from the adult brain, auto segmentation of the infant brain is especially challenging due to the reduced tissue contrast, poor spatial resolution, severe partial volume effect, and the ongoing maturation and myelination processes. The first-year infant brain is usually divided into three distinct stages: infantile stage (5months), (ii) isointense stage (6-8 months), and (iii) early adult like isointense stage, it is particularly difficult to discriminate WM from GM in brain magnetic resonance (MR) images because of overlapping areas with low tissue contrast. The traditional multi-atlas and label fusion (MALF) method uses the registration from a group of atlases with manually segmented labels. This approach has the limitation of treating different available imaging modalities equally and is often computationally expensive.

Deep learning techniques have emerged as powerful methods for integrating the information from multiple modalities and capturing a wide range of highly discriminative imaging features. With an increased number of parameters and intensive memory and computational requirements, the 3-dimensional (3D) fully convolutional neural network (FCNN) offers more accurate productivity by using more complex hierarchical features for its dense layers, small kernels and deeper architectures. Patch based FCNNs usually focus on the local tissue structures instead of the regional location information, while full-3Dimagenetworkswithend-to-end predictions often require multiple graphic processing units (GPUs), adequate random access memory(RAM) to load a sufficient number of samples, and much longer time to train. To grasp both the local structure and global spatial information with limited computational power and RAM, developed a label fusion-aided convolutional neural network (LFA-FCNN). The key idea is to apply the FCNN onto subregions that are defined by a traditional registration-based segmentation method such as MALF rather than training a single model for the whole brain, and then combine the segmentation results from those subregions by label fusion. In this way, the proposed approach captures more region-specific features and yields more refined segmentation results. The approach was evaluated by the dataset from the iSEGMICCAI Grand Challenge 2017, which consists of 10training and 13 testing isointense infant brain subjects.

Brain tumor is one of the dangerous diseases in the world. So early recognition of the cancer is key to its cure. As human brain is very complex structure analysis of tumor in this region is difficult process. Medical images have different textures depending on area of body considered classification of images becomes challenging problem. Existing system uses different algorithms like k-means for segmentation which has more disadvantages like it is slow, it expects user to specify cluster number, heavily dependent on initial cluster centers. A

very difficult problem in classification is choice of features to distinguish between classes. So this current procedure is extremely time consuming and more inclined to mistakes. In order to overcome the drawbacks of existing system this project aims to provide an efficient system by using adaptive multi scale patch driven active contour for segmentation and FCNN for accurate classification of MRI scan into normal and abnormal based on features. A correct classification of brain prompts right choice and gives great and right treatment.

II. LITERATURE SURVEY

Fractal analysis is appropriate for MR image analysis. For tumor detection, existing fractal-based techniques are described and three modified algorithms using fractal analysis models are proposed. For each new method, the brain MR images are divided into a number of pieces. The first method involves thresholding the pixel intensity values and the technique is called as piecewise-threshold-box-counting (PTBC) method. Then the improved piecewise-modified-box-counting (PMBC) and piecewise-triangular-prism-surface-area (PTPSA) methods are implemented. With the PTBC method, there are differences in intensity histogram and fractal dimension between normal and tumor images. Using PMBC and PTPSA methods, it is possible to detect and locate the tumor in the brain MR images more accurately.

Markov Random Fields (MRFs) are a popular and well-motivated model for many medical image processing tasks such as segmentation. Discriminative Random Fields (DRFs), a discriminative alternative to the traditionally generative MRFs, allow tractable computation with less restrictive simplifying assumptions, and achieve better performance in many tasks. Here, the tumor segmentation performance of a recent variant of DRF models that takes advantage of the powerful Support Vector Machine (SVM) classification method is proposed. Combined with a powerful Magnetic Resonance (MR) preprocessing pipeline and a set of 'alignment-based' features, the use of SVMs, MRFs, and two types of DRFs as classifiers for three segmentation tasks related to radiation therapy target planning for brain tumors are investigated. Two of which do not rely on 'contrast agent' enhancement. The results indicate that the SVM-based DRFs offer a significant advantage over the other approaches.

An extended graph-shifts algorithm for image segmentation and labeling is proposed. This algorithm performs energy minimization by manipulating a dynamic hierarchical representation of the image. It consists of a set of moves occurring at different levels of the hierarchy where the types of move, and the level of the hierarchy, are chosen automatically so as to maximally decrease the energy. Extended graph-shifts can be applied to a broad range of problems in medical imaging. It can be used for the detection of pathological brain structures: (i) segmentation of brain tumors, and (ii) detection of multiple sclerosis lesions. The energy terms in these tasks are learned from training data by statistical learning algorithms. It provides accurate results, precision and recall in the order of 93%, and also show that the algorithm is computationally efficient, segmenting a full 3D volume in about one minute.

