Hierarchical Convolutional-Deconvolutional Neural Networks for Automatic Liver and Tumor Segmentation

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Abstract—Automatic segmentation of liver and its tumors is an essential step for extracting quantitative imaging biomarkers for accurate tumor detection, diagnosis, prognosis and assessment of tumor response to treatment. MICCAI 2017 Liver Tumor Segmentation Challenge (LiTS) provides a common platform for comparing different automatic algorithms on contrast-enhanced abdominal CT images in tasks including 1) liver segmentation, 2) liver tumor segmentation, and 3) tumor burden estimation. We participate this challenge by developing a hierarchical framework based on deep fully convolutional-deconvolutional neural networks (CDNN). A simple CDNN model is firstly trained to provide a quick but coarse segmentation of the liver on the entire CT volume, then another CDNN is applied to the liver region for fine liver segmentation. At last, the segmented liver region, which is enhanced by histogram equalization, is employed as an additional input to the third CDNN for tumor segmentation. Jaccard distance is used as loss function when training CDNN models to eliminate the need of sample re-weighting. Our framework is trained using the 130 challenge training cases provided by LiTS. The evaluation on the 70 challenge testing cases resulted in a mean Dice Similarity Coefficient (DSC) of 0.963 for liver segmentation, a mean DSC of 0.657 for tumor segmentation, and a root mean square error (RMSE) of 0.017 for tumor burden estimation, which ranked our method in the first, fifth and third place, respectively.

I. INTRODUCTION

Liver cancer is the second leading cause of global cancer mortality (after lung cancer), and is one of the most rapidly increasing cancers in terms of incidence and mortality worldwide and in the United States [1], [2]. Although contrast-enhanced computed tomography (CT) has been widely used for liver cancer screening, diagnosis, prognosis, and the assessment of its response to treatment, proper interpretation of CT images is normally time-consuming and prone to suffer from inter- and intra-observer variabilities. Therefore, computerized analysis methods have been developed to assist radiologists and oncologists for better interpretation of liver CT images.

Automatically segmenting liver and viable tumors from other tissue is an essential step in quantitative image analysis of abdominal CT images. However, automatic liver segmentation is a challenging task due to the low contrast inside liver, fuzzy boundaries to its adjacent organs and highly varying shape. Meanwhile, automatic tumor segmentation on liver normally suffers from significant variety of appearance in size, shape, location, intensity, textures, as well as the number of occurrences. Although researchers have developed various methods to conquer these challenges [3], [4], [5], interactive approaches are still the only way to achieve acceptable tumor segmentation.

In this paper, we present a fully automatic framework based on deep fully convolutional-deconvolutional neural networks (CDNN) [6], [7], [8] for liver and liver tumor segmentation on contrast-enhanced abdominal CT images. Similar to [9], our framework is hierarchical and includes three steps. In the first step, a simple CDNN model is trained to obtain a quick but coarse segmentation of the liver on the entire 3D CT volume; then another CDNN is applied to the liver region for fine liver segmentation; finally, the segmented liver region is enhanced by histogram equalization and serves as an additional input to the third CDNN for tumor segmentation. Instead of developing sophisticated pre- and post-processing methods and hand-crafted features, we focus on designing appropriate network architecture and efficient learning strategies such that our framework can handle images under various acquisition conditions.

II. DATASET AND PREPROCESSING

Only LiTS challenge datasets were used for model training and validation. The LiTS datasets consist of 200 contrast-enhanced abdominal CT scans provided by various clinical sites around the world, in which 130 cases were used for training and the rest 70 for testing. The datasets have significant variations in image quality, spatial resolution and field-of-view, with in-plane resolution ranging from $0.6 \times 0.6$ to $1.0 \times 1.0$ mm and slice thickness from $0.45$ to $6.0$ mm. Each axial slice has identical size of $512 \times 512$, but the number of slices in each scan varies from 42 to 1026.

As for pre-processing, we simply truncated the voxel values of all CT scans to the range of [-100, 400] HU to eliminate the irrelevant image information. While a comprehensive 3D contextual information could potentially improve the segmentation performance, due to the limited hardware resource, it is infeasible to perform a fully 3D CDNN on the volumetric CT scans in our experimental environment. Thus, our CDNN model is based on 2D slice and the CT volume is processed
slice-by-slice, with the two most adjacent slices concatenated as additional input channels to the CDNN model. Different resampling strategies were applied at different hierarchical levels and will be described below.

