

A fast and robust 2D-3D image registration: application to image-guided proton therapy in the presence of anatomical deformation

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Background and aims

Proton therapy takes advantage of the unique characteristics of the Bragg peak to deliver radiation precisely to the tumor while minimizing damage to surrounding tissues. Accurate image registration is essential to ensure precise treatment delivery. However, conventional global 2D-3D image registration often fails to converge in the presence of anatomical deformations between the reference positioning CT image and pre-treatment X-ray images. Therefore, a new registration method is needed to achieve fast and accurate results under complex geometric conditions.

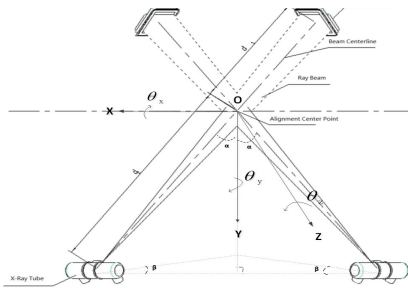


Fig. 1. a) the imaging geometry and 3D coordinate system of the imaging guided system.

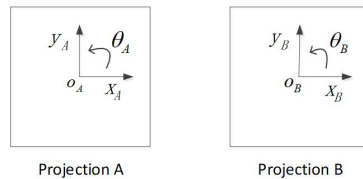


Fig. 1. b) the 2D coordinate system in projection A and B

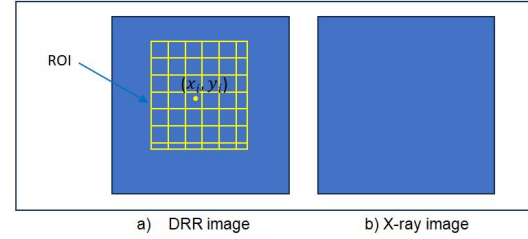


Fig. 2. ROI block sketch

Methods

To address this challenge, we propose a novel block-based similarity calculation method. The region of interest is divided into blocks, and similarity is independently evaluated for each block. The optimal rigid transformation is determined based on the number of similar blocks. Multithreading is incorporated to enhance computational speed. The algorithm's accuracy was validated using head, chest, and abdomen phantoms. Additionally, 468 registration pairs from 17 proton therapy patients (14 chest, 2 abdomen, 1 pelvis) were analyzed, covering 74 fractions with repeated X-rays (≥ 5 times) and deviated couch shifts that guided patients to accurate treatment positions. The couch shift values were used as the gold standard for both phantom and patient verifications. Similarity maps were generated for both the original and the proposed algorithm results, and the performance was assessed based on the principle that a larger region of similarity indicates superior registration accuracy.

Results

Phantom validation demonstrated that the maximum translation errors for the head, chest, and abdomen regions were all within 1 mm, while rotational errors were within 1° . Patient data analysis showed that the proposed method effectively identified optimal rigid registration regions even in the presence of deformations, achieving rapid convergence to the correct treatment position. The entire registration process was completed within 2 seconds.

Conclusions

The proposed block-based similarity calculation algorithm significantly reduces registration errors and improves both the efficiency and accuracy of image registration in proton therapy. Experimental results demonstrated that the algorithm effectively handles anatomical deformations by registering larger regions and converging to accurate positions more quickly. This method holds significant promise for enhancing the precision of image-guided proton therapy.

