Improving automated OAR segmentation for gynecological patients with data from prostate cancer patients

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INTRODUCTION

Accurate and robust segmentation of OARs on CT is essential for treatment planning, but this task is especially challenging when applying learning-based segmentation algorithms to gynecological cases due to the limited patients available for model training. While most of the research on learning from limited data aims to reduce over-fitting by either constructing a simplified learning model and/or imposing additional regularizations such as weight decay, we proposed to address this challenge by enlarging the training dataset and thus the discriminative capability of the segmentation model can be largely kept.

AIM

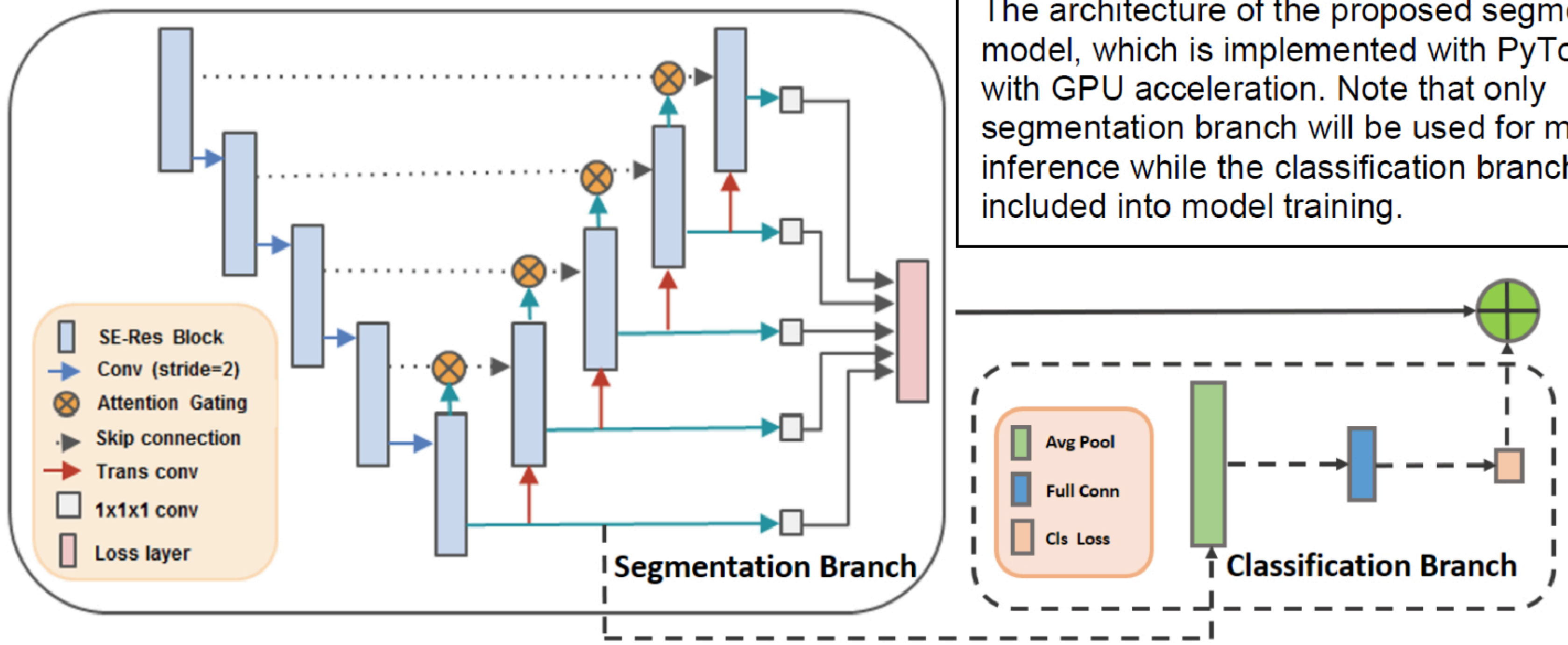
This work aims to investigate several strategies to improve the performance of deep-learning-based OAR segmentation, which usually suffers from limited training data due to the less patients available, by incorporating data from prostate cancer patients and optimizing network structure.

