# U-NET FOR PANCREAS SEGMENTATION IN ABDOMINAL CT SCANS

*Yijun Liu, Shuang Liu*

School of Electrical and Computer Engineering, Cornell University, Ithaca, NY, USA

## ABSTRACT

In this paper, we propose a U-Net based approach for pancreas segmentation. Under the same setting where bounding boxes are provided, this method outperforms previously reported results with a mean Dice Coefficient of 86.70 for the NIH dataset with 4-fold cross validation. Results show that a network trained from scratch with medical images can achieve a better performance with much less training time compared to fine-tuning the models that are pretrained on natural images.

## 1. INTRODUCTION

The fixed-point model [1] which fine-tuned an ensemble of networks pretrained on natural images with three views of CT volumes achieved the best result so far on the NIH pancreas dataset [2] while obtaining $83.18 \pm 4.81\%$ Dice Coefficient (DSC) given the pancreas bounding boxes. Our study shows that a single network trained only on axial view slices can push this limit to $86.70 \pm 3.51\%$ with much less training time.

## 2. METHOD

### 2.1. Preprocessing

Slices are cropped with bounding boxes and added with margins filled with original image data as reported in [1]. The images are then clipped between $[-100, 240]$ HU considering the common intensity distribution of pancreas, and scaled to the range $[0, 1]$. Only slices with at least 100 pancreas pixels are used for training.

### 2.2. Fully Convolutional Network

*2.2.1. Network Architecture*

The network is basically the same as the 2D U-Net [3] except that (1) all up-convolutions (upsampling + convolution) are replaced by transposed convolutions with size $2\times2$ and stride $2$, and (2) the final layer is set to one feature channel with sigmoid as the activation function.

*2.2.2. Dice Loss Function*

We use the negative of a softly defined Dice Coefficient as the loss function during network training, similar to the one applied in [1]. The loss is defined as

$$L(Y, \hat{Y}) = -\frac{2\sum_i y_i \hat{y}_i}{\sum_i y_i + \sum_i \hat{y}_i} \tag{1}$$

where $y_i \in Y$, $\hat{y}_i \in \hat{Y}$, and $Y$ is the ground truth, $\hat{Y}$ is the prediction.

*2.2.3. Training Settings*

The network is trained from scratch with Adam optimizer and a learning rate of $10^{-5}$ for 10 epochs with batch size of one. The network is implemented with Keras with Tensorflow backend. It takes ~3 hours to train the network with one NVIDIA Tesla K40c GPU which is less than 1/3 time needed by the approach in [1].

## 3. EXPERIMENTS

### 3.1. Dataset and evaluation

We evaluate the proposed method on the NIH pancreas segmentation dataset [2] with 4-fold cross validation under exactly the same test setting with oracle bounding boxes as used in [1]. Performance is evaluated by Dice Coefficient.

### 3.2. Results

Table 1. Test Results Comparison

| Method | DSC (%) | Min DSC (%) |
|---|---|---|
| Fixed-Point [1] | $83.18 \pm 4.81$ | 65.10 |
| Proposed Method | $86.70 \pm 3.51$ | 73.67 |

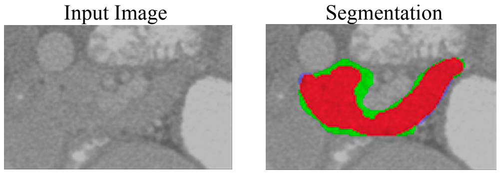

Fig. 1. Sample segmentation result (Green, blue and red indicate prediction, ground-truth and overlapped regions)

## 4. CONCLUSION

An efficient segmentation approach is presented which surpasses previous results. Training with medical images from scratch is shown to be more effective than fine-tuning models pretrained on natural images. In the future, a detection system is to be built to incorporate this segmentation model.

## 5. REFERENCES

[1] Y. Zhou, L. Xie, W. Shen, Y. Wang, E. Fishman and A. Yuille, "A Fixed-Point Model for Pancreas Segmentation in Abdominal CT Scans", *Proc. MICCAI, 2017*

[2] H. Roth, L. Lu, A Farag, H-C Shin, J Liu, E. Turkbey, and R. M. Summers, "DeepOrgan: Multi-level deep convolutional networks for automated pancreas segmentation", *Proc. MICCAI*, 2015.

[3] O. Ronneberger, P. Fischer, and T. Brox, "U-Net: Convolutional Networks for Biomedical Image Segmentation", *Proc. MICCAI*, 2015.