

# 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 Method

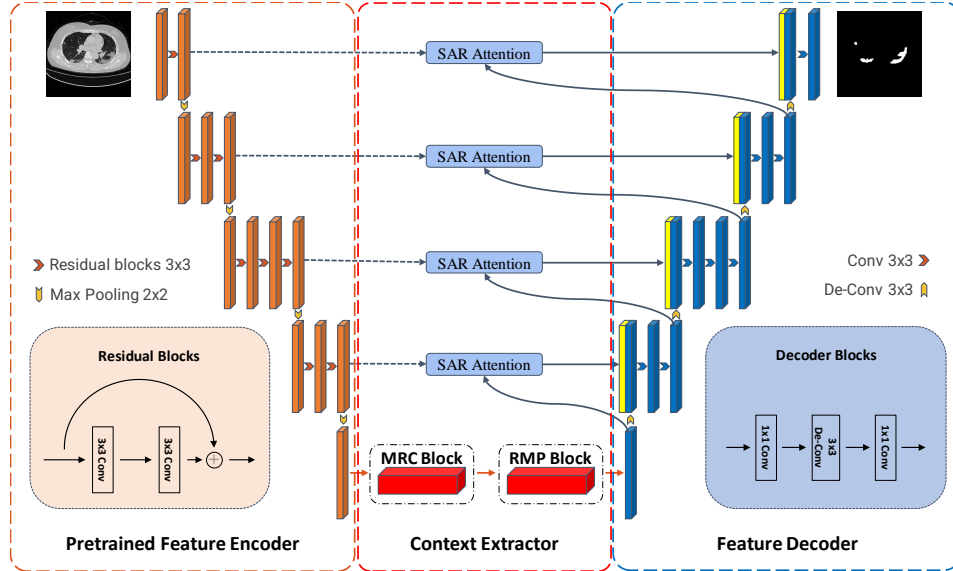


Figure 1: Illustration of our proposed network.

Table 1: Memorize Cost Comparison With Different Methods In Bottleneck

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

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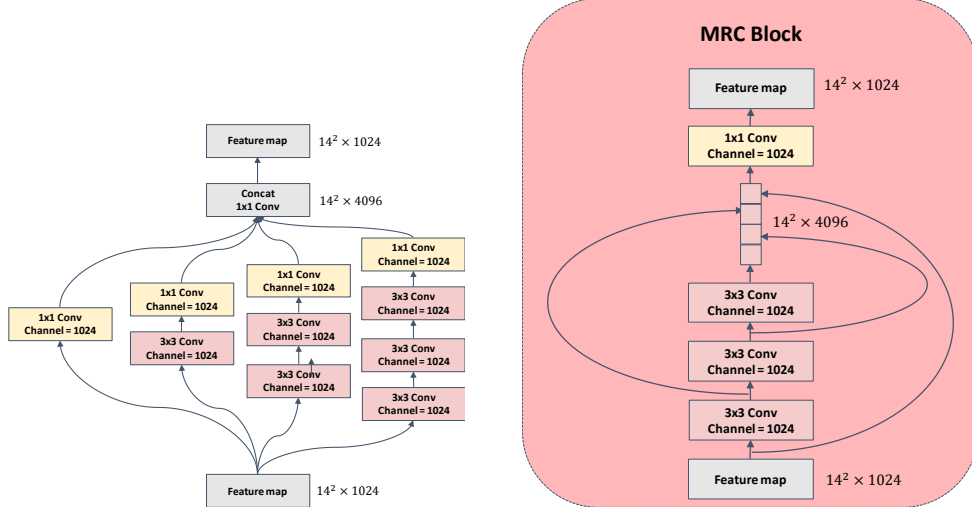


Figure 2: (1) is the illustration of DAC Block. (1) is the illustration of MRC Block.

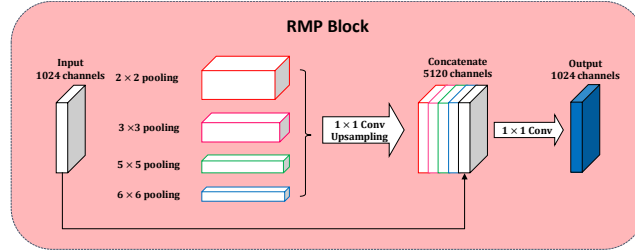


Figure 3: Illustration of RMP Block.

