CAggNet: Crossing Aggregation Network for Medical Image Segmentation

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Abstract—In this paper, we present Crossing Aggregation Network (CAggNet), a novel densely connected semantic segmentation method for medical image analysis. The crossing aggregation network absorbs the idea of deep layer aggregation and makes significant innovations in layer connection and semantic information fusion. In this architecture, the traditional skip-connection structure of general U-Net is replaced by aggregations of multi-level down-sampling and up-sampling layers. This enables the network to fuse information interactively flows at different levels of layers in semantic segmentation. It also introduces weighted aggregation module to aggregate multi-scale output information. We have evaluated and compared our CAggNet with several advanced U-Net based methods in two public medical image datasets, including the 2018 Data Science Bowl nuclei detection dataset and the 2015 MICCAI gland segmentation competition dataset. Experimental results indicate that CAggNet improves medical object recognition and achieves a more accurate and efficient segmentation compared to existing improved U-Net and UNet++ structure.

I. INTRODUCTION

Image segmentation is one of the core jobs of image processing and analysis. During the segmentation process, original images or videos are separated into different regions based on plenty of semantic features and recover to pixel-wised probability maps at the end of the model. These features can be extracted from pixel intensity value, crossing pattern, geometric shape, etc[1]. In general, image segmentation by deep learning can be defined as detecting pixel-wise region categories by network’s parameter training.

Among plenty of image segmentation jobs, medical image segmentation is one of the most challenging tasks due to its lack of samples and labels. In clinical research and application, medical image segmentation is a significant procedure for clinical evaluation and diagnosis. It includes all kinds of segmentation tasks from the cell level to the organ and system level of human bodies. Fig1 shows an example of detecting cell nuclei in microscopy images. The shape and area of unusual objects in medical images such as CT images, nuclear magnetic images, and microscopy images can offer clinicians crucial insight into patients’ severity and plan for treatment. It has become a consensus of clinical researchers using computers to assist in the diagnosis of medical images nowadays.

Recently, CNN gradually replaced traditional vision methods to solve medical image segmentation tasks. In the medical image object detection area, Faster R-CNN[11] is gradually becoming the backbone of various new models. Similarly, in the medical image segmentation area, the ideas of U-Net[12] and ResNets[3] have also been absorbed by many new medical image semantic segmentation networks. Deep learning approaches have been demonstrated exceptional performance and better robustness in medical image research[1]. However, it is still a challenging task to design new models that can more effectively capture fine-grained details of the input image.

In order to implement the request for more accurate segmentation in medical images, we propose Crossing Aggregation Network (CAggNet) that incorporates nested skip connection from UNet++[19] and residential blocks from ResNets. In CAggNet, we introduce two sub-structures: crossing aggregation module (CAM) and weighted aggregation module (WAM). CAM focuses on merging features from different layers on different levels while WAM focuses on aggregating multi-scale output information. This framework fully embeds dense skip connections into U-Net’s encoder-decoder structure.

Our main contributions in this paper include three points:

- Propose a crossing aggregation module to densely and iteratively integrate information in the U-Net structure.
- Redesign a novel deep layer aggregation method by combining crossing aggregation and weighted aggregation.
- Introduce focal loss in medical image segmentation and prove its robustness in our model.

The next section provides a brief description of some traditional medical image segmentation research-related work.
Then section 3 introduces the Crossing Aggregation Network (CAggNet) in detail. Section 4 presents and compares the experimental results among our CAggNet and other baseline segmentation methods such as U-Net. In the final section, we summarized the whole paper and offered some possible improvement direction for future research.

II. RELATED WORK

After the discovery of fully convolutional networks (FCN)[9], U-Net[12] and residual networks (ResNets)[3], a large number of image segmentation framework in Kaggle medical image segmentation competition have adopted their skip connection and residual block idea. FCN originated from the study of VGG-Net[11]. In FCN, the last fully connected layers of the VGGNet is replaced by convolutional layers output the same size probability mask of the input image. The U-Net architecture further applies skip-connection to combine low-level feature maps from the encoder sub-network with higher-level feature maps from the decoder sub-network, which enables a more precise pixel-level localization. The skip connection in U-Net can restore the information loss caused by the down-sampling process, which produces similar effects to the residual block in ResNets.