An automated system for brain tumor segmentation that provides objective, reproducible segmentations that is close to the manual results. Additionally, the method segments white matter, grey matter, cerebrospinal fluid, and edema. The segmentation of pathology and healthy structures is crucial for surgical planning and intervention. The method performs the segmentation of a registered set of MR images using an Expectation-Maximization scheme. The segmentation is guided by a spatial probabilistic atlas that contains expert prior knowledge about brain structures. This atlas is modified with the subject specific brain tumor prior that is computed based on contrast enhancement. Five cases with different types of tumors are evaluated. The results obtained from the automatic segmentation program are then compared with results done using manual and semi-automated methods. The automated method yields results that have surface distances roughly 1–4 millimeters compared to the manual results. The brain atlas was created by averaging manual segmentations of normal brains that have been registered using affine transformation. The atlas performs two critical functions. It provides spatial prior probabilities and it is used to estimate the initial intensity distribution parameters for the normal tissue classes. For each dataset, the three different image channels are first registered to a common space and then registered to the brain atlas. The registration process is done using affine transformation and the mutual information metric. Since the atlas is a normal brain atlas, it does not contain the prior probabilities for the tumor and edema. It is necessary to obtain prior probabilities for tumor and edema. Otherwise, the voxel would be incorrectly classified as normal tissue. The problem is tackled by artificially generating prior probabilities for tumor and edema.

The fractal texture feature is useful to detect pediatric brain tumor in multimodal MRI. The efficacy of using several different image features such as intensity, fractal texture, and level-set shape in segmentation of posterior-Fossa (PF) tumor for pediatric patients is investigated. It explores effectiveness of using four different feature selection and three different segmentation techniques, respectively, to discriminate tumor regions from normal tissue in multimodal brain MRI. The selective fusion of these features for improved PF tumor

segmentation is proposed. The result suggests that Kullback–Leibler divergence measure for feature ranking and selection and the expectation maximization algorithm for feature fusion and tumor segmentation offer the best results for the patient data. It shows that for T1 and fluid attenuation inversion recovery (FLAIR) MRI modalities, the best PF tumor segmentation is obtained using the texture feature such as multi-fractional Brownian motion (mBm) while that for T2 MRI is obtained by fusing level-set shape with intensity features. In multimodality fused MRI (T1, T2, and FLAIR), mBm feature offers the best PF tumor segmentation performance. The different similarity metrics are used to evaluate quality and robustness of these selected features for PF tumor segmentation in MRI for ten pediatric patients.

III. PROPOSED SYSTEM

To develop a fast and reliable automatic segmentation approach that is competitive with manual segmentation, first used an atlas-based approach to obtain a rough segmentation result, and then applied the FCNN model onto each individual sub region derived from the initial result to generate refined segmentation results. For each subject, need the T1-, T2-weighted MR images and manual segmentations for training purposes. Before started, some preprocessing steps were necessary including within-subject T1 and T2 registration, resolution standardization, skull stripping, intensity in homogeneity correction and removal of the cerebellum and brain stem.

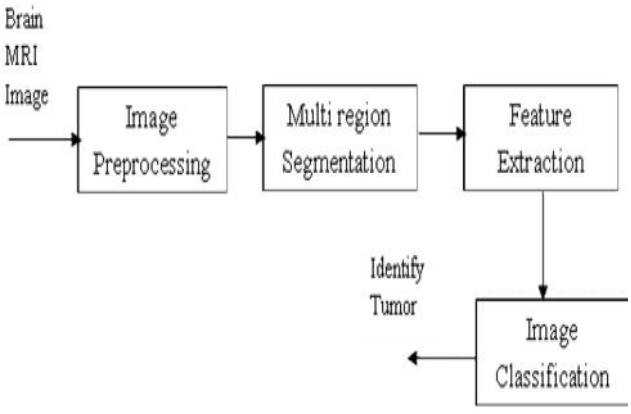


Fig 1 Proposed Block Diagram

Multi-Atlas Label Fusion

After preprocessing, used atlas-based segmentation to segment the WM, GM and CSF regions. This type of methods have an advantage over the level set method and watershed transform by borrowing prior knowledge about the shape and distribution of the segmented structures from a pre-segmented reference atlas. Assume have N subjects. For real data, N is the number of training subjects. A target image is segmented by treating images of all the other N-1 subjects as atlases. First, performed rigid, affine and then differ morphism registration (with mutual information as the loss function) using the Advanced Normalization Tools software to align all the T1-weighted images from atlases to the target T1 weighted image. Then transferred the annotation results from those atlases to the target space and obtained N-1 candidate labels for the target. The next step is to combine the candidate labels by label fusion. Define the Normalized Cross-Correlation (NCC) between registered image I1 and target image I2:

