Semi-Supervised 3D U-Net Learning Based on Meta Pseudo Labels

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Abstract. Deep learning models have demonstrated promising performance for segmenting medical images and are significantly dependent on a huge amount of well-annotated data. However, it is difficult to get a large amount of data, particularly in clinical practices. Likewise, high-performance deep learning models have an enormous model size, restricting their use in actual applications. In order to reduce the burden of both expensive annotations and computational expenses, we design a semi-supervised knowledge-based method which is on top of 3D U-Net and Meta Pseudo Labels. We validate our trained model on 20 cases of validation set on FLARE2022 grand challenge dataset and achieve 86.61% of DSC.

Keywords: Meta Pseudo Labels · Semi-Supervise · One-step gradient

1 Introduction

Abdomen organ segmentation is essential and plays an important role in artificial intelligence-based clinical diagnosis and treatment such as organ quantification and surgical planning etc [1]. In order to accelerate such research and developments, Fast and Low-resource semi-supervised Abdominal oRgan sEgmentation in CT (FLARE 2022) challenge has been introduced, that uses semi-supervised settings and focuses on the usage of unlabeled data. Though it is not easy to segment multiple organs automatically. For instance, multiple organs may vary in shape and size, and thus, organ lesions lead to abnormal segmentation. Similalrly, multi-center data with different scan ranges, and high computing resource

are required. However, it is also not easy to collect large amount of annotated data. Thus, semi-supervised learning techniques are efficient to generate labeled data from unlabeled data. Therefore, we propose a 3D U-Net Meta pseduo labels (MPL) method [2], which is a semi-supervise learning approach for segmenting multiple abdominal organs. The proposed method has the following features.

1. Using the MPL semi-supervise method with 3D U-Net[3] can perform automatic segmentation of multiple organs in abnormal CTs.
2. Combine the nnU-Net[4] framework, a surpervise learning framework, with the semi-supervise learning.

2   Method

We proposed a pair of networks entails a teacher and student network based on Meta Pseudo Labels. In the proposed network, teacher module generates pseudo labels from unlabeled data. Further, the pseudo labels and labeled images are utillized for training the student module. The teacher network receives feedback from the student network regarding their performance for the improvement of their predictions. The schematic diagram of teacher-student network is depicted in Fig. 1.

Fig. 1. The teacher-student semi-supervised network. When training the models, teacher model would inference the unlabeled data and use the pseudo-labeled data from teacher model to train the student model. The student model provides the feedback to teacher model.

2.1   Pre-processing

Our preprocessing approach is similar to that of nn U-Net . In the preprocessing step, the computed tomography (CT) images were left uncropped. However, for anisotropic images (maximum axis spacing > 3), in-plane resampling is performed with third order spline whereas out of plane interpolation is performed

with nearest neighbor interpolation. Furthermore, we use 0.5 and 99.5 percentiles of the foreground voxels for clipping as well as the global foreground mean (a standard deviation) for normalization on all images.

2.2 Proposed method

One-step gradient. For the proposed method we formulate our model as follows. Where T and S refer to teacher and student networks, respectively, whereas w_T and w_s refer to their parameters. Let (x_l, y_l) is a batch of images and their labels, and define x_u as a batch of unlabeled images. p denotes the soft prediction and L for the loss function. In our method, the loss function is cross-entropy loss and dice loss.

Algorithm 1 One-step gradient on MPL

1: Input: Labeled data x_l, y_l and unlabeled data x_u
2: Initialization:$\omega_t^{(0)}, \omega_s^{(0)}, t \leftarrow 0$
3: **repeat**
4:    Sample a labeled example x_l, y_l and an unlabeled example x_u
5:    Put x_l, x_u into teacher network get soft prediction p_l^T, p_u^T:

$$p_l^T = T(x_l; \omega_T^{(t)}), p_u^T = T(x_u; \omega_T^{(t)})$$

6:    Generate pseudo label $\hat{y}_u : \hat{y}_u = Argmax(Softmax(p_u^T))$
7:    Feed x_l, x_u into student network get soft prediction p_l^S, p_u^S :

$$p_l^S = S(x_l; \omega_S^{(t)}), p_u^S = S(x_u; \omega_S^{(t)})$$

8:    Update the student using the pseudo label $\hat{y}_u$:

$$\omega_S^{(t+1)} = \omega_S^{(t)} - \alpha_s \nabla_{\omega s} L(\hat{y}_u, p_u^S)$$

9:    Feed x_l into student network get soft prediction: $p_l^{S'} = S(x_l; \omega_S^{(t+1)})$
10:   Compute the teacher's gradient $g_T^{(t)}$ from student's feedback:

$$g_T^{(t)} = \nabla_{\omega_T}(L(\hat{y}_u, p_l^{S'}) - L(\hat{y}_u, p_l^S) \cdot L(p_u^T, \hat{y}_u))$$

