

Learning Multi-Class Segmentations From Single-Class Datasets: Supplementary Material

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Base model

Below are the details on the architecture of the base model.

Encoder	Input	Decoder
	Conv 2	
	DenseBlock 16x3 + MaxPooling	
	DenseBlock 32x3 + MaxPooling	
	DenseBlock 64x3 + MaxPooling	
	DenseBlock 128x3 + MaxPooling	
	DenseBlock 256x3 + MaxPooling	
	DenseBlock 512x3 + MaxPooling	
	TransConv 512 + DenseBlock 256x3	
	TransConv 256 + DenseBlock 128x3	
	TransConv 128 + DenseBlock 64x3	
	TransConv 64 + DenseBlock 32x3	
	TransConv 32 + DenseBlock 16x3	
	TransConv 16 + DenseBlock 8x3	
	Conv 32	
	Conv 1	
	Output	

Table 1. Architecture details of the base model. We utilize 2D or 3D convolutional and transposed convolutional (*TransConv*) layers, depending on the experiment. Each *DenseBlock* $X \times N$ contained N densely connected convolutional layers with X filters each.

References

- [1] Tobias Heimann, Bram Van Ginneken, Martin A Styner, Yulia Arzhaeva, Volker Aurich, Christian Bauer, Andreas Beck, Christoph Becker, Reinhard Beichel, György Bekes, et al. Comparison and evaluation of methods for liver segmentation from CT datasets. *IEEE Transactions on Medical Imaging*, 28(8):1251–1265, 2009.
- [2] Roth Holger, Farag Amal, Turkbey Evrim, Lu Le, Liu Jiamin, and Summers Ronald. Data from pancreas – CT. *Cancer Imaging Archive*, 2016.

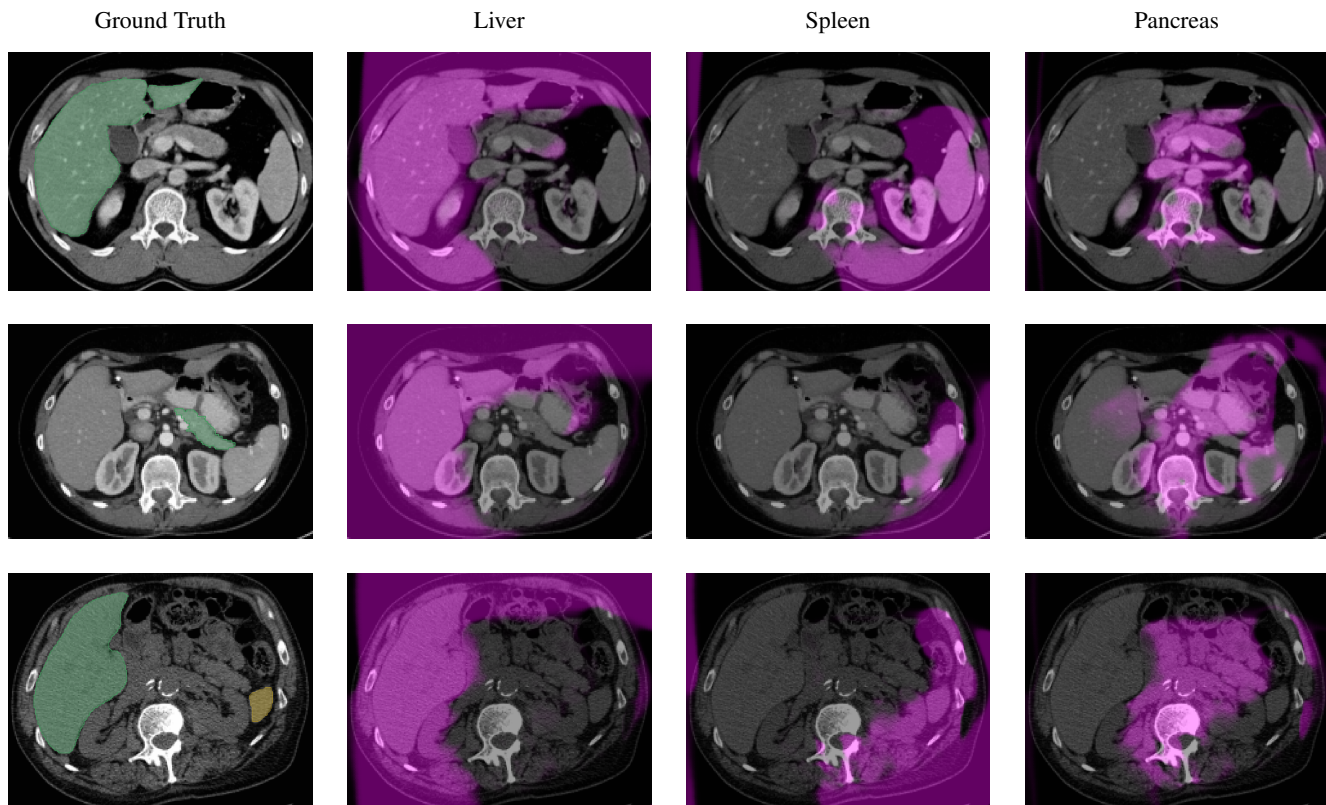


Figure 1: Examples of segmentation predictions for CT images from different testing sets generated by the `no_cond` model. The results are presented in 2D for illustrative purposes, but actual results are in 3D. Rows from top to bottom: Sliver07 [1], NIH Pancreas [2], our own additional dataset of liver and spleen segmentations. From left to right: available ground truth outlines in the datasets (green and yellow), segmentation results from each additional channel. Although the segmentation outlines for our additional dataset are shown together (green and yellow), they were generated and stored separately in a form of binary masks.