

# DNN Training Using Multiple GPUs for Medical Image Recognition

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Recently, CAD (Computer-Assisted Detection) that identifies the position of a lesion by analyzing a CT or MRI images has been introduced in the medical field. Moreover, CNN (Convolutional Neural Networks) has been studied for medical image segmentation by learning, and the accuracy of CAD has been drastically improved. On the other hand, training by a GPU time takes a long time and mini batch size is too small due to complicated neural network model. In this study, we aimed to improve the performance of training by large amount of GPUs with good accuracy for the segmentation task of using U-Net model.

## U-NET MODEL

As a CNN model, we use the U-Net model shown in Figure 1[1]. U-net is a model that extracts local features of the entire image by performing convolution processing and pooling processing(Encode Process), and restores the overall location information by using convolution processing and amplification processing(Decode Process). In this study, we focus on the lung nodule detection by applying U-net model to chest CT images(Figure 2[2]).

In fact, the U-Net model has many parameters such as image size of 3D data, number of 3D data samples, U-net layer depth, filter size, kernel size, batch size, and initial learning rate. Therefore, we need to determine these parameters dynamically by parameter search.

## IMPLEMENTATION OF U-NET BY CHAINER

Chainer is a Python-based, standalone open source framework for deep learning models and ChainerMN(one of Chainer's additional packages) enables machine learning using multiple GPUs with only a few changes to machine learning code written on the Chainer base. In this research, we used ChainerMN to perform data parallel using multiple GPUs.

In this research, the convolution processing executed twice in the Encode process (Left of Figure 1) is defined as one model (UNetEncodeModel), and the Encode process is realized defining the model (EncodeModel) that performs pooling processing for multiple UNetEncodeModel separately. Similarly, for the Decode process(Right of Figure 1), the U-Net model is implemented by defining the convolution process as one model (UNetDecodeModel) and defining the upsampling process as another model(DecodeModel).

## PRELIMINARY EVALUATION

For preliminary evaluation, we use Reedbush-H and -L system as GPU cluster operated by Information Technology Center, the University of Tokyo. In this case, a Dice coefficient  $DSC(A, B) = \frac{2|A \cap B|}{|A| + |B|}$  is used as the evaluation function and we applied the parameters

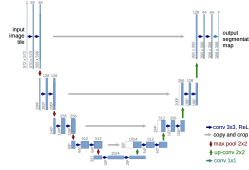


Figure 1: U-net model[1]

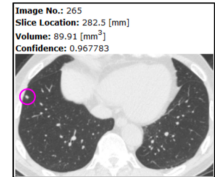


Figure 2: Chest CT images[2]

Table 1: Specification of Reedbush-H (RB-H) and -L (RB-L)

	RB-H	RB-L
CPU	Intel Xeon E5-2695v4 (Broadwell-EP) 2 socket (36 core) 2.4 GHz	
Memory	256 GB	
GPU	NVIDIA Tesla P100 x2	NVIDIA Tesla P100 x4
Interconnect	InfiniBand EDR 100 Gbps	

that maximize validation Dice Score of 1 GPU to multiple GPUs. When using 1 GPU, the same Dice Score of validation as the previous research using Keras[2] was obtained, and when using 2 GPU to 64 GPU, the execution time was inversely proportional to the number of GPUs. On the other hand, with 2 GPU to 8 GPU, the same Dice Score of validation as with 1GPU, 16 to 32 GPU, about 95% of Score, and 64 GPU, about 85% of Score were obtained.

## CONCLUSION AND FUTURE WORK

In this study, we applied the best parameters of 1 GPU to multiple GPUs and evaluated their performance. As the future work, we would like to study the Bayesian optimization when using multiple GPUs and improve the accuracy of lung nodules.

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