

ABSTRACT

PURPOSE - To generate synthetic CT (sCT) from routine site-specific MRI without requiring an additional designated sequence that prolongs simulation.

METHODS - A unified nnsyn strategy supported one-sequence prostate MRI and two-sequence abdomen and brain MRI. Site-specific models were developed using 235 patients.

RESULTS - Compared with CycleGAN, nnsyn reduced body and bone MAE in abdomen and reduced body MAE while improving PSNR in prostate. Brain sCT preserved fine anatomical detail.

CONCLUSION - Flexible MRI inputs support a practical MR-only workflow; dosimetric and multi-center validation are ongoing.

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Flexible Synthetic CT Generation Using nnsyn Deep Learning Network with Single- and Multi-Sequence Clinical MRI

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INTRODUCTION

- Magnetic resonance (MR)—only radiotherapy planning requires accurate synthetic CT (sCT) generation from images acquired using standard clinical MRI simulation protocols [1].
- However, MRI acquisition protocols vary substantially across anatomical sites, and many existing sCT models rely on a designated sequence (e.g., T1-weighted mDixon) necessitating inclusion of this sequence in all site-specific protocols. [2]
- This requirement is suboptimal, as it extends simulation scan time by about 5 minutes per patient.
- In this study, we developed and evaluated a site-specific sCT generation method that uses only routinely acquired clinical MR sequences and supports heterogeneous single- and multi-sequence inputs across multiple anatomical sites.

METHODS AND MATERIALS

- Patients Data
 - Brain: 62; POST T1 GRE 3D + POST T1 TSE 3D
 - Abdomen: 83; T2 MVXD 2D + T2 MVXD SPIR 2D
 - Prostate: 90; T2 TSE 3D only
- A deep learning–based sCT generation model adapted from the no-new synthetic network (nnsyn) architecture was developed with a flexible input design to accommodate heterogeneous MR sequences[3].
- Separate models were trained for each anatomical site using a unified network structure and training strategy.
- Prostate cases utilized a single standard MR sequence, while abdominal and brain cases used two routinely acquired MR sequences.
- The quality of sCT was quantitatively evaluated for each site using voxel-wise mean absolute error (MAE) and peak signal-to-noise ratio (PSNR), computed within the body contour and bony regions.
- The proposed model was compared with the in-house cycle generative adversarial network (CycleGAN) as a baseline for each site[4].

RESULTS

- Table 1 summarizes the image-quality results for abdomen and prostate.
- Abdomen body MAE decreased from 90.8 to 78.6 HU (13%), and bone MAE decreased from 166.4 to 139.7 HU (16%); both differences were significant.
- Prostate body MAE decreased from 66.3 to 42.9 HU (35%), while PSNR increased from 30.5 to 32.3 dB; both differences were significant.
- Brain performance was 98.7 ± 7.1 HU body MAE, 219.9 ± 24.7 HU bone MAE, and 25.2 ± 0.8 dB PSNR; no baseline comparator was available.
- Figures 1 and 2 demonstrate accurate reconstruction of bony structures across diverse anatomical sites, with preserved skull-base detail and more anatomically consistent sCT intensity patterns.

DISCUSSION

- The flexible-input strategy used routine site-specific MRI while maintaining one common learning framework for single- and multi-sequence inputs.
- Eliminating a designated mDixon acquisition can reduce simulation time by approximately 5 minutes per patient.
- The largest improvement was observed in prostate body MAE; abdomen showed significant reductions in both body and bone MAE. Qualitative findings were consistent with the quantitative results.
- The models remain site-specific, and a matched brain baseline was unavailable. Cross-site generalizability has not yet been established.
- Dosimetric accuracy, robustness across institutions, and performance in downstream treatment planning require further validation.

Table 1. Abdomen and prostate image metrics (mean ± SD). An asterisk indicates a statistically significant difference. For the brain, no baseline model was available for comparison.

