

# Utilizing the Clique Atrous Spatial Pyramid Pooling for Pancreas Segmentation

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## INTRODUCTION

Automatic organ segmentation is a challenging problem in medical image analysis and is well studied with good performance for organs such as heart, kidneys, liver. achieving high accuracy in pancreas segmentation is challenging due to its significant shape differences of anatomical structures across patients and atypical pancreas shapes. Many methods that have been shown to be good in natural images are not effective in improving the results of pancreas segmentation. Built upon atrous convolution, the pyramid pooling module, which empirically proves to be an effective way to generate multi-scale features, was proposed to encode information using parallel convolution with different dilation rates. In order to deal with complex pancreas segmentation scenarios, we propose a method that can produce multi-scale features by using clique atrous spatial pyramid pooling module. The proposed method achieved improvements over methods without clique atrous spatial pyramid pooling module.

## AIM

Combining Atrous spatial pooling pyramid and Cliquenet's recurrent feedback structure generate multi-scale features to remedy the various different sizes in pancreas segmentation.

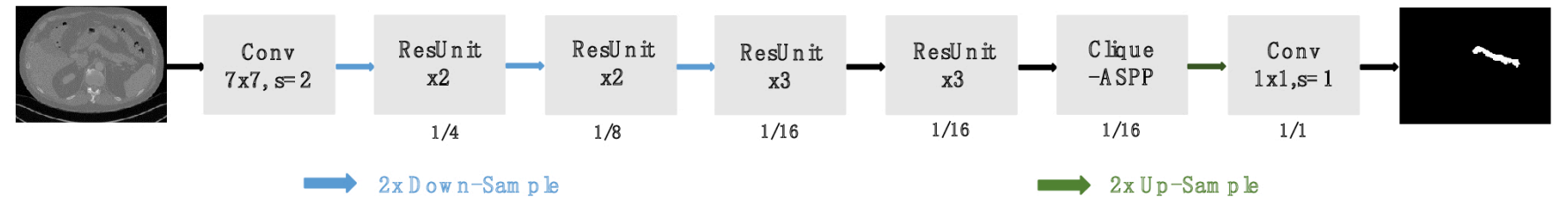
Achieve end-to-end, pixel-level segmentation on pancreas segmentation.

## CONCLUSIONS

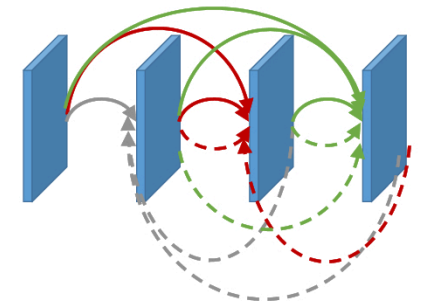
Combining atrous spatial pooling pyramid and cliquenets recurrent feedback structure, the proposed method can generate multi-scale features to remedy the various different sizes in pancreas segmentation to achieve better performance. For a dataset with 12 pancreas volumes, the averaged Dice is 0.678 while the method without CliqueASPP module is 0.675.

## METHOD

- ASPP(Atrous Spatial Pyramid Pooling) was introduced in the literature to handle objects in semantic segmentation with very different sizes.
- Motivated by CliqueNet, we proposed a model named CliqueASPP (Clique Atrous Spatial Pyramid Pooling) module. There are both forward and backward connections between any two layers.
- In Stage-I, we put layers with small dilation rates in lower part, while put layers with large dilation rates in upper part. The output of each atrous layer is concatenated to feed into the following layers.
- In Stage-II, we concatenate newly updated features to re-update previously updated layer, and reuse the convolution filters with same dilation rates as Stage-I.
- This recurrent feedback structure not only stacks all dilated layers together (including the features generated by Stage-I and Stage-II) to encode multi-scale information, but also bring higher level visual information back to refine low-level filters and achieve spatial attention.
- The CT images with size of 320x384 for pancreas patients were fed into the proposed Network in Fig. 1. After passing the convolution layer with filter size of 7x7, and a down-sampling layer, the feature map becomes 1/4 of the input in size. The feature is extracted through several residual blocks, including 2, 2, 3 and 3 residual units respectively.
- The feature map is then sent to the CliqueASPP module to extract multi-scale features which will be concatenated together and pass through the convolution and up-sampling layer to obtain the final segmentation result.



(a) Whole Network proposed in the work

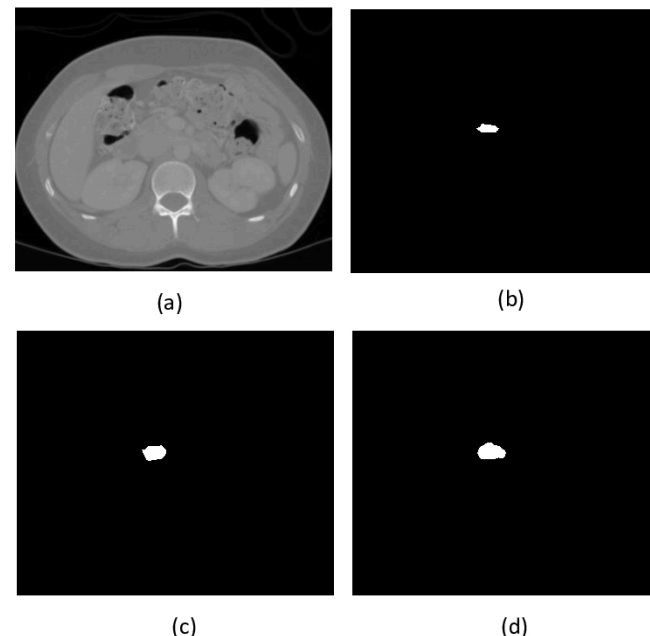


(b) CliqueASPP module

## RESULTS

Method	DSC
Without CliqueASPP	0.675
With CliqueASPP	0.678

**Table. 1.** The mean of DSC of all methods



**Fig. 1.** Visualization results on the dataset with 12 pancreas volumes when employing CliqueASPP module and not employing it. (a) Input, (b) The segmentation result without CliqueASPP, (c) The segmentation result with CliqueASPP, (d) Ground Truth.

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## ACKNOWLEDGEMENTS

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## CONTACT INFORMATION

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