Recently, a series of U-Net improvement architectures came into researchers’ sight. Ternaus-Net[5] applied the idea from transfer learning to replace the encoder part of general U-net by a pre-trained VGG-11 network. W-Net[14] achieved two-stage segmentation by connecting two U-Nets in series. Res U-net[15] and Dense U-net[2] replaced each U-Net’s encoder block and decoder block with residual connections and dense connections while attention U-Net[10] added self-attention block into the skip connection pathway of U-Net. Despite there are differences in the substructure of these models, they all share the same general encoder-decoder U-Net backbone.

Although U-Net has skip-connection pathways to combine features, its direct fusion of semantics can not achieve good results on issues with blurred and sophisticated shape[17]. Another improvement idea is to apply a nested structure to reduce the semantic gap between the feature maps of the encoder and decoder sub-networks, including deep layer aggregation (DLA)[16] and UNet++[19]. Both deep layer aggregation and UNet++ absorb the idea of nested skip connection from densely connected networks (DenseNets)[4]. DenseNets are a series of improved architectures of ResNets that concatenate all the layers in different stages by propagating features and losses through skip connections[4]. Like ResNets, DenseNets can also achieve more accuracy by deepening the network to achieve more accuracy as well as obtain better parameters and better memory efficiency. Deep layer aggregation structure iteratively and hierarchically merge the feature by a group of convolutional layers in each depth of the encoder-decoder structure. Similarly, UNet++ connects the encoder and decoder sub-network through a series of nested dense convolutional blocks. The core hypothesis of these two architectures is that the densely and nested encoder-decoder model can capture some more fine-grained details of the foreground objects from the shallower network level to the high-resolution feature maps. In contrast to general U-Net structure, DLA and UNet++ add more convolution layers and dense skip connections on skip pathways. These models’ segmentation results show better fusions of semantic information and more precise feature extraction.

To strengthen the skip connection and improve the efficiency of U-Net, we present CAggNet, a new segmentation architecture based on a densely crossing connection method to replace traditional skip connections. This model can address the need for more accurate segmentation in medical images.

III. PROPOSED NETWORK

Fig.3 illustrates the overall framework of our crossing aggregation network, which is primarily based on an encoder-decoder network, with multiple convolutional layers in each level’s skip connection pathways. This network can be divided into two parts: crossing the aggregation module and weighted aggregation module. In crossing aggregation module, the parameters are transferred among convolutional layers through up-sampling, down-sampling and direct concatenate operation. Then, the weighted aggregation module merges the outputs of the cross-aggregation module layer by layer in order to recover the probability predicted map that equal in size to the original input image.

A. Deep Aggregation

Since the skip connections in general U-Net are linear and shallow, much significant semantic information is lost before entering the decoder path. To handle this problem, Yu et al.[16] introduce a method called deep layer aggregation (DLA), which shares the same idea with UNet++. DLA contains two sorts of aggregation: Iterative Deep Aggregation (IDA) and Hierarchical Deep Aggregation (HDA)[16]. IDA is an iterative structure that progressively aggregates and deepen the feature resolution by extending additional layers between the original skip connection path. HDA embodies the idea of Semantic Embedding. It makes shallower and deeper layers combine together that span more of the feature hierarchy[6].

![Fig. 2: Deep layer aggregation consists of IDA (orange arrow) and HDA (red box). This tree-shaped encoder-decoder structure has been proven to be robust in nuclei segmentation task.[16.]](image)

Fig.2 shows the architecture of DLA combining by IDA and HDA. IDA connections join adjacent layers to gradually deepen and spatially refine features’ representation. HDA connections use a tree structure to involve more semantic information from high-level features fusing into low-level features.
Although deep layer aggregation performs well in many semantic segmentation tasks, its iterative fusion modus makes the advantage of the original U-Net direct skip connection weakened. In UNet++, Zhou et al. apply dense connections to keep the skip connection path still available after adding aggregation layers. However, the application of dense connections also means that the number of parameters in the model will increase significantly. These defects make DLA and UNet++ weaker than the original U-Net in terms of model versatility.

In CAggNet, we redesign a novel aggregation module: Crossing Aggregation Module (CAM). The input of CAM contains three different level feature maps: stage N-1 feature map, stage N feature map, and stage N+1 feature map. As Fig. 4 shows, CAM first concatenates the stage N feature map and down-sampling stage N-1 feature map and up-sampling stage N+1 feature map. Then, it passes through two $3 \times 3$ convolutional layers connected with the Relu function. At last, the output feature map of the last Relu function is summed up with the input stage N-1 feature map. The practical effect of CAM is to use the idea of residual blocks to fuse different pyramid levels of information while the connection of CAMs can also iteratively deepens each level of the network. Similar to the effect of ResNets, this aggregation method can avoid the network from losing parameters due to the increase in depth.

