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## Deep learning for online adaptive radiotherapy

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## Appendix of chapter 5

In this appendix we provide a detailed results for the proposed methods and associated experiments in terms of DSC and %95 HD.

Table 1: The effect of network input for the different architectures on the validation set (HMC) in terms of DSC. Higher values are better. Here,  $\oplus$  is the concatenation operation, and  $\cdot\|\cdot$  represents the inputs to the segmentation network (left of  $\|\|$ ) and the inputs to the registration network (right of  $\|\|$ ).

Network	Input	Output path	Prostate		Seminal vesicles		Rectum		Bladder	
			$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median
Seg	$I_f$		0.84 ± 0.03	0.84	0.60 ± 0.14	0.62	0.75 ± 0.10	0.77	0.90 ± 0.07	0.93
	$I_f \oplus S_m$		0.85 ± 0.05	0.86	0.66 ± 0.16	0.72	0.79 ± 0.12	0.82	0.93 ± 0.03	0.94
	$I_f \oplus I_m$		0.66 ± 0.08	0.67	0.39 ± 0.21	0.40	0.39 ± 0.21	0.41	0.91 ± 0.08	0.93
	$I_f \oplus I_m \oplus S_m$		0.86 ± 0.04	0.87	0.64 ± 0.16	0.70	0.78 ± 0.08	0.78	0.93 ± 0.03	0.94
Reg	$I_f \oplus I_m$		0.85 ± 0.06	0.86	0.62 ± 0.18	0.68	0.79 ± 0.08	0.81	0.82 ± 0.10	0.84
	$I_f \oplus I_m \oplus S_m$		0.82 ± 0.08	0.83	0.60 ± 0.17	0.65	0.77 ± 0.08	0.80	0.79 ± 0.13	0.83
JRS-reg	$I_f \oplus I_m$		0.87 ± 0.04	0.87	0.68 ± 0.14	0.72	0.82 ± 0.06	0.84	0.87 ± 0.08	0.91
	$I_f \oplus I_m \oplus S_m$		0.87 ± 0.04	0.87	0.67 ± 0.15	0.72	0.83 ± 0.06	0.84	0.87 ± 0.08	0.91
Cross-stitch	$I_f \ \  I_f \oplus I_m$	Segmentation	0.85 ± 0.03	0.85	0.57 ± 0.19	0.60	0.81 ± 0.08	0.83	0.93 ± 0.05	0.94
		Registration	0.87 ± 0.03	0.88	0.67 ± 0.15	0.70	0.82 ± 0.06	0.84	0.87 ± 0.08	0.91
	$I_f \ \  I_f \oplus I_m \oplus S_m$	Segmentation	<b>0.88 ± 0.04</b>	0.88	<b>0.70 ± 0.11</b>	<b>0.74</b>	<b>0.86 ± 0.05</b>	<b>0.88</b>	<b>0.94 ± 0.02</b>	<b>0.95</b>
		Registration	0.87 ± 0.03	0.88	0.68 ± 0.15	0.73	0.84 ± 0.05	0.85	0.88 ± 0.08	0.91
	$I_f \oplus S_m \ \  I_f \oplus I_m \oplus S_m$	Segmentation	0.77 ± 0.11	0.79	0.52 ± 0.19	0.57	0.80 ± 0.05	0.80	0.93 ± 0.03	0.94
		Registration	0.85 ± 0.04	0.85	0.66 ± 0.14	0.72	0.80 ± 0.06	0.82	0.87 ± 0.08	0.90
$I_f \oplus I_m \oplus S_m \ \  I_f \oplus I_m \oplus S_m$	Segmentation	0.88 ± 0.04	<b>0.89</b>	0.67 ± 0.15	0.72	0.85 ± 0.05	0.86	0.94 ± 0.03	0.95	
	Registration	0.86 ± 0.04	0.87	0.67 ± 0.16	0.72	0.83 ± 0.06	0.84	0.88 ± 0.08	0.91	

Table 2: The effect of network input for the different architectures on the validation set (HMC) in terms of %95 HD (mm). Lower values are better. Here,  $\oplus$  is the concatenation operation, and  $\cdot\|\cdot$  represents the inputs to the segmentation network (left of  $\|\|$ ) and the inputs to the registration network (right of  $\|\|$ ).

