
Paper Title

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Abstract

Graph Neural Networks (GNN) is an emerging field for learning on non-Euclidean data. Recently, there has been great interest in designing GNN that scales to large graphs. Most existing techniques use “graph sampling” or “layer-wise sampling” technique to reduce training time.

1 Experiments

1.1 Baseline and implementation

We used a server equipped with an Intel Core i9-9980XE CPU @ 3.00GHz with 64GB RAM and 12GB of RTX2080Ti GPU for our proposed networks training. The operating system of the sever is 64-bits Ubuntu 18.04. The structure of the network is implemented under the open source deep learning library Pytorch with VSCode implementation.

1.2 Dataset

For this study, we conduct our experiments on four differents segmentation tasks. Covering lesions/organs from most commonly used medical imaging modalities including microscopy, computed tomography (CT), and magnetic resonance imaging (MRI). Table 3 summarize those datasets in our study.

Table 1: Summaey Of Biomedical Image Segmentation Datasets Used In Our Experiments

Dataset	Image	Input Size	Modality	Provider
Cell	30	512×512	EM	ISBI 2012[1]
Liver	4,000	512×512	CT	MICCAI 2017 LiTS[3]
DSB2018	670	256×256	EM	Kaggle[2]
COVID19	1,800	630×630	CT	Web[10, 5]

Cell The datset is the segmentation of neuronal structures in electron microscopic recordings. The dataset is provided by the EM segmentation challenge[1] that is started at ISBI 2012. The data is a set of 30 images (512×512 pixels) from serial section transmission electron microscopy of the Drosophila first instar larva ventral nerve cord (VNC). Each image comes with a corresponding fully annotated ground truth segmentation map for cells (white) and membranes (black).

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Nuclei This dataset is a large number of segmented nuclei images[2] and is created for the Kaggle 2018 Data Science Bowl and consists of 670 segmented nuclei images (256×256 pixels) from different modalities (brightfield vs. fluorescence). We resized them to 512×512 for our experiments.

Liver Liver tumor Segmentation Challenge (LiTS)[3] contain 131 contrast-enhanced CT images provided by hospital around the world with 512×512 resolution. The ground truth segmentation provides two different labels: liver and lesion. For our experiments, we only consider liver as positive class and others as negative class.

COVID19 Dataset[10] includes whole volumes and includes, therefore, both positive and negative slices (373 out of the total of 829 slices have been evaluated by a radiologist as positive and segmented). Dataset[5] contains 20 CT scans of patients diagnosed with COVID-19 as well as segmentations of lungs and infections made by experts. These volumes are converted and normalized in a similar way as above, meanwhile we resize the data to 512×512 .

Lung Dataset[5] also contains 20 CT scans of patients as well as segmentations of lungs made by experts with 630×630 resolution. We converted and normalized in a similar way as above, meanwhile we resize the data to 512×512 .

1.3 Evaluation metrics

The experiments are implemented using the Pytorch framework. We use Adam optimizer[6] as our models' optimizer with a learning rate of 0.00001, batch size of 2. All of datasets are splitted into training set and validation set with the ratio of 8:2 using sklearn library. To numerically evaluate, we use five widely adopted metrics, *i.e.*, the Dice similarity coefficient(Dice.), F1 score., Sensitivity(Sen.), Iou. and hausdorff distance(Hd), the expressions of them are defined as follows:

$$\text{Sensitivity} = \frac{TP}{TP + FN} \quad (1)$$

$$\text{DSC}(G, S) = \frac{2|G \cap S|}{|G| + |S|} \quad (2)$$

$$\text{IOU}(G, S) = \frac{|G \cap S|}{|G| \cup |S|} \quad (3)$$

$$F_1 = 2 \cdot \frac{\text{precision} \cdot \text{recall}}{\text{precision} + \text{recall}} \quad (4)$$

$$h(G, S) = \max_{g \in G} \left\{ \min_{c \in C} \|g - c\| \right\} \quad (5)$$

1.4 Semantic Segmentation Results

For comparison, we use five original network FCN with 32s[7], U-Net[8], U-Net++[11], CE-Net[4] and U-Net with Attention Gate[9] to evaluate our proposed method.

Table 2: Comparison With Other Methods In Liver[3] Dataset

Dataset	Shape Loss	Dice.	F1 score.	Iou.	Sens.	Hd.
Our proposal	✓	0.9392	0.9392	0.8965	0.9261	3.8854
U-Net++	×	0.9351	0.9351	0.8781	0.9156	5.8218
Attention UNet	×	0.9346	0.9346	0.8776	0.9056	4.836
CENet	×	0.9315	0.9315	0.8721	0.9045	4.904
U-Net	×	0.9253	0.9253	0.8615	0.9106	6.6785
FCN32s	×	0.9065	0.9065	0.8300	0.9381	7.97

Table 3: Comparison With Other Methods In Lung[5] Dataset

Dataset	Shape Loss	Dice.	F1 score.	Iou.	Sens.	Hd.
Our proposal	✓	0.9392	0.9392	0.8965	0.9261	10.19714
UNet++	×	0.9351	0.9351	0.8781	0.9156	5.8218
Attention UNet	×	0.9346	0.9346	0.8776	0.9056	4.836
CENet	×	0.9315	0.9315	0.8721	0.9045	4.904
UNet	×	0.9253	0.9253	0.8615	0.9106	6.6785
FCN32s	×	0.9065	0.9065	0.8300	0.9381	7.97

2 Conclusion

Acknowledgments

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