Our crossing aggregation module is defined by:

$$Z = \text{Concatenate}(X_{i,j-1}, DS(X_{i-1,j}), US(X_{i+1,j}))$$

$$X_{i,j} = X_{i,j-1} + \sigma_2(W_2\sigma_1(W_1Z + b_1) + b_2)$$

where DS and US are down-sampling and up-sampling operation respectively. $\sigma$ is the Relu activation, and $W$ and $b$ are the weights in the convolutional layer. CAM also apply the batch normalization operation to accelerate training process and prevent overfitting.

Finally, CAggNet iteratively connects all CAM, as Fig. 3 shows. Further, we can find that the composition of CAggNet can be split into multiple sub-encoder-decoder structures. This iterative network framework significantly promotes the fusion of semantic information.
will also increase. Lin et al.[8] also found that focal loss work best in our experiments if \( \gamma \) and background classes and focusing parameter to rescale the parameters respectively denote for balanced variant of foreground as:

\[
\text{D. Focal Loss}
\]

Most of medical image segmentation problems can be defined as foreground-background class imbalanced problems. This is because there is often a lot of noise and background interference in medical images. Most of the time, the foreground objects we need to detect are only distributed in a small range in original images. Cross entropy loss is not conducive to the training process of these imbalanced class situation. In order to handle these problems, Lin et al.[8] introduced focal loss, a method that is applied to train on sparse sets. The focal loss is defined as:

\[
\text{FocalLoss}(P_t) = -\alpha_t(1-P_t)^{\gamma} \log(P_t)
\]

where \( P_t \) is predicted probability, \( \alpha \) and \( \gamma \) are two hyper-parameters respectively denote for balanced variant of foreground and background classes and focusing parameter to rescale the loss. When \( \gamma = 0 \), the focal loss is equivalent to Weighted BCE loss. If \( \gamma \) increase, the effect of the modulating factor will also increase. Lin et al.[8] also found that focal loss work best in our experiments if \( \gamma = 2 \) and \( \alpha = 0.5 \).

IV. EXPERIMENT

The models are implemented in Pytorch. Adam optimizer[7] is used to optimize models and the learning rate is set to 1e-3. Batch size is set to 5 for the CELL dataset and 2 for the GLAND dataset. Early-stopping on the validation set is applied with a patience of 32 epochs. The models generally converge within 100 epochs. The IOU and F1-score are computed on the validation set. All models are trained on an Nvidia 1080Ti GPU.

A.Datasets

We evaluated our method on two public datasets. The first dataset (referred to as CELL) is 2018 Data Science Bowl aiming to detect the nuclei in divergent microscopy cell images. In this dataset, there are 670 cell images in total, 509 for training, and 161 for validation. We also resized each images of the dataset to 256×256. The challenge of this task is that cell type, magnification, and imaging modality have a variety of conditions, so the model need to handle nuclei segmentation in different environment. The second dataset (referred to as GLAND) is from the MICCAI 2015 Gland Segmentation Challenge Contest[13] (Warwick-QU dataset). In this dataset, there are 165 microscopy gland images in total, 85 images for training, and 60 (Part A) + 20 (Part B) for validation. These training and testing images were collected from healthy glandular tissue and glandular tissue of different degrees of malignancy. We resized each images of the dataset to 512×512, so the training set and testing set are increasing to 158 and 144 respectively.

B. Evaluation Metrics

We use intersection over union (IOU) and F1-score to evaluate the performance of models.

\[
P_r = \frac{\text{True Positives}}{\text{True Positives} + \text{False Positives}}
\]

\[
S_e = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}}
\]

\[
IOU = \frac{P_r \cdot S_e}{P_r + S_e - P_r \cdot S_e}
\]

\[
F_1 = 2 \cdot \frac{P_r \cdot S_e}{P_r + S_e}
\]

Where \( P_r \) stands for precision and \( S_e \) stands for sensitivity.