Metric	Baseline	Proposed	Change
Abdomen body MAE	90.8 ± 10.5	78.6 ± 9.9*	-13%
Abdomen bone MAE	166.4 ± 18.3	139.7 ± 19.7*	-16%
Abdomen PSNR	29.0 ± 0.7	29.3 ± 0.8	+0.3 dB
Prostate body MAE	66.3 ± 13.7	42.9 ± 6.5*	-35%
Prostate bone MAE	162.0 ± 45.8	149.0 ± 52.4	-8%
Prostate PSNR	30.5 ± 3.4	32.3 ± 2.7*	+1.8 dB
Brain body MAE	-	98.7 ± 7.1	-
Brain bone MAE	-	219.9 ± 24.7	-
Brain PSNR	-	149.0 ± 52.4	-

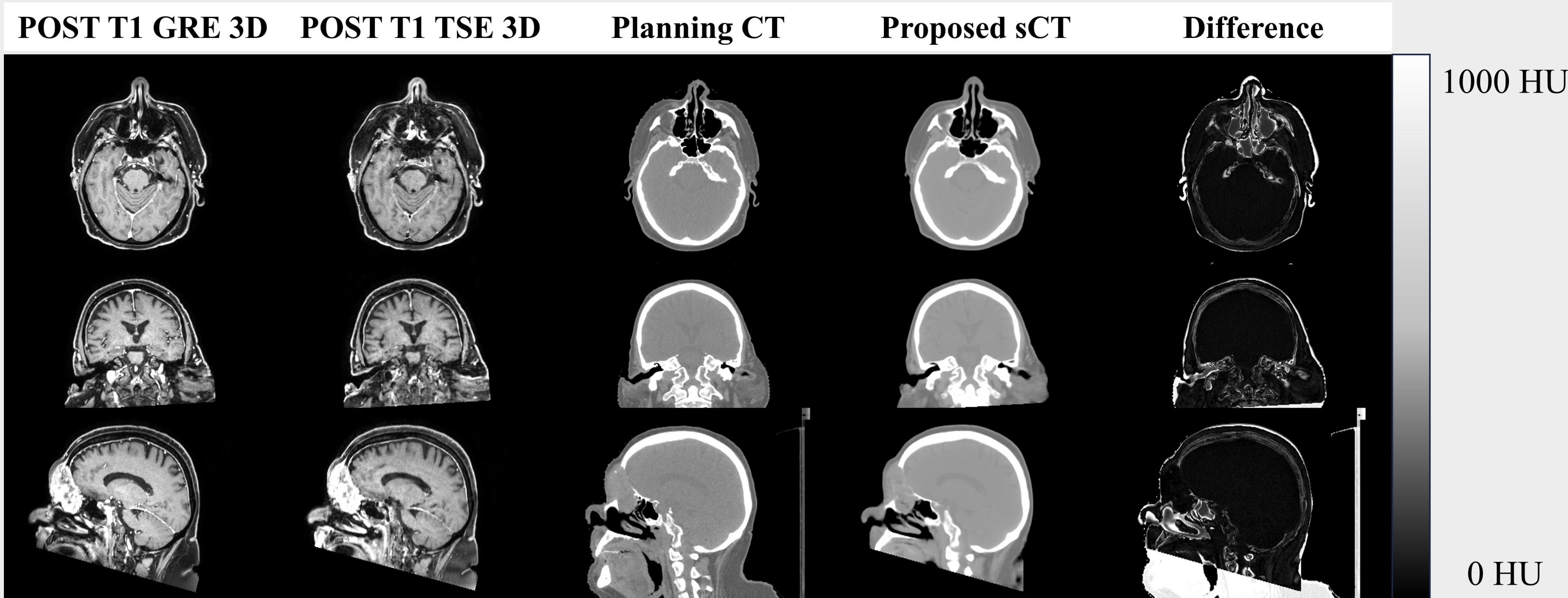


Figure 1. Brain MRI inputs, planning CT, proposed sCT, and voxel-wise difference maps.

