Herlev Hospital

REGION

MRI-only based radiotherapy

Creating a pseudo CT scan from a T_1-weighted MRI scan

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Background

In radiotherapy (RT) based on magnetic resonance (MR) as the only modality, the information on electron density which is usually obtained from the computed tomography (CT) must be derived from the MR. This is a challenging task, since no unique relationship between MR and electron density exists. Using a mathematical model trained on preexisting MR and CT correlated scans shows a promising approach to predict a so-called pseudo-CT (pCT) from the MR scan.

Recent attempts to create a pCT have involved the use of MR sequences such as the dual ultra short echo time (dUTE). Contrary to standard MR sequences, the dUTE sequence provides contrast between bone and air/tissue which is valuable discriminative information for a computational model. However, the dUTE sequence is non-clinical and not widely available. Furthermore, it may increase the scan time unacceptably for larger body parts such as the pelvis**.** In this work, we demonstrate that a pCT can be generated from a T_1-weighted (T1w) MR sequence using a patch-based (PB) method. We compare the accuracy of our predicted pCTs with those predicted using a multi-atlas approach based on T1w MR [1] and using a Gaussian Mixture regression (GMR) based on the dUTE sequence [2].

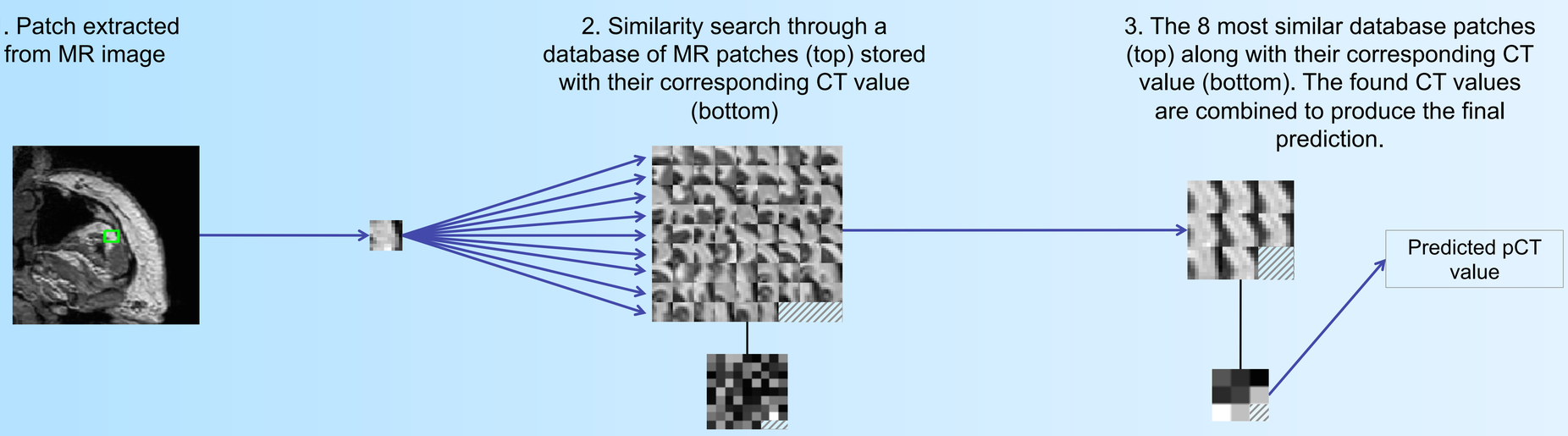
Data and Methods

Data

Head scans of 5 palliative patients fixated for cranial RT were acquired on a Philips Panorama 1 T open MR scanner with two flex coils. dUTE scans were recorded at flip angles 10 and 25 degrees, respectively. Echo- and repetition times were TE1/TE2/TR=0.09/3.5 /7.1 ms with a voxel resolution of 1x1x1 mm and a 256 mm FOV. The T1w scan was a 3D Fast Field Echo with TE/TR=6.9/25 ms, a voxel resolution of 0.85x0.85x1.2 mm and a 182.4 mm FOV. Corresponding CT head scans were also acquired using the same fixation. All scans were co-registered, resliced and cropped to the same resolution and FOV as the T1w.

Patch-based prediction

The idea behind the patch based (PB) prediction is that similarity in local anatomy between two patients' MR images translates to a similarity in their CT images. Contrary to traditional atlas based methods, PB prediction does not rely on non-linear registrations which can be slow and sensitive to interpatient variability. In the illustration below, the PB method is shown for a simplified 2D case - everything is actually done in 3D and methods for search space reduction are applied as in [3].



