

Automatic prostate bed target segmentation on daily cone-beam CT image using a 3D multi-path DenseNet

J. Fu¹, S. Yoon¹, A.U. Kishan¹, K. Singhrao¹, Z. Wang¹, J.H. Lewis², and D. Ruan¹

1. University of California, Los Angeles, Los Angeles, CA 2. Cedars-Sinai Medical Center, Los Angeles, CA, USA

INTRODUCTION

Automatic prostate bed target segmentation based on cone-beam CT (CBCT) imaging is important for adaptive therapy, but is extremely challenging. This is mainly because the soft-tissue contrast of the CBCT images is low and prostate bed targets are inferred geometries with large appearance variations. The implicit mapping between a planning CT and its associated prostate bed (PB_{CT}) contour could provide useful prior information in a convolutional neural network for generating CBCT prostate bed (PB_{CBCT}) contours. In this study, we proposed a novel 3D multi-path DenseNet for automatically generating the PB_{CBCT} contour from the image triplet (CBCT, CT, PB_{CT}). We hypothesized that a multi-path architecture, where each image has its own set of encoding filters, could achieve better segmentation performance than the single-path architecture, where all images share the same encoding filters, by capturing the image-specific features.

METHOD

Dataset

- 17 prostate cancer patients who received 5-fraction stereotactic body radiation therapy after radical prostatectomy
- Each patient had one planning CT and five daily set-up CBCT images
- CBCT images were rigidly aligned with the planning CT
- Prostate bed contours on CT images (PB_{CT}) and CBCT images (PB_{CBCT}) were drawn by an experienced oncologist
- All images and contours were resampled to 2.5 x 2.5 x 2.5 mm³ and cropped to a final dimension of 240 x 240 x 64
- Each patient has five image triplets (CBCT, CT, PB_{CT})

Single-path and multi-path DenseNets for segmentation

- Figure 1 shows the architecture of a 3-layer dense block used in the proposed 3D DenseNets.
- Figure 2 shows the architecture of the 3D single-path DenseNet
- Figure 3 (A) shows the architecture of the 3D multi-path DenseNet. The encoded feature maps from three different paths were concatenated and then fused by squeeze-and-excitation blocks (SEB) as shown in Figure 3 (B)

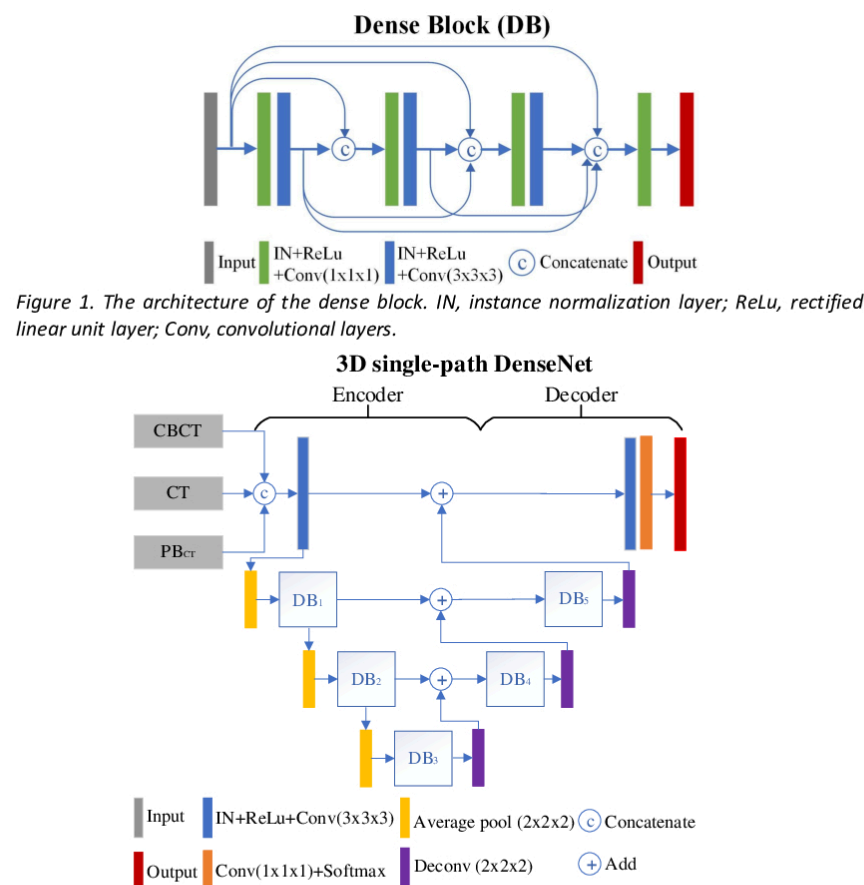


Figure 2. The architecture of the 3D single-path DenseNet. DB, dense block shown in Figure 1; Deconv, deconvolutional layer.