METHOD

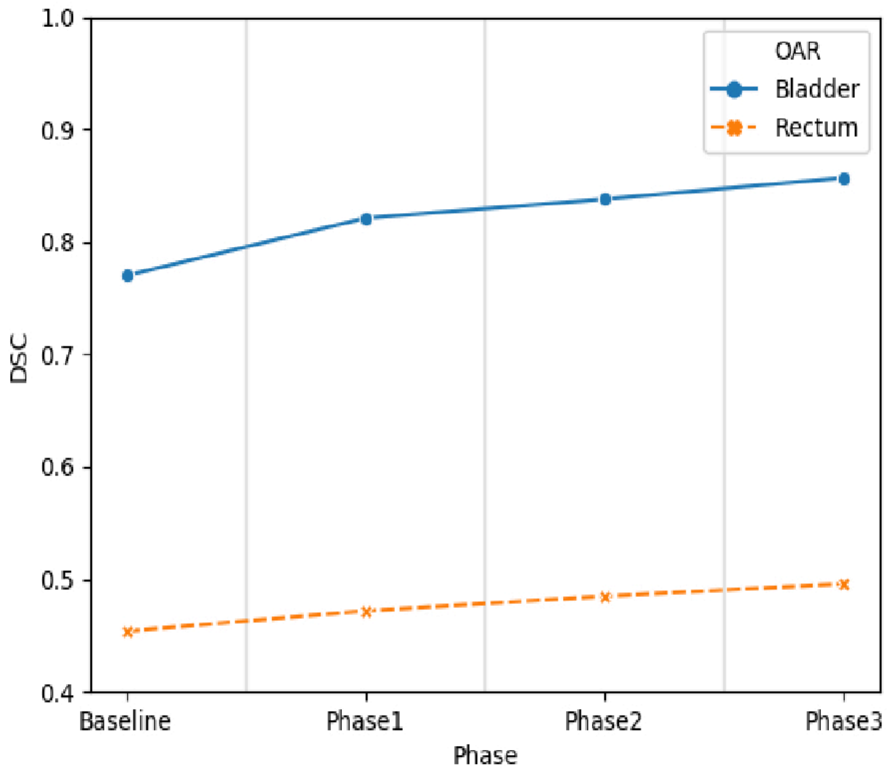
We employed U-Net [1] as the basic structure of our segmentation framework, but replace each convolutional building block with a residual block [2] where the input is directly added to the output of two consecutive convolutional operations. These long- and short-range skip connections greatly facilitate gradient back propagation and allow the decoding pathway to directly integrate high resolution features from the encoding pathway. In order to further boost its representative capability, we embedded channel-wise attention mechanism [3] into the model by recalibrating channel response at teach residual block. The direct application of this method to challenging segmentation task such as OAR contouring on gynecological patients will suffer from over-fitting due to limited training data. So, three strategies were investigated:

- Incorporating prostate cancer patients to enlarge training set;
- Adding a classification branch in the original network to differentiate gynecological patients from prostate cancer patients, which provides global prior information to characterize the anatomical difference between them;.
- Oversampling the gynecological cases to account for the sample imbalance between gynecological and prostate cancer patients.

KEY RESULTS



The architecture of the proposed segmentation model, which is implemented with PyTorch with GPU acceleration. Note that only segmentation branch will be used for model inference while the classification branch will be included into model training.



The figure on the left shows the segmentation results of each OAR at different evaluation phases:

Baseline: using 32 gynecological patients only, no classification branch (Bladder: 0.770, Rectum: 0.454)

Phase 1: adding 80 prostate cancer patients into model training, no classification branch (Bladder: 0.821, Rectum: 0.472)

Phase 2: oversampling gynecological patients by a factor of 2, no classification branch (Bladder: 0.838, Rectum 0.485)

Phase 3: oversampling gynecological patients with classification branch (Bladder: 0.857, Rectum 0.496)

RESULTS

The direct application of the original segmentation model on 32 gynecological cases resulted in a mean Dice-Similarity-Coefficient (DSC) of 0.770 on bladder and 0.454 on rectum under four-fold cross validation. The proposed strategies consistently improved the segmentation performance with 80 prostate cancer patients included, achieving a statistically significant improved DSC of 0.857 on bladder ($p = 0.003$) and DSC of 0.498 on rectum

CONCLUSIONS

Our preliminary results demonstrate that by carefully designing network structure and learning strategies, prostate cancer cases can be used to improve the segmentation performance of gynecological patients despite their significant anatomical deviations.

ACKNOWLEDGEMENTS

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