Method comparison

Nested cross-validation was carried out to find the optimal parameters for the PB method (patch size, search volume), multi-atlas method and GMR. A b-spline transform in Elastix was used for the deformable registration required for the multi-atlas method. Predictions were done in a leave-one-out manner in order to predict pCTs for each patient. . Each pCT was evaluated in terms of the mean absolute error (MAE) and Dice score (DSC) of bone using the real CT as reference:

$$MAE = \frac{1}{N}\sum_i |\, pCT(i) - CT(i) \,|$$ (N: size of data, *i:* index of spatially corresponding voxels).

$$DSC = \frac{2(V_{pCT} \cap V_{CT})}{V_{pCT} + V_{CT}}$$ (V_{pCT} , V_{CT}: bone volumes in pCT and CT, respectively)

A dose plan was made for 2 targets in all patients with static fields and 2 Gy to be delivered in 30 fractions. Dose calculation was carried out on the pCT and the plan was transferred to the real CT and re-calculated using fixed parameters. Percentage deviation was calculated in the Dose Volume Histogram (DVH) points: D_{median} – the dose received by 50% and less of the target, $D_{2\%}$ - the dose received by 2% and less of the target and $D_{98\%}$ - the dose received by 98% and less of the target.

Results

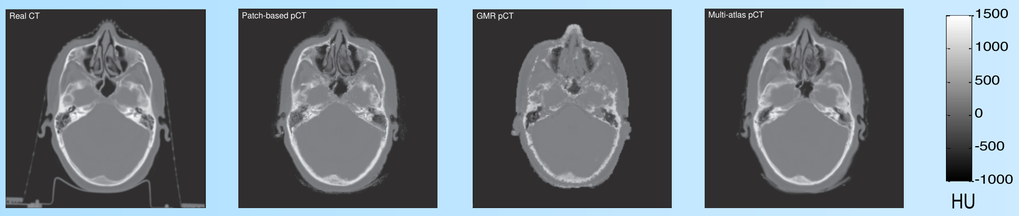
Table 1 shows the average MAE and DSC. Figure 1 shows the real CT and predicted pCTs. Figure 2 shows the position of the targets used for dose planning and the deviation in DVH points.

Accuracy of predictions

	Patch-based	GMR	Multi-atlas
MAE (5 patients)	85 HU (σ=14 HU)	148 HU (σ=22 HU)	97 HU (σ=19 HU)
DSC (5 patients)	0.84 (σ=0.02)	0.67 (σ=0.03)	0.83 (σ=0.01)

Table 1: Average and standard deviation of MAE and Dice score on bone. DSC=1 means perfect overlap of bone volumes.

Figure 1: Real CT and pseudo CTs



Dosimetric evaluation

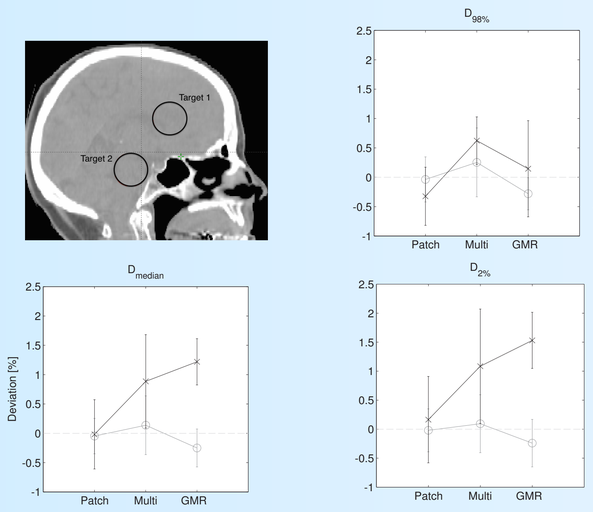


Figure 2: Top left panel: Position of the targets.
Other panels: Percentage deviation in DVH points. Grey lines and circles: Target 1. Black lines and crosses: Target 2.

Conclusion

There was an indication that the PB method is superior to GMR and multi-atlas in terms of the MAE and the dosimetric accuracy. A study with more patients should be carried out before drawing conclusions. The fact that the PB and multi-atlas methods use standard T1w MR images makes the them easily implementable in the clinical workflow.

References

[1] Burgos et al.: Attenuation Correction Synthesis for Hybrid PET-MR Scanners.

[2] Johansson et al.: CT Substitute Derived from MR Sequences with Ultrashort Echo Time.

[3] Coupé et al.: Patch-based Segmentation using Expert Priors: Application to Hippocampus and Ventricle Segmentation.

Presented at the Summer School on Deep Learning in Image Analysis, Langeland 2014. Corresponding author: Daniel Andreasen, dana@dtu.dk