Local-imbalance-based and Centerline-distance Weight Dice-loss for Airway Segmentation in CT

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Abstract. The most challenge part of airway segmentation in CT is that the segmentation of very small airways. Because of the imbalance of pixels between small airways and big ones, the CNN-based methods always ignore the performance of small airways segmentation. In the mean time, with a random crop on the whole CT volume, the probability of cropping small airways is also small. So we choose to combine two existed weight dice losses for airway segmentation, and we also oversample the small airways in the training stage.

1 Method

1.1 Local Imbalance Based Weight Dice Loss

As mentioned in [1], it is important to adjust the gradient according to the size of different sizes of branches. And the sizes of branches can be measured by the local class imbalance between foreground and background, as local foreground rate:

$$FR_p = \frac{1}{N} \sum_{x_i \in B} y_i \tag{1}$$

where FR_p denotes the foreground rate of point p, B is a pre-defines neighborhood with N voxels centered at p, x_i denotes a voxel within B and y_i is the corresponding label. We adopt a cubic neighbothood with a size of $7 \times 7 \times 7$. We use the general union loss [2] as out weight dice loss, which is defined as:

$$Loss = 1 - \frac{\sum_{i=1}^{N} \omega_i p_i^{\beta} g_i}{\sum_{i=1}^{N} \omega_i (p_i + g_i)} \tag{2}$$

As we want the small airways to have bigger weights on loss, following [1]:

$$\omega_p = (1 - \lambda)(f_c(-log_{10} FR_p))^r + \lambda \tag{3}$$

where r means the root, $f_c = min(x, 1)$ is applied to prevent the value greater than 1. We choose $\lambda = 0.05$, $\beta = 2$ and randomly select r from 2 to 3.

1.2 Centerline Distance Based Weight Dice Loss

After focus on the small airways, we should also pay more attention on the pixels near to centerlines. It is because that the airway segmentation result should be one single connected domain, and to keep branches coherent, more attention is needed near the centerlines. As used in [2], the centerline distance based weight is defined as:

$$\omega_{d_i} = (1 - \frac{d_i}{d_{max}})^2 \tag{4}$$

Then, the whole weight of each pixels can be defined as:

$$\omega_i = \omega_p + \omega_{d_i} \tag{5}$$

1.3 Small Airway Oversampling

As random crop sampling is used in training stage, to make sure the weight dice loss plays an important role, the small airways need oversampling. We extract the centerlines of the training labels, and calculate the minimal distances of pixels on centerlines to the backgrounds, which defined as d_{center}. We identify a pixel on centerline as the small airway centerline pixel if $d_{center} < 2\ pixels$. We will oversample the crops around these pixels for a small airway oversampling.

2 Experiments Details

2.1 Overall Implementation

We use WingsNet [2] as our backbone. We first extract the lung area of each training samples, and use a circumscribed rectangle of the lung area as target volume. $128 \times 128 \times 128$ randomly crop is used to extract training sample crops. We also use two channels for each crops. One channel is the original volume, the other one is the volume with a window width $Hu = 750$ and window level $Hu = -250$. We set the batch size as 32, and learning rate as 0.0001. An AdamW optimizer is used for the training stage.

During training, the training stage is separated into 3 parts. For the first part, we training the networks with only dice loss and randomly crop sampling for 100 epochs. For the second part, we use $\omega_i = \omega_p$ as the weight, and use weight dice loss for training. We also use hard-mining sampling (50%), small airway sampling (25%) and random crop sampling (25%) together in the second part. the second part is trained for 5 epochs. The we use $\omega_i = \omega_p + \omega_{d_i}$ as weight, and continue training for 45 epochs.

During testing, a overlap crop sampling is used. We used a crop size of $128 \times 128 \times 128$ and overlap size of $64 \times 64 \times 64$. The overlap prediction results is the mean values of all overlap crops. We use a threshold of 0.5 for binary results. We also only keep a maximum connected domain of the prediction, and fill all the holes.

References

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