$$NCC = \frac{Cov(I_1, I_2)}{\sqrt{var(I_1)}\sqrt{var(I_2)}}$$

The NCC was computed in an r x r square local neighborhood around each voxel, which characterizes the - local similarity. In this way, calculated the N-1 NCC maps between the N-1 atlases and the target T1-weighted image. Then, for a given voxel, from the N-1 registered local label maps, chose the one with the largest NCC at that voxel as its segmented label. This method is referred to as the NCC-based local weighted voting.

Integration of Label Fusion and FCNN

Based on the label fusion segmentation, developed two strategies to determine the subregions for building FCNN models separately. Strategy A: training two FCNN models, where in the first model the extracted patches are centered within the areas with NCC<0.85 while in the second model they were centered within those with NCC>0.85. Strategy B: training three FCNN models using patches centered. Within the two-voxel-dilated WM, GM and CSF areas. From the last subsection, had MALF segmentation for target images a1) and a2). By thresholding the NCC map, obtained b11) the (NCC<0.85) area and b12) the (NCC>0.85) area; by dilating the CSF, GM and WM areas by 2 voxels in a2), obtained the dilated CSF in b21), dilated GM in b22) and dilated WM in b23). can obtain those 5 areas in b11), b12), b21), b22) and b23) from the target image as well as from each atlas by alternating the atlas to a target. Next, extracted patches from the five areas of each atlas to train 5 FCNN models and predicted the target labels at their corresponding areas.

Pre-Processing

MRI images are altered by the bias field distortion. This makes the intensity of the same tissues to vary across the image. To correct it, applied the N4ITK method However, this is not enough to ensure that the intensity distribution of a tissue type is in a similar intensity scale a cross different

subjects for the same MRI sequence, which is an explicit or implicit assumption in most segmentation methods. In fact, it can vary even if the image of the same patient is acquired in the same scanner in different time points, or in the presence of a pathology. So, to make the contrast and intensity ranges more similar across patients and acquisitions, apply the intensity normalization method proposed by Nyul on each sequence.

After normalizing the MRI images, compute the mean intensity value and standard deviation across all training patches extracted for each sequence. Then, normalize the patches on each sequence to have zero mean and unit variance.

Fullyconvolutional Neural Network

FCNN were used to achieve some breakthrough results and win well-known contests. The application of convolutional layers consists in convolving a signal or an image with kernels to obtain feature maps. So, a unit in a feature map is connected to the previous layer through the weights of the kernels.

The weights of the kernels are adapted during the training phase by backpropagation, in order to enhance certain characteristics of the input. Since the kernels are shared among all units of the same feature maps, convolutional layers have fewer weights to train than dense FC layers, making FCNN easier to train and less prone to overfitting. Moreover, since the same kernel is convolved overall the image, the same feature is detected independently of the location – translation invariance. By using kernels, information of the neighborhood is taken into account, which is an useful source of context information. Usually, a non linear activation function is applied on the output of each neural unit.

Deeper Architectures/Small Kernels

Using cascaded layers with small 3 x3 kernels has the advantage of maintaining the same effective receptive field of bigger kernels, while reducing the number of weights, and allowing more non-linear transformations on the data. To evaluate the real impact of this technique on brain tumor segmentation, changed the cascaded convolutional layers before each max pooling of the proposed architecture by one layer with larger kernels with the equivalent effective receptive field. So, in HGG changed the groups of layers 1, 2, 3 and 5, 6, 7by one convolutional layer with 7 x7 kernels each, while in the LGG changed the groups of layers 1 and 2, and 4 and 5 by one layer with 5 x5 kernels each. Using these architectures, experimented two variants for both grades: 1) maintained the 64 feature maps in the first convolutional layer and 128 in the second; 2) increased the capacity of the FCNN by using wider layers, namely, 128 feature maps in the first convolutional layer and 256 in the second. Present the results obtained in the Leader board and Challenge data (Leader board: 3:1%, Challenge: 1:6%), while for variant it was 2:1% (Leader board: 2:4%, Challenge: 1:8%). In the majority of metrics, the proposed method obtained higher scores than both variants with bigger kernels, with some of them with statistical significance, while the variants achieved better scores in PPV (HGG in both data sets). In the boxplots, both variants seem to have larger dispersion and more outliers. In the segmentations, although the segmentations by the variants appear with good quality, the proposed method can capture more details, and variant 2 classified some non enhanced tumor inside the enhancing ring, which does not happen in the manual segmentation in HGG in LGG the architecture with bigger kernels also identified an excess of non-enhancing tumor.

