

MICCAI, KiTS19 Challenge

Automatic segmentation of kidney and kidney tumors using the cascaded dense network combined with cLSTM in CT scan

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Abstract

In this study, we develop the cascaded deep neural network model for automatic segmentation of the kidney and kidney tumors in CT scans. We used the fully dense network (to extract inner-slice image features) combined with bi-cLSTM (to extract inter-slice image features) for segmentation of kidney and kidney tumors. The whole CT scan is preprocessing for resizing (256*256) and intensity normalization (clipping between -600 and 400 and then normalizing between 0 and 1), and then entered into 1st neural network (growth factor = 8, and the consecutive slices = 3) for segmentation of kidney. And the output of 1st network is resized into 96*96, and entered into 2nd neural network, which is the same architecture of 1st network excepting growth factor = 16, and the consecutive slices = 5. Our cascaded deep neural network showed the dice scores of 0.932 (train), and 0.884 (validation) for segmentation of kidney and the dice scores of 0.845 (train), and 0.696 (validation) for segmentation of kidney tumors.

1. Introduction

The goal of this competition is to automatically segment kidney and kidney tumors in the contrast-enhanced CT scan. To segment kidney and kidney tumors, we use the cascaded deep neural network model for the segmentation of kidney and kidney tumors. The preprocessing steps and deep learning model used in this challenge are explained in detail in section 2. In section 3, we explain our experimental setting and preliminary results for deep learning.

2. Model description

2.1 Preprocessing

In our cascaded deep learning model, the whole CT scan is needed as input data for segmentation of kidney and then the CT scan within the segmented kidney region is need as input data for segmentation of kidney tumors. For preprocessing, the whole CT scan is clipped between -600 and

400 values in CT scans and then the clipped CT values are normalized into between 0 and 1. For segmentation of kidney, the CT scan is resized into 256 x 256 image size, and for segmentation of kidney tumors, the output from 1st deep learning model (the segmented kidney from 1st deep learning model) is resized into 96 x 96 image size.

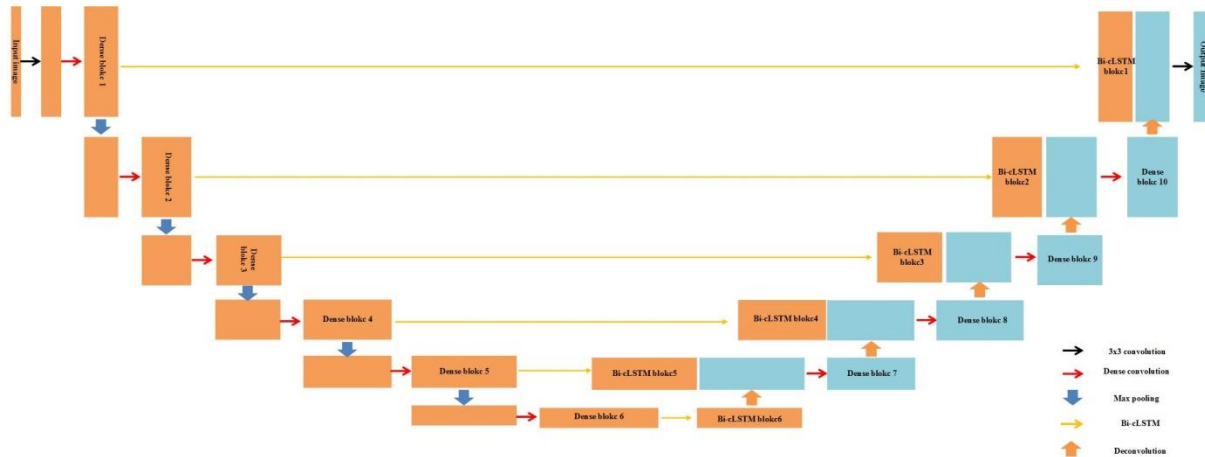


Figure 1 Deep learning model for segmentation

2.2 CNN and convolutional LSTM for segmentation of kidney and kidney tumors

Our basic model is based on Tiramisu model (fully convolutional dense network) combined with cLSTM for segmentation of kidney and kidney tumors as shown in Figure 1. We use same architecture for segmentation of kidney and kidney tumors excepting growth factor for dense network and the number of consecutive slices for bi-cLSTM. The encoding and decoding architecture is composed of dense blocks, which is similar to the Tiramisu architecture. But, in encoding part, the input of image (batch size, width, height, slice) is converted into the image (batch size * slice, width, height, 1) for extracting inner-slice image feature. Before skip connection, bi-cLSTM block was performed on the reformed image features (batch size, slice, width, height, channel) for extracting inter-slice image features. In decoding part, we performed convolution on the combined inner- and inter-slice image features for segmentation.

2.3 Postprocessing

We performed connected component analysis for segmentation of kidney (# of voxels > 5,000). We did not perform connected component analysis for segmentation of kidney tumors.

3. Experimental setting and results

We use 168 CT scans for training, and 42 scans for validation. The batch size for segmentation of kidney is 12, and that for segmentation of kidney tumors is 6. The learning rate is 0.0001 for starting train, and then is reduced half of the initial learning rate for every 50 epochs. The totals 300 epochs

are running during training. The growth factor is 8 for segmentation of kidney, and is 16 for segmentation of kidney tumors. We used bi-cLSTM for decoding of our deep learning model for 3 consecutive slices for segmentation of kidney and 5 consecutive slices for segmentation of kidney tumors. At last, we performed data augmentation (rotate, flip up and down, flip left and right, and scale) during training. For segmentation of kidney, training and validation dice scores are 0.932, and 0.884, and for segmentation of kidney tumors, training and validation dice scores are 0.845, and 0.696, respectively.