11:   Compute the teacher's gradient on labeled data:

$$g_{T,supervised}^{(t)} = \nabla_{\omega_T} L(p_l^T, y_l)$$

12:   Update the teacher: $\omega_T^{(t+1)} = \omega_T^{(t)} - \alpha_T(g_T^{(t)} + g_{(T,supervised)}^{(t)})$
13:   Update epoch: $t \leftarrow t + 1$
14: **until** $t > N - 1$
Output: Teacher model ω_T^{N-1}, Student model ω_S^{N-1}

The Backbone Network. Our backbone network utilizes 3D U-Net, which has four upsampling and downsampling layers. Each layer is composed of 3D convolutions, ReLU activations and batch normalization. The first level of the 3D U-Net extracts 32 feature maps and each downsampling process maximizes the extracted feature maps up to 512. The 3D U-Net backbone network is depecited in Fig. 2.

Fig. 2. The 3D U-Net network architecture.

Proposed semi-supervised method. Our semi-supervised learning method is based on MPL and 3D U-Net as shown in Fig. 3 and their symbolic representation described in One-step gradient(2.2), which having the detail of the method. In the proposed method, the teacher's model (M_t) is trained only by the labeled data which generates the pseudo data. After that, student's model (M_s) uses the pseudo data and unlabel data to train student model and uses the pseduo labels again by utilizing the gradient descent and update Ms to a new student model i.e., M_{s+1}. Finally, using the output from the M_s and M_{s+1} to calculate the student's model feedback, and utilized that for the updation of teacher model.

3   Experiments

3.1   Dataset and evaluation measures

The FLARE 2022 dataset is curated from more than 20 medical groups under the license permission including MSD [5], KiTS [6,7], AbdomenCT-1K [8], and TCIA [9]. The training set includes 50 labeled CT scans with pancreas disease and 2000 unlabeled CT scans with liver, kidney, spleen, or pancreas diseases. The validation set includes 50 CT scans with liver, kidney, spleen, or pancreas

Fig. 3. Our proposed semi-supervised method based on the Meta pseudo labels where the backbone model is a 3D U-Net. x denotes the input, y denotes the label or the output, M represents the model, and p denotes the softmax output.

diseases. The testing set includes 200 CT scans where 100 cases have liver, kidney, spleen, or pancreas diseases and the other 100 cases have uterine corpus endometrial, urothelial bladder, stomach, sarcomas, or ovarian diseases. All the CT scans only have image information and the center information is not available. The evaluation measures consist of two accuracy measures i.e., Dice Similarity Coefficient (DSC) and Normalized Surface Dice (NSD), and three running efficiency measures: running time, area under GPU memory-time curve (lower than 2048 MB is preferred), and area under CPU utilization-time curve. All measures are used to compute the ranking score.

3.2   Implementation details

Our implementation details with respect to configured environments and requirements are provided in Table.1. Training protocls for our model are provided in Table.2.

4   Results and discussions

4.1   Quantitative results on validation set

For ablation study to analyze the effect of unlabeled data and semi-supervised learning, the validation set we used was the official data of 20 abdominal CT

Table 1. Development environments and requirements.

Windows/Ubuntu version	Ubuntu 20.04.1 LTS
CPU	AMD EPYC 7742 64-Core Processor
RAM	1.8TB
GPU (number and type)	NVIDIA A100 40G($\times$8)
CUDA version	11.4
Programming language	Python 3.8
Deep learning framework	Pytorch (1.10)

Table 2. Training and Inference protocols.

Data augmentation	scaling, rotation, random crop, mirror
Network initialization	"He" normal initialization
Batch size	8
Patch size	$32\times64\times160\times160$
Total epochs	1000
Optimizer	SGD with nesterov momentum(μ=0.99)
Weight decay	3e-5
Initial learning rate (lr)	0.01
Lr scheduler	ReduceLROnPlateau
Training time	5 days
Loss function	Dice + Cross Entropy Loss

cases. For labeled data, 50 cases of data were used to train a 3D U-Net model as the baseline segmentation model. For unlabeled data, only 1000 cases of data were used to train the semi-supervised data model, and the MPL student's model was used to segment organs. The ablation study results are provided in the Table 3, containing the Dice of MPL and baseline method for 13 organs and mean Dice for all classes. Baseline is the 3D U-Net method using all labeled data belonging to supervised learning and MPL is the 3D U-Net method based on proposed MPL, belonging to semi-supervised-based learning. The results show that MPL is better than baseline method.

4.2 Qualitative results

Fig. 4 shows successful segmentation of 4 cases including case0002 and case0006 which are easy cases and the two other cases are challenging. From the results we can see that the proposed 3D U-Net MPL method can perform well than baseline method.