Patch Extraction Plane

The use of 2D patches in a MRI image requires that define a plane perpendicular to an axis to extract patches. So, following the procedure defined in the previous subsection, investigated the use of patches extracted in a plane perpendicular to the Axial, Coronal, and Sagittal axis. The results in both the Leader board and Challenge data sets. As can be observed, extracting patches in the plane perpendicular to the Axial axis presented the best overall performance with a mean gain of 2:33% relative to the Coronal plane and 4:00% relative to the Sagittal plane. The Axial plane presented better DSC and PPV scores for both data sets than the Sagittal plane, but worst sensitivity for the Challenge data set and for the complete region in the Leaderboard data set.

Considering, this can be explained by an over-segmentation of the tumor, which is corroborated by the lower PPV score. A similar pattern is found for the Coronal plane, which was better in the enhanced region for the PPV score and in the complete region for the Sensitivity score. The better performance obtained using patches extracted in the axial plane can be explained by some acquisitions having lower spatial resolution in the Coronal and Sagittal planes, which can be considered a limitation of the BRATS databases.

Finally, as an overall analysis, note some general trends across all experiments. Considering the boxplots, verify a lower dispersion for the complete region, presenting also a higher mean value for the same region. This lower dispersion is less expressive in the Leaderboard than in the Challenge data set, which may be explained by the worst performance of the algorithms on LGG subjects in this data.

Gliomas are the brain tumors with the highest mortality rate and prevalence. These neoplasms can be graded into Low Grade Gliomas (LGG) and High Grade Gliomas (HGG), with the former being less aggressive and infiltrative than the latter. Even under treatment, patients do not survive on average more than 14 months after diagnosis. Current treatments include surgery, chemotherapy, radiotherapy, or a combination of them. MRI is especially useful to assess gliomas in clinical practice, since it is possible to acquire MRI sequences providing complementary information.

The accurate segmentation of gliomas and its intra-tumoral structures is important not only for treatment planning, but also for follow-up evaluations. However, manual segmentation is time-consuming and subjected to inter- and intra-rater errors difficult to characterize. Thus, physicians usually use rough measures for evaluation. For these reasons, accurate semiautomatic or automatic methods are required. However, it is a challenging task, since the shape, structure, and location of these abnormalities are highly variable. Additionally, the tumor mass effect change the arrangement of the surrounding normal tissues. Also, MRI images may present some problems, such as intensity inhomogeneity, or different intensity ranges among the same sequences and acquisition scanners.

In brain tumor segmentation, find several methods that explicitly develop a parametric or non-parametric probabilistic model for the underlying data. These models usually include a likelihood function corresponding to the observations and a prior model. Being abnormalities, tumors can be segmented as outliers of normal tissue, subjected to shape and connectivity constrains. Other approaches rely on probabilistic atlases. In the case of brain tumors, the atlas must be estimated at segmentation time, because of the variable shape and location of the neoplasms.

Tumor growth models can be used as estimates of its mass effect, being useful to improve the atlases. The neighborhood of the voxels provides useful information for achieving smoother segmentations through Markov Random Fields (MRF).Zhao at alalso used a MRF to segment brain tumors after a first over segmentation of the image into super voxels, with a histogram-based estimation of the likelihood function. As observed by Menze et al. generative models generalize well in unseen data, but it may be difficult to explicitly translate prior knowledge into an appropriate probabilistic model. Another class of methods learns a distribution directly from the data.

