

# AutoDenseSeg ([pxln@hotmail.com](mailto:pxln@hotmail.com))

## ***Abstract***

This document briefly describes techniques we used in automatic segmentation of the prostate in transversal T2-weighted MR images for the PROMISE12 challenge. We use a densely connected CNN with 3D convolutions for semantic segmentation to tackle this problem. Details of each step are described next in each section.

## ***Data processing***

Each volume is normalized to have a zero mean and a unit variance. The training data is augmented by rotations (90, 180, 270 degrees) and flipping in axial plane. For training, we first crop a ROI region that encompasses the prostate for each volume. Then we randomly cropped 16x64x64 sub-volumes from this ROI region and background parts for training. The batch size is 8.

## ***Network Structure***

The proposed network consists of a down-sampling path and an up-sampling path, followed by a softmax layer for prediction. The down-sampling path follows a DenseNet-like network structure, including several dense blocks and transition blocks with 3D pooling. The up-sampling path uses transpose convolutions with stride 2 to restore the high-resolution signal. 3D convolutions are used to exploit spatial correlations in a 3D volume.

For better regularization, a dropout layer with a ratio 0.2 (80% probability to keep) is added after each convolution.

## ***Deep supervision***

Except the final main prediction, we take the smaller volumes with  $\frac{1}{2}$  of the original resolution produced during the down-sampling path to get an auxiliary prediction. Again, transpose convolutions are used for the up-sampling. Both predictions are used in loss metric.

## ***Loss metric***

We use cross entropy for the loss metric. For deep supervision, the weighted loss of the two predictions are used.

## ***Evaluation***

### ***Implementation***

The algorithm is implemented in a modified caffe, supporting 3D convolution and 3D pooling. We use a GeForce GTX 1080 Ti GPU for training. The input size is 16x64x64 with a batch size of 8 for training.

### ***Inference process***

During inference, we use overlapped sub-volumes for prediction. Only the main prediction is utilized. For overlapped regions, the prediction probabilities are averaged to get the final prediction. As a post-processing, we only retain the largest connected set with a label "foreground" as the prostate. No other post-processing is used.

## *Results*

We split the 50 training cases into a training set with 45 cases and a validation set with 5 cases, i.e. 0, 10, 20, 30 and 40. The proposed scheme achieves a dice score of 0.879 on the validation set and 0.883 on the training set.