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.

解决了什么问题?论文主要工作?效果如何?

1 Method

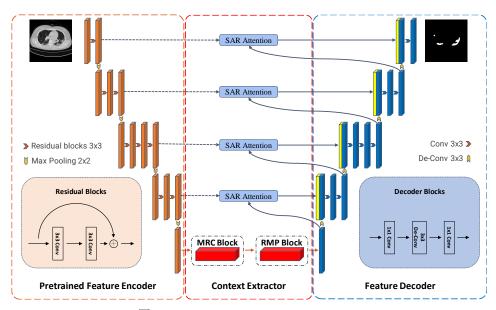


图 1: Illustration of our proposed network.

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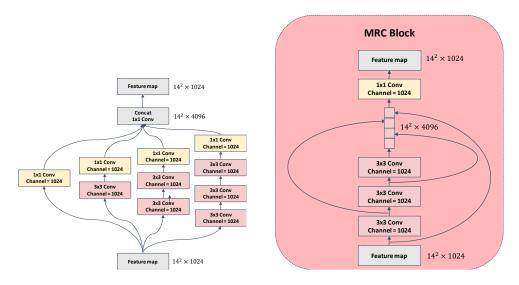


图 2: (1) is the illustration of DAC Block. (1) is the illustration of MRC Block.

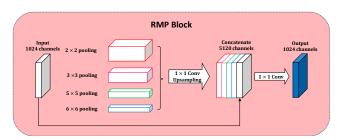


图 3: Illustration of RMP Block.

Backbone	Components	Params	Params size	
ResU-Net	SAR+DAC+RMP(CE-Net)	135,571,137	517.16	
ResU-Net	SAR+ASPP	92,573,377	353.14	
ResU-Net	SAR+MRC+RMP	94,669,505	361.14	

表 1: Memorize Cost Comparison With Different Methods In Bottleneck

2 Experiments

2.1 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.

2.2 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 2.2 summarize those datasets in our study.

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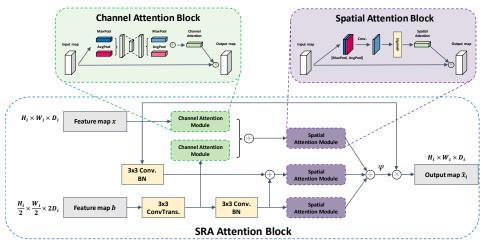


图 4: Illustration of SRA Attention Block.								
Dataset	Image	Input Size	Modality	Provider				
Cell	30	512×512	EM	ISBI 2012[1]				
Liver	4,000	512×512	CT	MICCAI 2017 LiTS[3]				
DSB2018	670	256×256	EM	Kaggle[2]				
COVID19	1,800	630×630	CT	Web[11, 6]				

表 2: Summaey Of Biomedical Image Segmentation Datasets Used In Our Experiments

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).

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[11] 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[6] 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 .

2.3 Evaluation metrics

The experiments are implemented using the Pytorch framework. We use Adam optimizer[7] 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:

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

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

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

$$F_1 = 2 \cdot \frac{\text{precision \cdot recall}}{\text{precision + recall}} \tag{4}$$

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

2.4 Medical image Segmentation Results

For comparsion, we use five original network FCN with 32s[8], U-Net[9], U-Net++[12], CE-Net[5] and U-Net with Attention Gate[10] to evaluate our proposaed method.

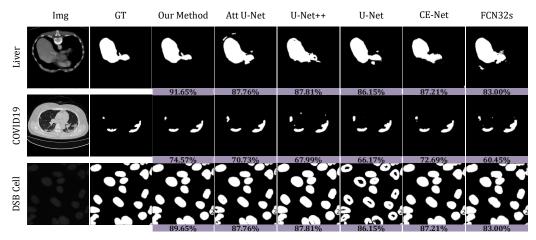


图 5: Medical image segmentation examples.

我们利用 U-Net, ResU-Net 作为 baseline,与我们提出的模型分别在 Cell, Liver, COVID19 三个数据集上进行对比,每次实验所使用的参数,训练集,验证集,测试集均相同。Segmentation results of cell segmentation are shown in tables 2.4,在 Dice. and F1 score 指数上相比于 CE-Net, U-Net++, U-Net with Attention Gate, U-Net and FCN32s 分别提升了 1.30%, 1.49%, 4.35%, 6.11% and 16.95%. 在 Iou. 指数上,分别提升了 2.05%, 2.27%, 6.08%, 7.30% and 19.70%. 在 Sens. 指数上分别提升了 9.80%, 6.53%, 7.39%, 11.81% and 15.36%. 在 Hd. 指数上分别降低了-0.4074, -0.9083, -0.7471, -0.8825 and -2.4968.

Methods	Shape Loss	Dice.	F1 score.	Iou.	Sens.	Hd.
Our proposal	\checkmark	0.8588	0.8588	0.7623	0.9296	4.6224
CENet	×	0.8458	0.8458	0.7418	0.8316	5.2098
UNet++	×	0.8439	0.8439	0.7396	0.8643	5.5307
Attention UNet	×	0.8153	0.8153	0.7015	0.8557	5.3695
UNet	×	0.7977	0.7977	0.6893	0.8115	5.5049
FCN32s	×	0.6895	0.6895	0.5653	0.7760	7.1192

表 3: Comparsion With Other Methods In Cell[2] Dataset

Segmentation results of cell segmentation are shown in table 2.4, 在 Dice. and F1 score 指数上相比于 CE-Net, U-Net++, U-Net with Attention Gate, U-Net and FCN32s 分别提升了 2.01%, 2.05%,

2.36%, 2.98% and 4.86%. 在 Iou. 指数上,分别提升了 3.84%, 3.89%, 4.44%, 5.50% and 8.65%. 在 Sens. 指数上分别提升了 2.33%, 3.33%, 3.44%, 2.83% and 0.08%. 在 Hd. 指数上分别降低了-1.9362, -0.9506, -1.0186, -2.7931 and -4.0846.