III. METHOD

A. CDNN model

Our CDNN model [8] belongs to the category of fully convolutional network (FCN) that extends the convolution process across the entire image and predicts the segmentation mask as a whole. This model performs a pixel-wise classification and essentially serves as a filter that projects the 2D CT slice to a map where each element represents the probability that the corresponding input pixel belongs to liver (or tumor). This model consists two pathways, in which contextual information is aggregated via convolution and pooling in the convolutional path and full image resolution is recovered via deconvolution and up-sampling in the deconvolutional path. In this way, the CDNN model can take both global information and fine details into account for image segmentation.

We fix the stride as 1 and use Rectified Linear Units (ReLUs) [10] as the activation function for each convolutional/deconvolutional layer. For output layer, we use sigmoid as the activation function. Batch normalization is added to the output of every convolutional/deconvolutional layer to reduce the internal covariate shift [11].

We employ a loss function based on Jaccard distance proposed in [8] in this study:

\[
L_{d_j} = 1 - \frac{\sum_{i,j} (t_{ij}p_{ij})}{\sum_{i,j} t_{ij}^2 + \sum_{i,j} p_{ij}^2 - \sum_{i,j} (t_{ij}p_{ij})},
\]

where \( t_{ij} \) and \( p_{ij} \) are target and the output of pixel \((i, j)\), respectively. As compared to cross entropy used in the previous work [9], [12], the proposed loss function is directly related to image segmentation task because Jaccard index is a commonly used metric to assess medical imaging segmentation. Meanwhile, this loss function is well adapted to the problems with high imbalance between foreground and background classes as it does not require any class re-balancing. We trained the network using Adam optimization [13] to adjust the learning rate based on the first and the second-order moments of the gradient at each iteration. The initial learning rate was set as 0.003.

In order to reduce overfitting, we added two dropout layers with \( p = 0.5 \) - one at the end of convolutional path and the other right before the last deconvolutional layer. We also employed two types of image augmentations to further improve the robustness of the proposed model under a wide variety of image acquisition conditions. One consists of a series of geometric transformations, including randomly flipping, shifting, rotating and scaling. The other type focuses on randomly normalizing the contrast of each input channels in the training image slices. Note that these augmentations only require little extra computation, so the transformed images are generated from the original images for every mini-batch within each iteration.

B. Liver localization

This step aims to locate the liver region by performing a fast but coarse liver segmentation on the entire CT volume, thus we designed a relatively simple CDNN model for this task. This model, named CDNN-I, includes 19 layers with 230, 129 trainable parameters and its architectural details can be found in [8]. For each CT volume, the axial slice size was firstly reduced to \( 128 \times 128 \) by down-sampling and then the entire image volume was resampled with slice thickness of 3 mm. We found that not all the slices in a CT volume were needed in training this CDNN model, so only the slices with liver, as well as the 5 slices superior and inferior to the liver were included in the model training. For liver localization and segmentation, the liver and tumor labels were merged as a single liver label to provide the ground truth liver masks during model training.

During testing, the new CT images were pre-processed following the same procedure as training data preparation, then the trained CDNN-I was applied to each slice of the entire CT volume. Once all slices were segmented, a threshold of 0.5 was applied to the output of CDNN and a 3D connect-component labeling was performed. The largest connected component was selected as the initial liver region.

C. Liver segmentation

An accurate liver localization enables us to perform a fine liver segmentation with more advanced CDNN model while reducing computational time. Specifically, we firstly resampled the original image with slice thickness of 2 mm, then the bounding-box of liver was extracted and expanded by 10 voxels in \( x, y \) and \( z \) directions to create a liver volume of interest (VOI). The axial dimensions of VOI were further adjusted to \( 256 \times 256 \) either by down-sampling if any dimension was greater than 256, or by expanding in \( x \) and/or \( y \) direction otherwise. All slices in the VOI were used for model training.

The CDNN model used in the liver segmentation (named CDNN-II) includes 29 layers with about \( 5M \) trainable parameters. As compared to CDNN-I, the size of local receptive field (LRF), or filter size, is reduced in CDNN-II such that the network can go deeper, i.e. more number of layers, which allows applying more non-linearities and being less prone to overfitting [14]. Meanwhile, the number of feature channels is doubled in each layer. Please refer to [15] for more details.

During testing, liver VOI was extracted based on the initial liver mask obtained in the liver localization step, then the trained CDNN-II was applied to each slice in the VOI to yield a 3D probability map of liver. We used the same post-processing as liver localization to determine the final liver mask.

