

An MRI sequence independent convolutional neural network for synthetic head CT generation in proton therapy

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Objective

MRI is an essential image modality in radiation oncology to delineate target structures and organs at risk. For an MRI-only workflow the MRI has to be converted into a synthetic CT (sCT) which is dependent on the input sequence and scanner typ. This requires a repeated process of training models with new sequences.

Aim: Development of an MRI sequence independent deep learning technique for synthetic CT (sCT) generation for proton therapy patients.

Patients and Methods

Data collection and pre-processing:

- 47 meningioma patients treated with proton therapy at the MedAustron Center for Ion Beam Therapy (Wiener Neustadt, Austria)
- All patients received CT and MRI on the same day in treatment position employing the identical immobilization devices.
- Selected MRI sequences: T1, T2, and T1 with contrast media (CM).
- CT and MRI were rigidly registered

Model training specification:

- 33/6/8 patients (training/validation/testing)
- Base model: 3D U-Net architecture (Figure 1) with ResNet-Blocks between down- and up-sampling
- Augmentation techniques were considered to reduce overfitting (flipping, spatial transforms, cropping)
- Hyperparameter search: network depth, activation function, loss function and crop size

Evaluation:

- Conversion quality: structural similarity metric (SSIM) and the mean absolute error (MAE)
- Plan quality: The clinical treatment plans were re-calculated on the sCT and the dose distributions were compared by DVH parameters and spot differences.

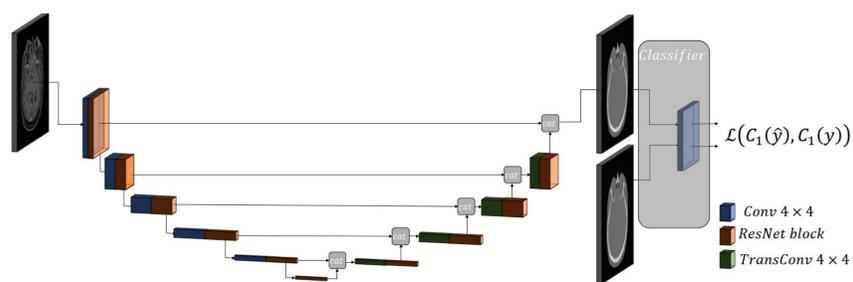


Figure 1: Final architecture schematics with the generated features of the pre-trained classifier. Blue blocks are the output of the convolution layers and green blocks the output of the transpose convolution layers. Orange blocks are ResNet blocks.

Results

Hyperparameter Search and Metric Evaluation:

The final model was trained with fixed features per group, six down-convolution steps, an input image size of 128×192×192, and feature loss. The model applied to the test dataset was trained with all MRI sequences and 98k iterations, the results are summarized in Table 1. Visual comparison for an example patients is illustrated in Figure 2.

	MAE body [HU]	MAE bone [HU]	SSIM
T1	79.8±5.9 [71.1,86.5]	216.3±29.6 [178.9,278.5]	0.97±0.01 [0.96,0.97]
T2	71.1±3.1 [66.7,76.6]	186.1±25.7 [155.4,242.4]	0.98±0.00 [0.97,0.98]
T1CM	82.9±6.1 [75.1,93.4]	236.4±41.4 [195.8,331.4]	0.96±0.01 [0.95,0.97]

Table 1: Metric results of the test dataset

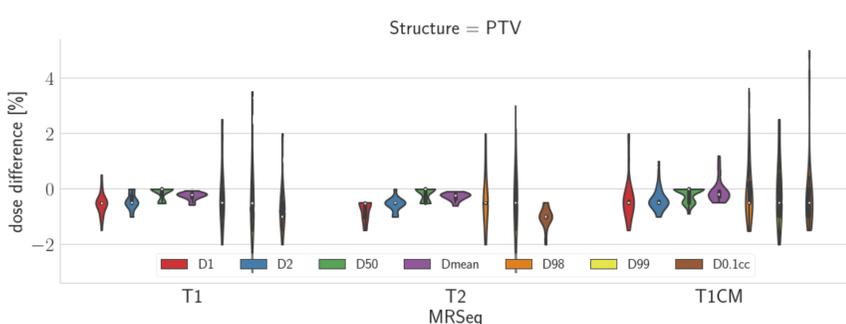


Figure 3: Difference of DVH parameters for the PTV.