Table 1 Results of head, chest and abdomen simulation phantom

Body Site	Couch shift						Registration result						Registration error					
	x(mm)	y(mm)	z(mm)	pitch	roll	rotation	x(mm)	y(mm)	z(mm)	pitch	roll	rotation	x(mm)	y(mm)	z(mm)	pitch	roll	rotation
Head	0	0	0	0	0	0	-0.33	0.73	0.86	0.05	0	0.13	0	0	0	0	0	0
	2	2	2	2	2	2	-2.42	-1.64	-1.83	-1.94	-2.31	-1.74	-0.09	-0.37	-0.69	0.01	-0.31	0.13
	-2	-2	-2	-2	-2	-2	1.66	1.1	2.2	2.73	2.08	1.92	-0.14	-0.35	0.31	0.15	-0.28	0.02
Chest	0	0	0	0	0	0	-0.2	0.18	0.52	-0.03	0.3	0.19	0	0	0	0	0	0
	2	2	2	2	2	2	-2.38	-1.64	-1.82	-1.93	-1.94	-2.1	-0.18	0.18	-0.34	0.1	-0.24	-0.29
	-2	-2	-2	-2	-2	-2	2.03	2.37	2.16	2.24	2	2.09	-0.51	0.37	-0.07	0.26	0	-0.02
Abdomen	0	0	0	0	0	0	-0.54	0	-0.28	-0.01	0.42	0.21	0	0	0	0	0	0
	2	2	2	2	2	2	-2.52	-2.36	-2.19	-2.78	-1.03	-2.01	0.02	-0.36	0.09	-0.77	0.55	-0.22
	-2	-2	-2	-2	-2	-2	1.66	2.74	1.71	2.54	1.22	2.37	-0.36	-0.17	-0.67	0.22	-0.27	0.32

Table 2. Results of real patient data

Patient No.	Fraction No. (X-ray No.)	Original result					the registration result of this method					Similarity degree	
		x	y	z	pitch	roll	x	y	z	pitch	roll	Original	This method
1	100	184	-2.53	269	0.12	-0.58	1.77	123	-0.27	0.86	-0.53	0.18	-0.05
	5(11)	039	-0.09	126	-1.11	-0.65	-0.79	084	-0.05	1.05	-0.52	-0.76	-0.51
	4(18)	346	-3.62	041	-0.43	-3.55	-0.95	335	-4.72	022	-0.98	-0.34	-0.02
	7(31)	846	-8.62	041	-0.43	-3.55	-0.95	256	-3.18	115	-0.6	-0.35	-0.51
	8(39)	167	-2.18	372	-0.51	-1.82	-0.88	123	-4	137	-0.77	-0.78	-0.39
	10(47)	328	-2.18	345	-1.85	1	-1.86	179	2	118	-0.84	-0.46	-0.05
	3(2)	844	0.91	152	-2.67	0.86	110	-0.20	0.18	1.95	1.27	0.89	1.11
	4(16)	012	0.55	-0.96	0.98	0.20	1.11	-1.48	118	-1.21	103	1.01	1.10
	7(27)	230	-0.72	037	1.25	1.01	-0.03	006	0.73	056	0.03	2.32	0.54
	8(32)	123	-1.48	-0.08	1.59	-0.10	-0.19	-2.49	-1.62	1.77	0.69	1.41	1.84
2	1(0)	205	1.84	03	0.73	0.07	2	281	2.19	-0.91	-0.19	1.16	0.3
	3(7)	188	-1.45	-0.01	-0.21	0.79	-0.15	2	-1.64	-0.47	-0.75	0.65	-0.22
	4(13)	-0.18	-1.44	2.01	0.64	-1.56	0	-1.09	1.85	0.42	-1.25	-1.13	
	6(22)	579	-2.36	188	0.52	1.36	0.32	561	-0.09	-1.06	0.86	1.31	-1.06
	9(50)	1.14	0.72	291	0.05	-1.29	0.27	-0.06	0.01	0.97	-1.22	-0.93	0.4
	9(41)	487	-0.75	128	1.54	1.02	0.25	637	-0.18	-4.17	-0.06	2.23	0.88
	1(0)	-0.05	-0.74	-3.44	-1.1	0.83	1.37	0.84	0.97	-0.12	1.55	0.06	
	8(28)	-4.79	-4.38	-1.77	-2.09	2.02	0.35	-1.21	-5.1	-1.62	-1.13	2.15	-0.69
	9(46)	-0.83	-1.85	2.28	-2.13	2.02	-0.73	-0.13	-2.38	1.79	-1.79	1.8	-0.97
	11(80)	119	-5.1	-4.19	-1.33	2.97	-0.62	1.71	-5.82	4.41	-1.19	2.12	-0.49
	18(70)	337	-6.75	-1.01	-1.42	2.5	-2.86	1.25	-7.05	-0.39	-1.71	0.4	-0.09

Fig. 3. adding a similarity map on the DRR image. Green color indicates the similarity value high, yellow color indicates the similarity value medium, and red color indicates the similarity value low.