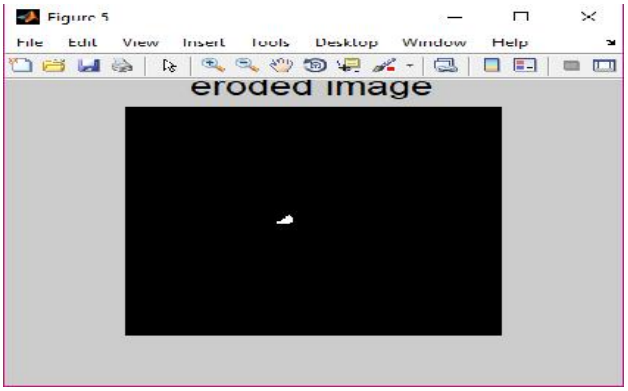
Although a training stage can be a disadvantage these methods can learn brain tumor patterns that do not follow a specific model. This kind of approaches commonly consider voxels as independent and identically distributed, although context information may be introduced through the features. Because of this, some isolated voxels or small clusters may be mistakenly classified with the wrong class, sometimes in physiological and anatomically unlikely locations. To overcome this problem, some authors include information of the neighborhood by embedding the probabilistic predictions of the classifier into a Conditional Random Field. Classifiers such as Support Vector Machines and, more recently, Random Forests (RF) were successfully applied in brain tumor segmentation.

Other methods known as Deep Learning deal with representation learning by automatically learning an hierarchy of increasingly complex features directly from data. So, the focus is on designing architectures instead of developing handcrafted features, which may require specialized knowledge.

FCNNs have been used to win several object recognition and biological image segmentation challenges. Since a FCNN operates over patches using kernels, it has the advantages of taking context into account and being used with raw data. In the field of brain tumor segmentation, recent proposals also investigate the use of FCNNs. Used a shallow FCNN with two convolutional layers separated by max-pooling with stride 3, followed by one fully-connected (FC) layer and a soft max layer. Urban et al. evaluated the use of 3D filters, although the majority of authors opted for 2D filters. 3D filters can take advantage of the 3D nature of the images, but it increases the computational load. Some proposals evaluated two-pathway networks to allow one of the branches to receive bigger patches than the other, thus having a larger context view over the image. In addition to their two-pathway network, built a cascade of two networks and performed a two-stage training, by training with balanced classes and then refining it with proportions near the originals. Use a binary FCNN to identify the complete tumor. Then, a cellular automata smooths the segmentation, before a multiclass FCNN discriminates the sub-regions of tumor. Extracted patches in each plane of each voxel and trained a FCNN in each MRI sequence; the outputs of the last FC layer with softmax of each FCNN are concatenated and used to train a RF classifier. divided the brain tumor regions segmentation tasks into binary sub-tasks and proposed structured predictions using a FCNN as learning method.