D. Tumor segmentation

The VOI extraction in tumor segmentation was similar to that in liver segmentation, except that the original image
resolution was used to avoid potentially missing small lesions due to image blurring from resampling. Instead of using all the slices in the VOI, we only collected those slices with tumor as training data so as to focus the training on the liver lesions and reduce training time. Besides the original image intensity, a 3D regional histogram equalization was performed to enhance the contrast between tumors and surrounding liver tissues, in which only those voxels within the 3D liver mask were considered in constructing intensity histogram. The enhanced image served as an additional input channel to another CDNN-II model for tumor segmentation. We found this additional input channel could further boost tumor segmentation performance.

During testing, liver VOI was extracted based on the liver mask from the liver segmentation step. A threshold of 0.5 was applied to the output of CDNN-II model and liver tumors were determined as all tumor voxels within the liver mask.

E. Implementation

Our CDNN models were implemented with Python based on Theano [16] and Lasagne2 packages. The experiments were conducted using a single Nvidia GTX 1060 GPU with 1280 cores and 6GB memory.

We used five-fold cross validation to evaluate the performance of our models on the challenge training datasets. The total number of epochs was set as 200 for each fold. When applying the trained models on the challenge testing datasets, a bagging-type ensemble strategy was implemented to combine the outputs of six models to further improve the segmentation performance [8].

An epoch in training CDNN-I model for liver localization took about 70 seconds, but the average time per epoch became 610 seconds and 500 seconds when training CDNN-II models for liver segmentation and tumor segmentation, respectively. This increase was primarily due to larger slice size and more complicated CDNN models. Applying the entire segmentation framework on a new test case was, however, very efficient, taking about 33 seconds on average (8, 8 and 17 s for liver localization, liver segmentation and tumor segmentation, respectively).

IV. Results and Discussion

We applied the trained models to the 70 LiTS challenge test cases (team: deepX). Based on the results from the challenge organizers, our method achieved an average dice similarity coefficient (DSC) of 0.963 for liver segmentation, a DSC of 0.657 for tumor segmentation, and a root mean square error (RMSE) of 0.017 for tumor burden estimation, which ranked our method in the first, fifth and third place, respectively. The complete evaluation results are shown in Table I-III.

To summarize our work, we develop a fully automatic framework for liver and its tumor segmentation on contrast-enhanced abdominal CT scans based on three steps: liver localization by a simple CDNN model (CDNN-I), liver fine segmentation by a deeper CDNN model with doubled feature channels in each layer (CDNN-II), and tumor segmentation by CDNN-II model with enhanced liver region as additional input feature. Our CDNN models are fully trained in an end-to-end fashion with minimum pre- and post-processing efforts.

While sharing some similarities with previous work such as U-Net [12] and Cascaded-FCN [9], our CDNN model is different from them in the following aspects: 1) The loss function used in CDNN model is based on Jaccard distance that is directly related to image segmentation task while eliminating the need of sample re-weighting: 2) Instead of recovering image details by long skip connections as in U-Net, the CDNN model constructs a deconvolutional path where deconvolution is employed to densify the coarse activation map obtained from up-sampling. In this way, feature map concatenation and cropping are not needed.

Due to the limited hardware resource, training a complex CDNN model is very time consuming and we had to restrict the total number of epochs to 200 in order to catch the deadline of LiTS challenge submission. While upgrading hardware is clearly a way to speed up the model training, we plan to improve our network architectures and learning strategies in our future work such that the models can be trained in a more effective and efficient way. Other post-processing methods, such as level sets [17] and conditional random field (CRF) [18], can also be potentially integrated into our model to further improve the segmentation performance.

| TABLE I | LIVER SEGMENTATION RESULTS (DEEPX) ON LITS TESTING CASES |
|---------------------------------|-----------------|-----------|-----------|-----------|-----------|
| Dice / case | Dice global | VOE | RVD | ASSD | MSD | RMSD |
| 0.9630 | 0.9570 | 0.071 | -0.010 | 1.104 | 23.847 | 2.303 |

| TABLE II | TUMOR SEGMENTATION RESULTS (DEEPX) ON LITS TESTING CASES |
|---------------------------------|-----------------|-----------|-----------|-----------|-----------|
| Dice / case | Dice global | VOE | RVD | ASSD | MSD | RMSD |
| 0.6570 | 0.8200 | 0.378 | 0.288 | 1.151 | 6.209 | 1.078 |

| TABLE III | TUMOR BURDEN RESULTS (DEEPX) ON LITS TESTING CASES |
|---------------------------------|-----------|-----------|
| RMSE | Max Error |
| 0.0170 | 0.0490 |

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