4.3 Segmentation efficiency results

According to official information, If the GPU memory is less than 2GB when segmenting the organs, the participants would get the prefect score on the AUC_GPU_Time metric, but our model actually used GPU memory which is

Table 3. Quantitative results on 20 cases of validation set.

Method	Baseline(Dice)	Baseline+MPL(Dice)
Liver	0.9651	0.9752
RK	0.8643	0.8840
Spleen	0.8580	0.9390
Pancreas	0.8530	0.8777
Aorta	0.9510	0.9624
IVC	0.8777	0.8909
RAG	0.8083	0.8076
LAG	0.8100	0.8066
Gallbladder	0.7143	0.7540
Esophagus	0.8794	0.8781
Stomach	0.8633	0.8824
Duodenum	0.7220	0.7520
LK	0.8712	0.8499
mDSC	0.8491	0.8661

Fig. 4. Qualitative results on challenging and easy cases. The case2 and case6 are the easy inference cases , the case33 and case38 are the challenging cases.

nearly with 7GB memory. So it indicated that the nnU-Net framework has the defect of too high GPU memory and leads to a relatively large AUC_GPU_Time.

The main reason is that model trained by nnU-Net framework is too large, which leads to a long running time and high GPU occupancy.

5 Conclusion

In this paper, we proposed a 3D U-Net semi-supervised approach based on Meta Pseudo Labels (MPL) for training the neural networks with limited labeled data and a large number of unlabeled images for medical image segmentation. We trained baseline method using labeled data and 3D U-Net MPL on labeled data and unlabeled data. DSC are used to assess the accuracy. Three different running computational efficiency measures were also computed which proved the effectiveness of our semi-supervised approach experimentally compared to baseline method.

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References

1. Eli Gibson, Francesco Giganti, Yipeng Hu, Ester Bonmati, Steve Bandula, Kurinchi Gurusamy, Brian Davidson, Stephen P Pereira, Matthew J Clarkson, and Dean C Barratt. Automatic multi-organ segmentation on abdominal ct with dense v-networks. *IEEE transactions on medical imaging*, 37(8):1822–1834, 2018. 1
2. Hieu Pham, Zihang Dai, Qizhe Xie, and Quoc V Le. Meta pseudo labels. In *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*, pages 11557–11568, 2021. 2
3. Olaf Ronneberger, Philipp Fischer, and Thomas Brox. U-net: Convolutional networks for biomedical image segmentation. Number: arXiv:1505.04597. 2
4. Fabian Isensee, Jens Petersen, Andre Klein, David Zimmerer, Paul F Jaeger, Simon Kohl, Jakob Wasserthal, Gregor Koehler, Tobias Norajitra, Sebastian Wirkert, et al. nnu-net: Self-adapting framework for u-net-based medical image segmentation. *arXiv preprint arXiv:1809.10486*, 2018. 2
5. Amber L Simpson, Michela Antonelli, Spyridon Bakas, Michel Bilello, Keyvan Farahani, Bram Van Ginneken, Annette Kopp-Schneider, Bennett A Landman, Geert Litjens, Bjoern Menze, et al. A large annotated medical image dataset for the development and evaluation of segmentation algorithms. *arXiv preprint arXiv:1902.09063*, 2019. 4
6. Nicholas Heller, Fabian Isensee, Klaus H Maier-Hein, Xiaoshuai Hou, Chunmei Xie, Fengyi Li, Yang Nan, Guangrui Mu, Zhiyong Lin, Miofei Han, et al. The state of the art in kidney and kidney tumor segmentation in contrast-enhanced ct imaging: Results of the kits19 challenge. *Medical Image Analysis*, 67:101821, 2021. 4

7. Nicholas Heller, Sean McSweeney, Matthew Thomas Peterson, Sarah Peterson, Jack Rickman, Bethany Stai, Resha Tejpaul, Makinna Oestreich, Paul Blake, Joel Rosenberg, et al. An international challenge to use artificial intelligence to define the state-of-the-art in kidney and kidney tumor segmentation in ct imaging. *American Society of Clinical Oncology*, 38(6):626–626, 2020. 4

8. Jun Ma, Yao Zhang, Song Gu, Cheng Zhu, Cheng Ge, Yichi Zhang, Xingle An, Congcong Wang, Qiyuan Wang, Xin Liu, Shucheng Cao, Qi Zhang, Shangqing Liu, Yunpeng Wang, Yuhui Li, Jian He, and Xiaoping Yang. Abdomenct-1k: Is abdominal organ segmentation a solved problem? *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 2021. 4

9. Kenneth Clark, Bruce Vendt, Kirk Smith, John Freymann, Justin Kirby, Paul Koppel, Stephen Moore, Stanley Phillips, David Maffitt, Michael Pringle, et al. The cancer imaging archive (tcia): maintaining and operating a public information repository. *Journal of Digital Imaging*, 26(6):1045–1057, 2013. 4