## 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 le-sions/organs from most commonly used medical imaging modalities including microscopy, com-puted tomography (CT), and magnetic resonance imaging (MRI). Table 2 summarize those datasets in our study.

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

Dataset	Image	Input Size	Modality	Provider
Cell	30	$512 \times 512$	EM	ISBI 2012[1]
Liver	4,000	$512 \times 512$	CT	MICCAI 2017 LiTS[3]
DSB2018	670	$256 \times 256$	EM	Kaggle[2]
COVID19	1,800	$630 \times 630$	CT	Web[11, 6]

**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 ( $512 \times 512$  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).

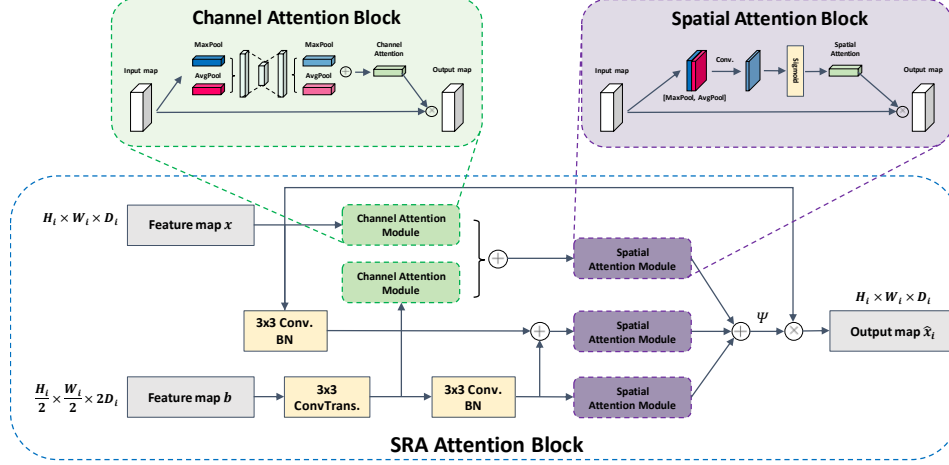


Figure 4: Illustration of SRA Attention Block.

**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 ( $256 \times 256$  pixels) from different modalities (brightfield vs. fluorescence). We resized them to  $512 \times 512$  for our experiments.

**Liver** Liver tumor Segmentation Challenge (LiTS)[3] contain 131 contrast-enhanced CT images provided by hospital around the world with  $512 \times 512$  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  $512 \times 512$ .

**Lung** Dataset[6] also contains 20 CT scans of patients as well as segmentations of lungs made by experts with  $630 \times 630$  resolution. We converted and normalized in a similar way as above, meanwhile we resize the data to  $512 \times 512$ .

### 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:

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

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

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

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

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

## 2.4 Semantic Segmentation Results

For comparison, we use five original network FCN with 32s[8], U-Net[9], U-Net++[13], CE-Net[5] and U-Net with Attention Gate[10] to evaluate our proposed method.

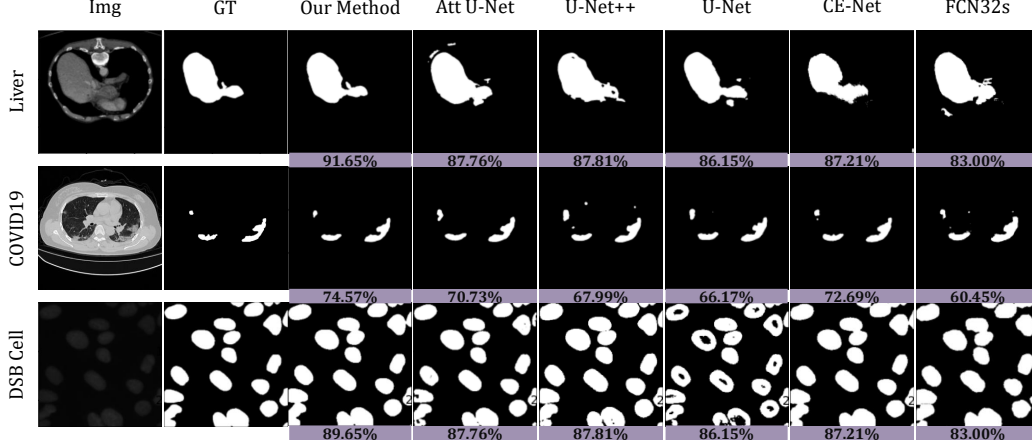


Figure 5: Medical image segmentation examples.