Treatment Outcome Analysis:

- Summary of the percentage dose differences between re-calculated and originally calculated plans for the PTV (Figure 3)
- The varying input MRI sequences provided similar results (<1%), with slight advantage for T1CM
- The spot difference analysis (Figure 4) peaks at ±0.2 cm. For 95% of all spots the absolute differences was below 0.6 cm

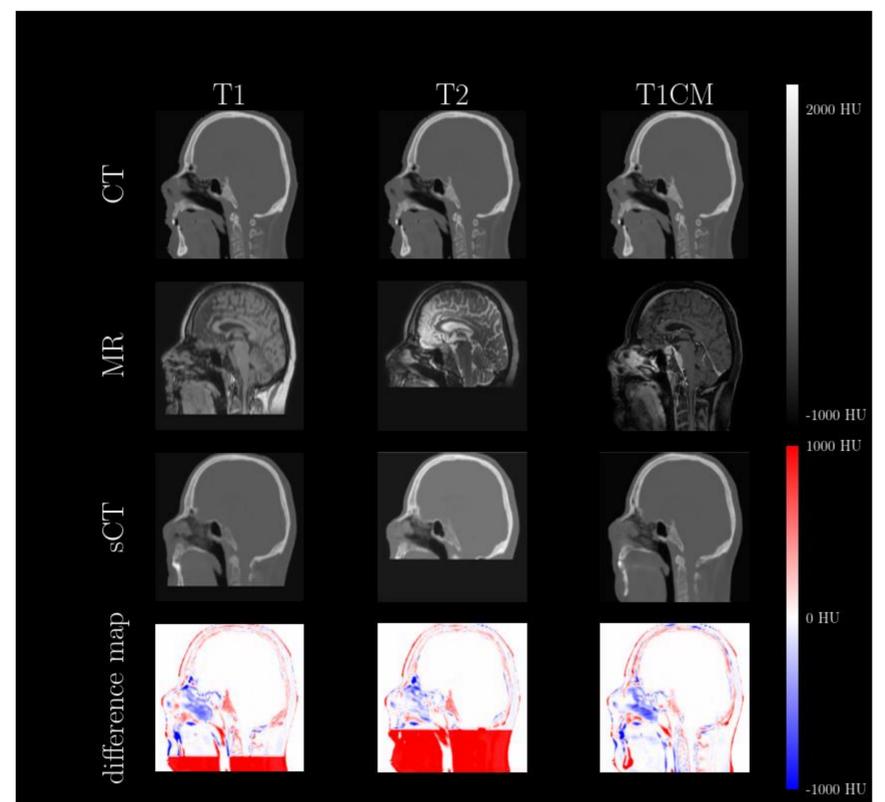


Figure 2: Generated sCTs with corresponding MRI sequence (T1, T2, T1CM) and CT images. Difference maps between the planning CT and sCT in the last row.

Discussion & Conclusion

- Training on multiple sequences was possible without compromising quality for any sequences
- The sCT quality is independent of the input MRI sequence. Thus, clinical MRI sequences can be used without hampering the clinical workflow.
- Dosimetric comparison (<1%) and spot difference maps showed a very good agreement
- The use of a universal sCT generator based on neural networks is an important step to enable translations of different MRI acquisition protocols

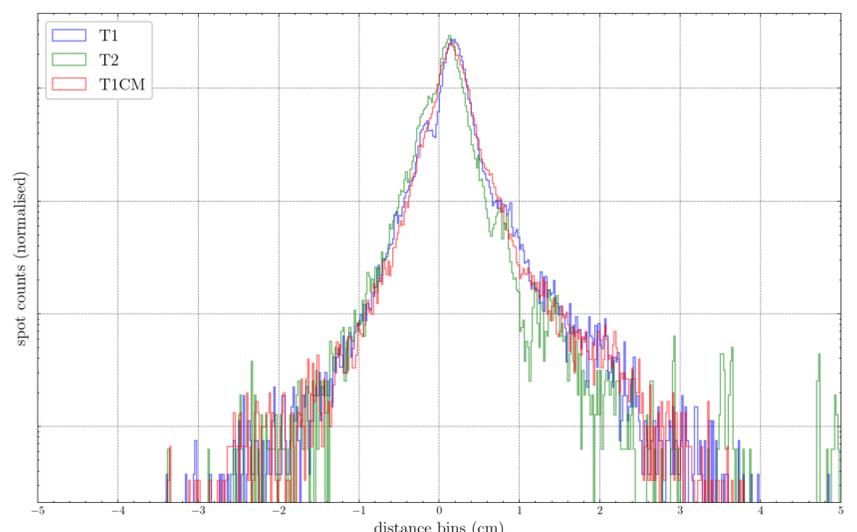


Figure 4: Spot difference between the planning CT and sCT. Values are normalized so that area under the histogram integrates to unity.

References

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