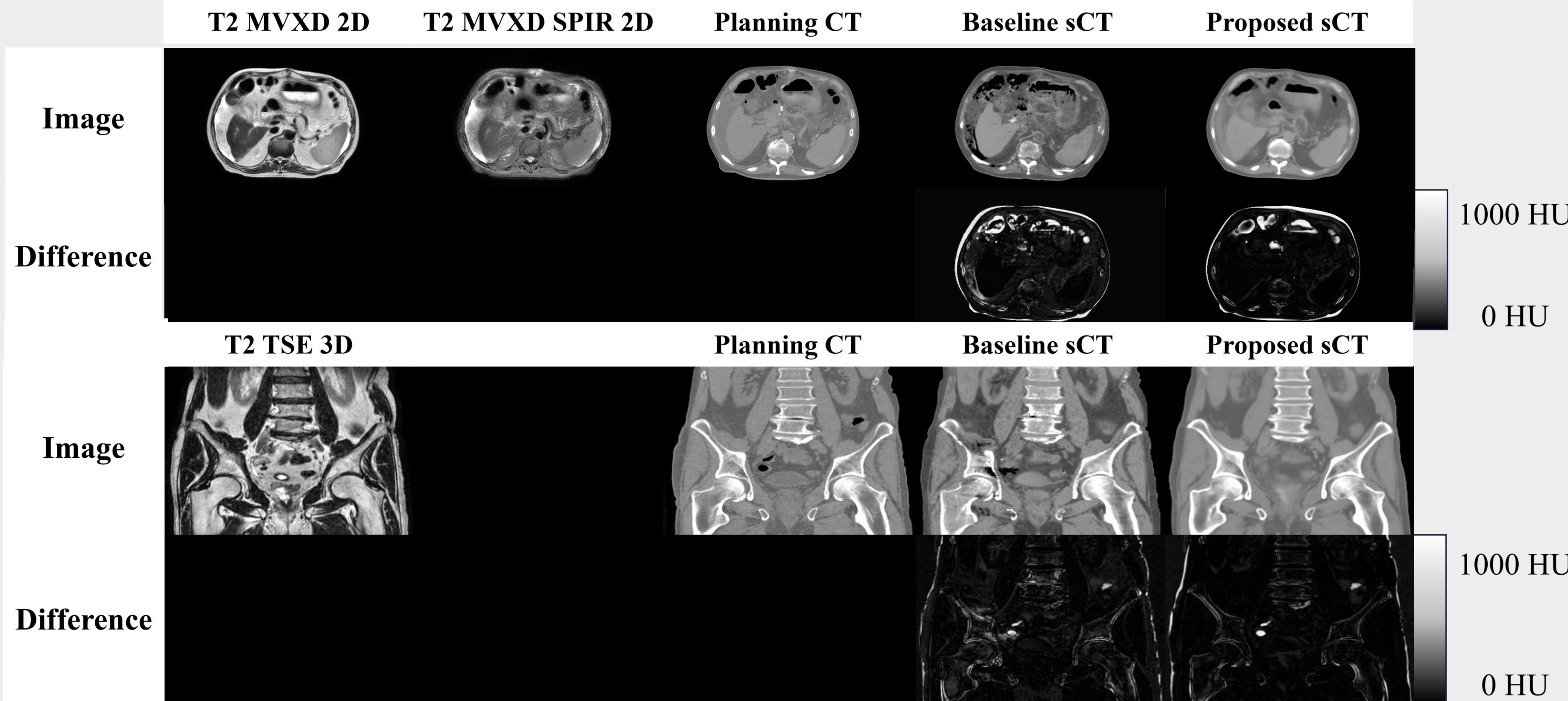


Figure 2. Abdomen and prostate comparison of baseline and proposed sCT with difference maps.

CONCLUSIONS

The nnsyn framework generated sCT images from routine single- and multi-sequence MRI in 235 patients. Compared with CycleGAN, it improved image metrics in the abdomen and prostate while preserving brain anatomy. This approach may support MR-only planning without requiring an additional dedicated MRI sequence.

REFERENCE

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