C. Baselines

In order to prove the robustness of our model, we compare CAggNet with other deep learning models in semantic segmentation, including U-Net[12], UNet++[19] and a fully convolutional network (FCN)[9]. We chose U-Net and UNet++ because their performances are well in many MICCAI contests. The DLA is not in the baseline list because its performance is almost the same to UNet++. In this baseline comparison, all models are trained under the binary cross entropy (BCE) loss.

\[
BCE(x) = -[y \log f(x) + (1 - y) \log(1 - f(X))]
\]
Where $x$ is the model input, $f(x)$ is the model output and $y \in \{0, 1\}$ is the ground truth label. In Table I and Table II, we compare CAggNet with its baseline models in terms of the IOU and F1-score after repeating the experiment many times. As shown, CAggNet outperforms U-Net, UNet++ and the FCN consistently on both datasets. As a qualitative result, Fig.6 shows example predictions on the CELL and GLAND validation sets.

| Architecture | CELL | GLAND |
|--------------|------|-------|
| FCN[9]       | 0.3698 | 0.5400 |
| U-Net[12]    | 0.8459 | 0.7873 |
| UNet++[19]   | 0.8489 | 0.7919 |
| CAggNet      | 0.8537 | 0.7922 |

**TABLE I: Performance of CAggNet and baselines in IOU**

| Architecture | CELL | GLAND |
|--------------|------|-------|
| FCN[9]       | 0.5293 | 0.6923 |
| U-Net[12]    | 0.9166 | 0.8810 |
| UNet++[19]   | 0.9188 | 0.8836 |
| CAggNet      | 0.9216 | 0.8845 |

**TABLE II: Performance of CAggNet and baselines in F1-score**

### D. Study on Loss Functions

To evaluate the contribution of the focal loss, we trained CAggNet with different loss function settings on the GLAND dataset. In Table III, we compared the BCE loss function and focal loss function with varying hyperparameters. Models trained with the focal loss generally gain performance against the model trained with BCE loss. By applying a modulating term to the cross-entropy loss, the focal loss allows the model to focus on learning hard positive examples instead of being distracted by the easy negatives, which boosts the performance of our model significantly. Finally, the model trained with focal loss ($\alpha = 0.25, \gamma = 2$) outperforms the other models and achieves a performance of 0.8063/0.8927 (IOU/F1-score).

| Method                  | IOU   | F1-score   |
|-------------------------|-------|------------|
| BCELoss                 | 0.7922 | 0.8845     |
| FocalLoss($\alpha = 0.5, \gamma = 1$) | 0.8020 | 0.8907     |
| FocalLoss($\alpha = 0.25, \gamma = 2$) | **0.8063** | **0.8927** |
| FocalLoss($\alpha = 0.5, \gamma = 2$) | 0.8048 | 0.8918     |

**TABLE III: Study on loss functions on the GLAND dataset**

### E. Final Results

Table IV and Table V demonstrates how much our model structure and the focal loss function contributed to the final result. As seen, CAggNet consistently outperforms UNet++ and general U-Net in both the CELL and GLAND datasets. Comparing to U-Net, our proposed architecture achieved an average of 0.94% gain on F1-score and 1.56% gain on IoU accuracy. As with UNet++, CAggNet yields average improvement of 0.70% and 1.18% points in F1-score and IoU. These results prove the effectiveness of our architecture on both datasets. Fig.6 shows a qualitative comparison between the results of U-Net, UNet++, and CAggNet.

| Method | IOU | F1-score |
|--------|-----|----------|
| U-Net  | √   | √        |
| UNet++ | √   | √        |
| CAggNet| √   | √        |
| Focal  |     |          |
| BCE    | 0.8459 | 0.9166  |
| BCE    | 0.8489 | 0.9188  |
| BCE    | 0.8537 | 0.9216  |
| CAggNet| **0.8581** | 0.9236  |

**TABLE IV: Final results on CELL dataset**

![Image](image_url)  

**Fig. 6:** Visualization of segmentation results of two public datasets.
TABLE V: Final results on GLAND dataset

| Model       | Accuracy | F1-score | IoU |
|-------------|----------|----------|-----|
| UNet++      | 0.7873   | 0.8845   | 0.7922 |
| CAggNet     | 0.8063   | 0.8927   | 0.8810 |

V. CONCLUSION

In this paper, we proposed Crossing Aggregation Network (CAggNet) for medical image segmentation. The suggested architecture consists of two aggregation sub-module: crossing aggregation module (CAM) and weighted aggregation module (WAM). CAM fuses three layers in different levels and computes their residuals as output. And then, groups of CAM connect iteratively in the skip-connection path of U-Net. WAM aggregates the output of the last layer of skip-connections in different levels through the mechanism of channel attention and up-sampling. Experimental results show that the proposed method outperforms several state-of-the-art semantic segmentation methods on two public datasets. The application of focal loss also successfully makes our proposed method avoid the foreground-background imbalance issue in the training process, and finally achieve the highest IoU and F1 score. The plan in the future is to test this model in more medical image segmentation tasks like video frames and CT images.

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