

2D to 3D Line Pattern Match (3DLM) Scheme in 6D for Marker **Based Image Guided Radiation Therapy**

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INTRODUCTION

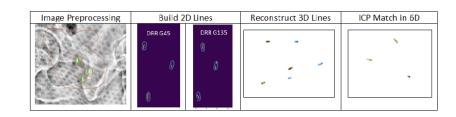
Maker image guided radiation therapy in clinic relies on visually match between the pre-treatment image to the reference image. Using paired-planar-image to verify the pretreatment position, operator typically manually matches the makers in translation. By reconstructing the makers in 3D, 2D paired-image can be automatically registered in 3D and can be computed both translation and rotation transformation accurately.

AIM

Develop a 2D to 3D line pattern automatic registration scheme (3DLM) in 6D for marker-based image guided radiation therapy.

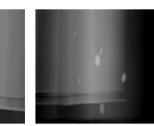
METHOD

- The markers on 2D paired-planar-image were identified using an enhanced sobel filter.
- Marker edges were then skeletonized to draw 2D line pattern on paired-planar- image.
- Central moment of the marker edges was utilized to reconstruct 2D lines to 3D lines.
- An iterative closest point (ICP) algorithm was followed to calculate the 6D transformation from 3D line pattern of the pretreatment paired-image to 3D line pattern of the DRR paired-
- The automatch software was validated by comparing the 6D transformation calculated from 3DLM to the 6D transformation after CBCT matched to the reference CT.
- A series of one marker-implanted prostate patient's pretreatment paired-images using manually match (MM) were used to compare registration results between 3DLM and MM.



RESULTS

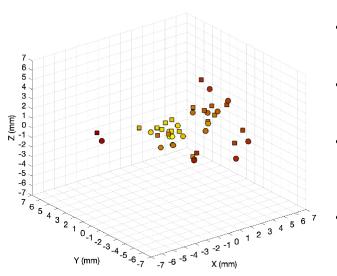
Validation of the 3DLM



CBCT to planning CT match phantom Paired X-ray image (45° & 315°) match to DRR using the 3DLM in 6D in 6D

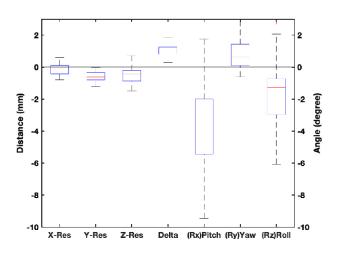
- Six phantom measurements were done to compare 3DLM with CBCT 3D/3D match.
- The mean±SD in each dimension was $(0.1\pm1.2\text{mm})_{x}$, $(0.5\pm0.6\text{mm})_{x}$, $(0.0\pm0.8\text{mm})_{z}$, $(0.2\pm0.1^{\circ})_{Rx}$, $(0.0\pm0.3^{\circ})_{Ry}$, $(0.5\pm0.7^{\circ})_{Rz}$ respectively.

Comparing Manual Match (performed with translation only, symbol) to the re-alignment using the 3DLM (in 6D, symbol):



- The mean±SD differences were: $(-0.1\pm0.4\text{mm})_{y}$, (- 0.6 ± 0.4 mm)_y, $(-0.5\pm0.5$ mm)_z
- The mean±SD vector distance from MM shift to 3DLM shift was $(1\pm0.4\text{mm})$.
- The rotational misalignments calculated from 3DLM were $(-3.9\pm2.8^{\circ})_{Rx}$, $0.8\pm0.9^{\circ})_{Ry}$, (- $1.6\pm2.7^{\circ}$)_{Rz}.
- Paired t-test showed insignificant different in the X direction (P=0.43).

Boxplot distribution of manual match residual error in 6D



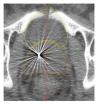
- 43% of the images showed pitch direction misaligned more than 5°;
- 10% showed roll direction miss-aligned more than 5°;
- no miss-alignment in yaw direction was more than 3°.

Example of 3DLM showed large rotational miss-alignment







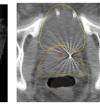


3DLM: Pitch: -6.3°: Roll: -2.1°: Yaw: 1.5°. CBCT: insufficient bladder volume.









3DLM: Pitch: -5.8°; Roll: -3.3°; Yaw: 0.2°. CBCT: insufficient bladder volume & large air gas level in rectum.

CONCLUSIONS

- The 3DLM scheme is feasible and has accuracy comparable to the 3D match of CBCT.
- Its clinical implementation is more efficient than taking CBCT, much robust than using 2D paired-image MM, and have both translational and rotational misalignment information as using CBCT.
- Weekly CBCT image showed that the pitch and yaw misalignments were mainly due to insufficient bladder filling and high level of air gas in rectum.
- This study didn't see a major discrepancy (~1mm) of position match comparing MM to 3DLM, however, 6D misalignment information would be helpful to prescreen and to suggest whether a further CBCT verification is needed to address the potential bladder and rectal problem.

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