Methods	Shape Loss	Dice.	F1 score.	Iou.	Sens.	Hd.
Our proposal	\checkmark	0.9551	0.9551	0.9165	0.9389	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

表 4: Comparsion With Other Methods In Liver[3] Dataset

Segmentation results of cell segmentation are shown in table 2.4, 在 Dice. and F1 score 指数上相比于 CE-Net, U-Net++, U-Net with Attention Gate, U-Net and FCN32s 分别提升了 1.41%, 4.75%, 2.60%, 6.15% and 10.80%. 在 Iou. 指数上,分别提升了 1.67%, 6.58%, 3.84%, 8.40% and 14.12%. 在 Hd. 指数上分别降低了-0.4581, -0.7171, -0.5715, -0.9101 and -1.5514. 敏感度方面,通过观察 Figure 5我们可以发现,其在分割目标图像时更加保守(改)。

Methods	Shape Loss	Dice.	F1 score.	Iou.	Sens.	Hd.
Our proposal	\checkmark	0.8489	0.8489	0.7457	0.8570	4.313
CENet	×	0.8348	0.8348	0.7290	0.9359	4.7711
UNet++	×	0.8014	0.8014	0.6799	0.9426	5.0301
Attention UNet	×	0.8229	0.8229	0.7073	0.9435	4.8845
UNet	×	0.7874	0.7874	0.6617	0.9528	5.2231
FCN32s	×	0.7409	0.7409	0.6045	0.9935	5.8644

表 5: Comparsion With Other Methods In COVID19[6] Dataset

综上所述,我们的模型在三个数据集上均 consistently outperforms CE-Net and U-Net with Attention-Gate. Figure 5展示了我们在三个数据集上与其余 5 个模型的对比示例。COVID-19 · · · · · · · , Liver · · · · · · · · , Cell · · · · · · · 。

2.5 Ablation study

To justify the effectiveness of the pretrained U-Net[9], Res-UNet[4], MRC(multi residual convolution) block, RMP block and SAR(spatial channel and gateway) Attention block in our proposed method, we conduct the following ablation study using the COVID19 and Cell dataset as examples:

Methods	Loss	Dice.	F1 score.	Iou.	Sens.	Hd.
Our proposal	BCE	0.8076	0.8076	0.6874	0.8772	5.0112
Our proposal	BCE+DiceLoss	0.8375	0.8375	0.7282	0.8827	4.7241
Our proposal	Ours	0.8489	0.8489	0.7457	0.8570	4.4313

表 6: Comparsion With Other loss functions In COVID19[11] Dataset

Methods	Loss	Dice.	F1 score.	Iou.	Sens.	Hd.
U-Net	BCE	0.7874	0.7874	0.6617	0.9528	5.2231
ResU-Net	BCE	0.8105	0.8105	0.6923	0.9601	5.0248
ResU-Net + MRC + RMP	BCE	0.8185	0.8185	0.7030	0.9295	4.8931
ResU-Net + SAR	BCE	0.7988	0.7988	0.6846	0.7969	5.1522
ResU-Net+SAR+MRC+RMP	BCE	0.8076	0.8076	0.6874	0.8772	5.0112
ResU-Net+SAR+MRC+RMP	Ours	0.8489	0.8489	0.7457	0.8570	4.313

表 7: Ablation study for each component on COVID19 dataset

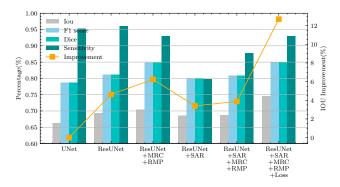
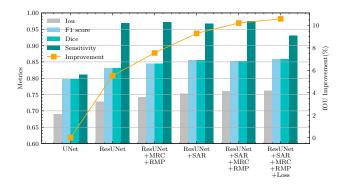


图 6: Metric results of COVID19 segmentation compared with different models.

Methods	Loss	Dice.	F1 score.	Iou.	Sens.	Hd.
U-Net	BCE	0.7977	0.7977	0.6893	0.8115	5.5049
ResU-Net	BCE	0.8314	0.8314	0.7274	0.9685	5.5861
ResU-Net + MRC + RMP	BCE	0.8448	0.8448	0.7414	0.9714	5.0647
ResU-Net + SAR	BCE	0.8545	0.8545	0.7534	0.9669	4.9601
ResU-Net+SAR+MRC+RMP	BCE	0.8525	0.8525	0.7598	0.9744	4.9210
ResU-Net+SAR+MRC+RMP	Ours	0.8588	0.8588	0.7623	0.9296	4.6224

表 8: Ablation study for each component on Cell dataset



 $\ensuremath{\mathbb{E}}$ 7: Metric results of Cell segmentation compared with different models.

3 Conclusion

Acknowledgments

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