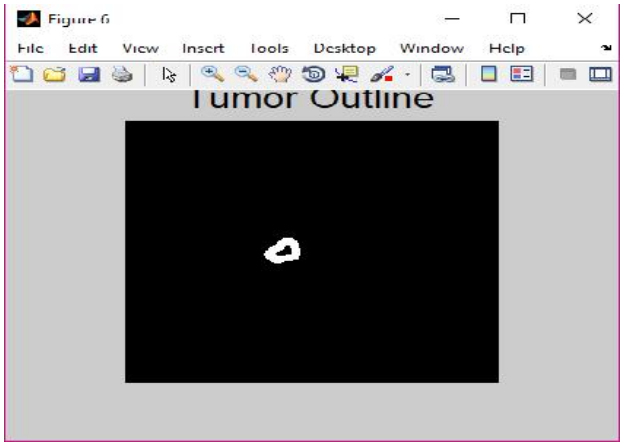
IV. SCREEN SHOTS

Input Image

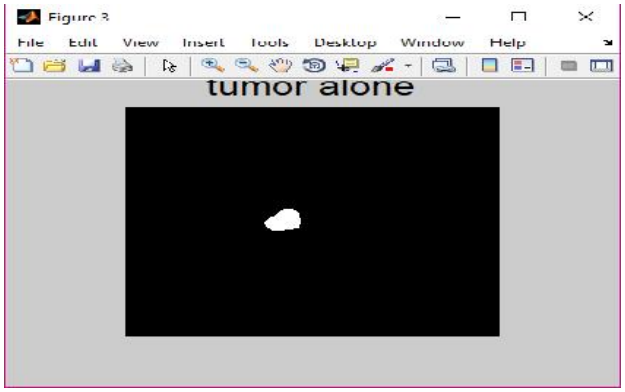


Eroded Image

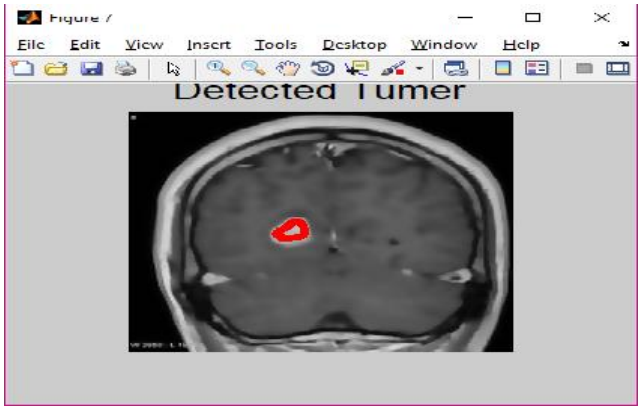
Filtered Image



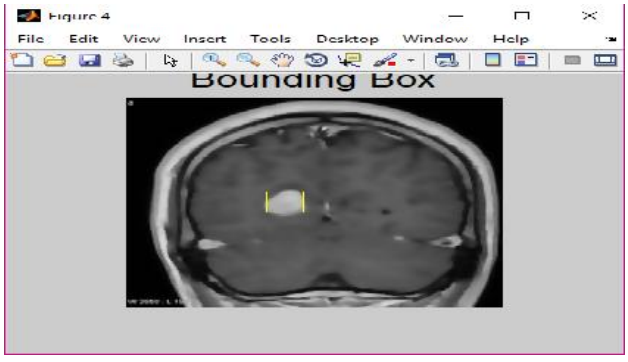
Tumor Outline



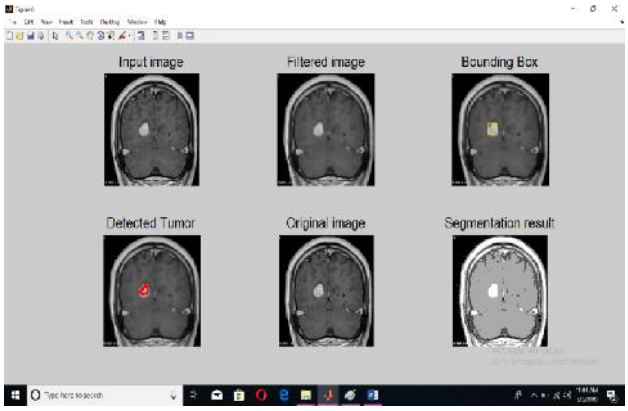
Tumor Alone



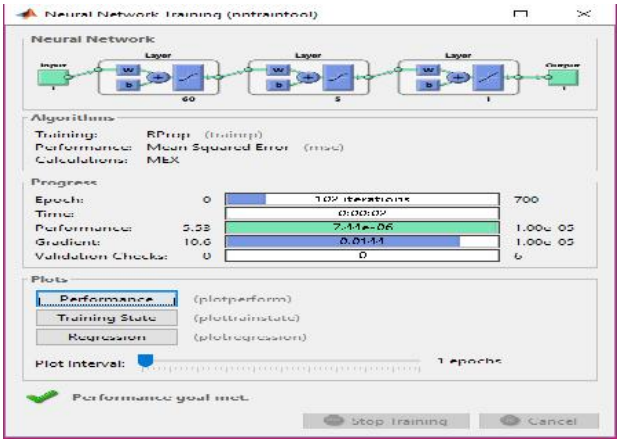
Detect Tumor



Bounding Box



Segmentation Result



Fully Convolutional Neural Network

V. CONCLUSION

Thus a label-fusion aided deep-learning approach for automatically segmenting isointense infant brain images into white matter, gray matter and cerebrospinal fluid using T1- and T2-weighted magnetic resonance images. A key idea of our approach is to apply the fully convolutional neural network (FCNN) to individual brain regions determined by a traditional registration-based segmentation method instead of training a single model for the whole brain. This provides more refined segmentation results by capturing more region specific features. The GM and WM were more difficult to discriminate; compared with MALF, deep-learning based methods performed much better; the Strategy-B-based FCNN method outperformed the FCNN-only method. A two-sample paired t-test shows that the Dice coefficients of all the three labels by Strategy are significantly larger than using MALF and FCNN. Compared with the top ranking team, it is competitive on CSF segmentation. The low standard deviation on test set implies this approach is robust. Believe that using more complex brain parcellations to train a variety of FCNN models may capture more region-specific features, but training multiple models undoubtedly increases the computational burden.

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