### 2.4.1 Performance in Cell segmentation task

Segmentation results of cell segmentation are shown in table3,

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

Methods	Shape Loss	Dice.	F1 score.	Iou.	Sens.	Hd.
Our proposal	✓	<b>0.8588</b>	<b>0.8588</b>	<b>0.7623</b>	<b>0.9296</b>	<b>4.6224</b>
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

### 2.4.2 Performance in liver segmentation task

Segmentation results of cell segmentation are shown in table4,

Table 4: Comparison With Other Methods In Liver[3] Dataset

Methods	Shape Loss	Dice.	F1 score.	Iou.	Sens.	Hd.
Our proposal	✓	<b>0.9551</b>	<b>0.9551</b>	<b>0.9165</b>	<b>0.9389</b>	<b>3.8854</b>
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

### 2.4.3 Performance in covid19 lesion segmentation task

Segmentation results of cell segmentation are shown in table5,

Table 5: Comparision With Other Methods In COVID19[6] Dataset

Methods	Shape Loss	Dice.	F1 score.	Iou.	Sens.	Hd.
Our proposal	✓	<b>0.8489</b>	<b>0.8489</b>	<b>0.7457</b>	<b>0.8570</b>	<b>4.313</b>
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

#### 2.4.4 Performance in lung segmentation task

Segmentation results of cell segmentation are shown in table6,

Table 6: Comparision With Other Methods In Lung[6] Dataset

Methods	Shape Loss	Dice.	F1 score.	Iou.	Sens.	Hd.
Our proposal	✓	<b>0.9392</b>	<b>0.9392</b>	<b>0.8965</b>	<b>0.9261</b>	<b>10.19714</b>
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

#### 2.5 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:

Table 7: Comparision With Other loss functions In COVID19[11] Dataset

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

Table 8: Ablation study for each component on COVID19 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	<b>0.8489</b>	<b>0.8489</b>	<b>0.7457</b>	<b>0.8570</b>	<b>4.313</b>

Table 9: Ablation study for each component on Cell dataset

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	<b>0.8588</b>	<b>0.8588</b>	<b>0.7623</b>	<b>0.9296</b>	<b>4.6224</b>

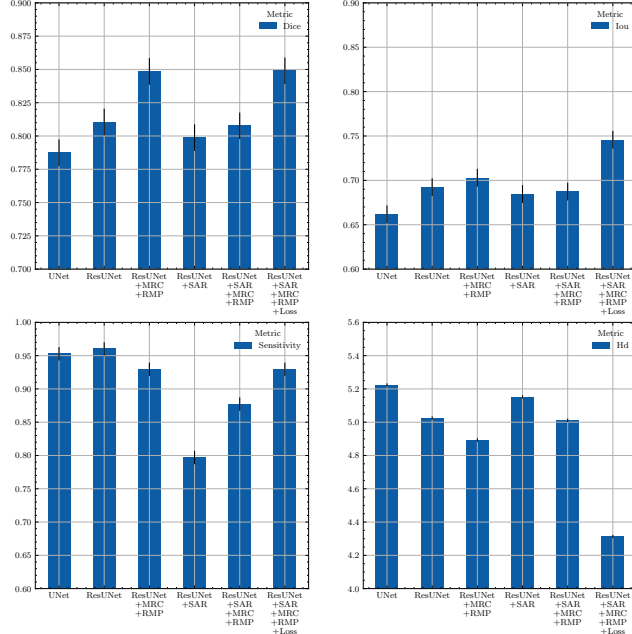


Figure 6: Fig 1 shows ; Fig 2 shows; Fig 3 shows; Fig 4 shows;Fig5 shows.