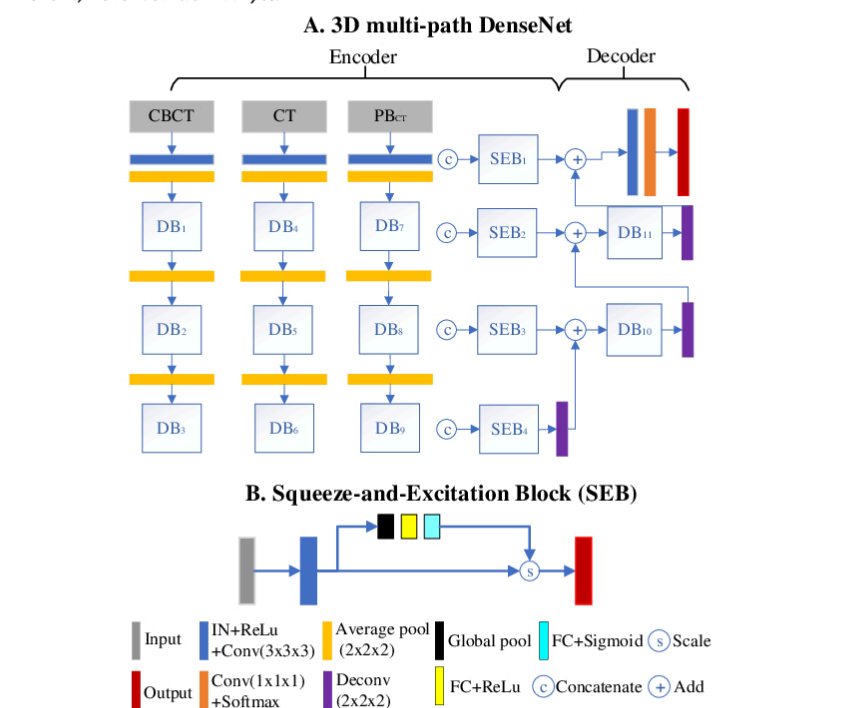


Figure 3. (A) The architecture of the 3D multi-path DenseNet. (B) The architecture of the squeeze-and-excitation blocks (SEB).

- The number of convolutional filters was set to ensure the single-path DenseNet has a similar number of trainable parameters as the multi-path DenseNet.

- 3D UNet¹ was constructed for model comparison

Model training

- The patient cohort was randomly split into a training set of 12 patients, a validation set of 2 patients, and a testing set of 3 patients
- The Adam stochastic gradient descent method was used to minimize the Dice loss
- A batch size of 1 was used for training
- The initial learning rate and the stopping epoch number were tuned using the validation set

Model evaluation

- Trained models were applied to 15 image triplets of the testing patients to generate their autosegmented PB_{CBCT} contours
- Model performance was evaluated using Dice similarity coefficient (DSC)
- Friedman test for repeated measures and Wilcoxon signed-rank tests were conducted to compare the model differences

RESULTS

- Figure 4 shows the transverse slices of the co-registered CT and CBCT images along with the corresponding ground truth PBCBCT contour
- Figure 5 shows the ground truth PBCBCT contour and generated PBCBCT contours of a single fraction for the two testing patients
- Table 1 summarizes DSC statistics and the number of model trainable parameters
- Table 2 summarizes the results of the statistical tests

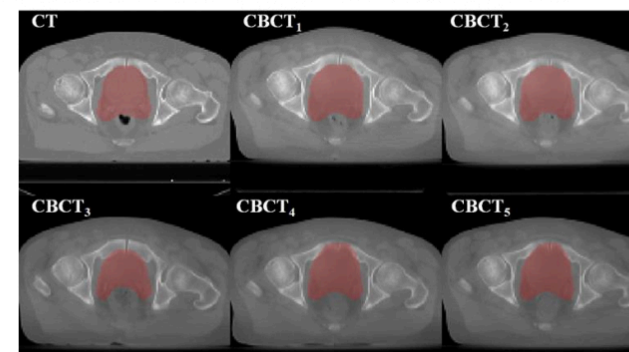


Figure 4. Transverse slices of the co-registered CT and CBCT images along with ground truth PB_{CBCT} contours for the example patient.

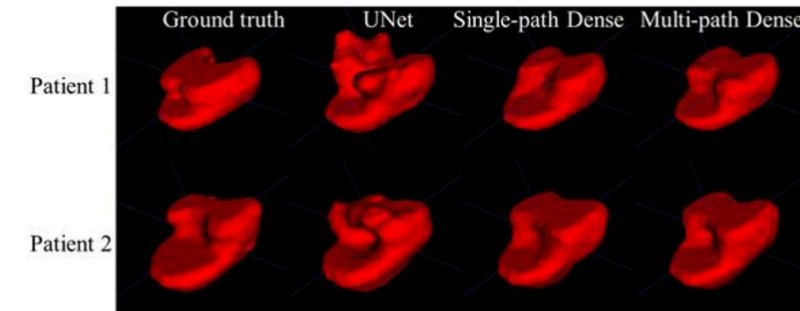


Figure 5. 3D shape of the ground truth and predicted PB_{CBCT} contours generated by three models

Model	UNet	Single-path Dense	Multi-path Dense
Dice	0.780±0.065	0.814±0.068	0.837±0.073
Parameters # (*10 ⁶)	4.77	0.38	0.36

Table 1. Statistics of the Dice coefficient and the number of trainable model parameters for three models. Results are averaged across 15 testing image triplets.

	Friedman	Wilcoxon		
		UNet vs Single-path DenseNet	UNet vs Multi-path DenseNet	Single-path vs Multi-path DenseNet
P-value	<0.01	0.04	<0.01	<0.01

Table 2. Statistical test results. A p-value of <0.05 is considered significant in the Friedman test. A p-value of < 0.0167 is considered significant in the Wilcoxon sign-rank test as per the Bonferroni correction.

CONCLUSIONS

Our proposed 3D multi-path DenseNet generated PB_{CBCT} contours with the highest clinical agreement. Statistical tests indicated significant differences between the multi-path DenseNet and the 3D UNet or single-path DenseNet. This pilot study demonstrates the promise of using the multi-path DenseNet for online contouring in an adaptive workflow. More patient data needs to be acquired to examine model robustness.

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CONTACT INFORMATION

jiefu@mednet.ucla.edu