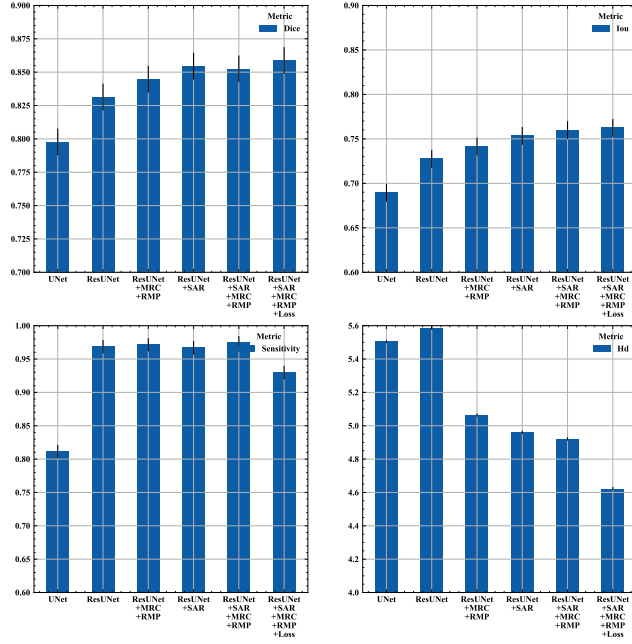


Figure 7: Fig 1 shows ; Fig 2 shows; Fig 3 shows; Fig 4 shows;Fig5 shows.

### 3 Conclusion

### Acknowledgments

## References

- [1] I. Arganda-Carreras, S. C. Turaga, D. R. Berger, D. Cirean, A. Giusti, L. M. Gambardella, J. Schmidhuber, D. Laptev, S. Dwivedi, J. M. Buhmann, T. Liu, M. Seyedhosseini, T. Tasdizen, L. Kamensky, R. Burget, V. Uher, X. Tan, C. Sun, T. D. Pham, E. Bas, M. G. Uzunbas, A. Cardona, J. Schindelin, and H. S. Seung. Crowdsourcing the creation of image segmentation algorithms for connectomics. *Frontiers in Neuroanatomy*, 9:142, 2015.
- [2] J. C. Caicedo, A. Goodman, K. W. Karhohs, and B. A. Cimini. Nucleus segmentation across imaging experiments: the 2018 data science bowl. *Nature Methods*, 16(12):1247–1253, Dec 2019.
- [3] P. Christ. Lits liver tumor segmentation challenge (lits17).
- [4] F. I. Diakogiannis, F. Waldner, P. Caccetta, and C. Wu. Resunet-a: A deep learning framework for semantic segmentation of remotely sensed data. *ISPRS Journal of Photogrammetry and Remote Sensing*, 162:94114, Apr 2020.
- [5] Z. Gu, J. Cheng, H. Fu, K. Zhou, H. Hao, Y. Zhao, T. Zhang, S. Gao, and J. Liu. Ce-net: Context encoder network for 2d medical image segmentation. *IEEE Transactions on Medical Imaging*, 38(10):22812292, Oct 2019.
- [6] M. Jun, G. Cheng, W. Yixin, A. Xingle, G. Jiantao, Y. Ziqi, Z. Mingqing, L. Xin, D. Xueyuan, C. Shucheng, W. Hao, M. Sen, Y. Xiaoyu, N. Ziwei, L. Chen, T. Lu, Z. Yuntao, Z. Qiongjie, D. Guoqiang, and H. Jian. COVID-19 CT Lung and Infection Segmentation Dataset, Apr. 2020.
- [7] D. P. Kingma and J. Ba. Adam: A method for stochastic optimization. 2017.
- [8] J. Long, E. Shelhamer, and T. Darrell. Fully convolutional networks for semantic segmentation. *CoRR*, abs/1411.4038, 2014.
- [9] O. Ronneberger, P. Fischer, and T. Brox. U-net: Convolutional networks for biomedical image segmentation. *CoRR*, abs/1505.04597, 2015.
- [10] J. Schlemper, O. Oktay, M. Schaap, M. P. Heinrich, B. Kainz, B. Glocker, and D. Rueckert. Attention gated networks: Learning to leverage salient regions in medical images. *CoRR*, abs/1808.08114, 2018.
- [11] Websites. Covid-19 ct segmentation dataset.
- [12] S. Woo, J. Park, J.-Y. Lee, and I. S. Kweon. Cbam: Convolutional block attention module. In V. Ferrari, M. Hebert, C. Sminchisescu, and Y. Weiss, editors, *Computer Vision – ECCV 2018*, pages 3–19, Cham, 2018. Springer International Publishing.
- [13] Z. Zhou, M. M. R. Siddiquee, N. Tajbakhsh, and J. Liang. Unet++: Redesigning skip connections to exploit multiscale features in image segmentation, 2020.