Network	Input	Output path	Prostate		Seminal vesicles		Rectum		Bladder	
			$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median
Seg	$I_f$		4.4 ± 1.0	4.4	8.6 ± 8.6	7.3	16.5 ± 11.0	13.3	6.9 ± 6.6	4.0
	$I_f \oplus S_m$		3.9 ± 1.4	3.6	5.9 ± 5.9	4.1	12.1 ± 9.7	8.9	4.3 ± 3.2	3.0
	$I_f \oplus I_m$		9.1 ± 2.3	8.7	14.9 ± 10.5	11.7	45.1 ± 17.3	41.8	5.3 ± 5.6	3.6
	$I_f \oplus I_m \oplus S_m$		3.8 ± 1.1	3.6	7.3 ± 9.2	4.2	11.5 ± 6.7	9.6	3.3 ± 1.5	3.0
Reg	$I_f \oplus I_m$		5.5 ± 4.5	4.0	5.6 ± 4.1	4.3	11.0 ± 6.4	9.4	15.7 ± 9.6	12.1
	$I_f \oplus I_m \oplus S_m$		7.7 ± 6.3	5.5	6.2 ± 4.2	4.8	11.6 ± 6.8	9.2	17.0 ± 9.5	14.7
JRS-reg	$I_f \oplus I_m$		3.6 ± 1.3	3.0	4.5 ± 3.0	3.3	9.6 ± 5.7	8.2	13.1 ± 10.1	9.4
	$I_f \oplus I_m \oplus S_m$		3.6 ± 1.9	3.1	4.4 ± 2.8	3.7	9.8 ± 5.9	8.1	13.4 ± 10.7	10.6
Cross-stitch	$I_f \ \  I_f \oplus I_m$	Segmentation	5.1 ± 2.3	4.4	9.5 ± 9.6	6.1	17.2 ± 14.0	12.6	5.0 ± 6.6	3.0
		Registration	3.3 ± 0.9	3.0	4.7 ± 3.0	3.7	10.1 ± 6.3	9.0	12.6 ± 10.0	9.4
	$I_f \ \  I_f \oplus I_m \oplus S_m$	Segmentation	<b>3.0 ± 1.0</b>	<b>3.0</b>	<b>4.3 ± 1.7</b>	3.9	<b>9.5 ± 6.2</b>	<b>7.2</b>	<b>3.3 ± 2.9</b>	<b>2.3</b>
		Registration	3.2 ± 0.9	3.0	4.5 ± 3.3	3.6	9.8 ± 6.3	8.6	12.2 ± 10.1	9.7
	$I_f \oplus S_m \ \  I_f \oplus I_m \oplus S_m$	Segmentation	5.8 ± 2.0	5.9	11.0 ± 13.4	5.8	10.2 ± 4.9	8.5	4.5 ± 4.3	3.0
		Registration	4.4 ± 1.6	4.1	4.5 ± 3.3	3.6	10.2 ± 5.7	9.3	12.9 ± 9.3	11.1
$I_f \oplus I_m \oplus S_m \ \  I_f \oplus I_m \oplus S_m$	Segmentation	3.1 ± 1.0	3.0	5.4 ± 5.4	4.4	9.7 ± 5.6	8.9	4.2 ± 5.6	2.6	
	Registration	3.5 ± 1.2	3.2	4.4 ± 3.1	<b>3.4</b>	10.2 ± 6.3	9.1	12.5 ± 10.6	8.7	

Table 3: DSC values for the different networks and loss weighting methods for the HMC dataset. Higher values are better.

Network	Weight	Output path	Prostate		Seminal vesicles		Rectum		Bladder	
			$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median
JRS-reg	Equal	Registration	0.84 ± 0.16	0.89	0.67 ± 0.25	0.79	0.76 ± 0.14	0.79	0.79 ± 0.17	0.88
	Homoscedastic	Registration	0.84 ± 0.16	0.89	0.68 ± 0.25	0.77	0.76 ± 0.15	0.80	0.80 ± 0.18	0.89
	DWA	Registration	0.83 ± 0.16	0.88	0.66 ± 0.25	0.78	0.74 ± 0.15	0.79	0.76 ± 0.18	0.84
Dense	Equal	Segmentation	0.83 ± 0.15	0.88	0.55 ± 0.29	0.65	0.78 ± 0.16	0.81	0.88 ± 0.11	0.93
		Registration	0.83 ± 0.16	0.88	0.66 ± 0.25	0.75	0.76 ± 0.15	0.80	0.79 ± 0.16	0.87
	Homoscedastic	Segmentation	0.84 ± 0.16	0.89	0.63 ± 0.27	0.75	0.79 ± 0.16	0.82	0.87 ± 0.13	0.93
		Registration	0.84 ± 0.16	0.88	0.68 ± 0.25	0.78	0.77 ± 0.14	0.80	0.78 ± 0.17	0.86
	DWA	Segmentation	0.84 ± 0.15	0.89	0.58 ± 0.28	0.67	<b>0.79 ± 0.15</b>	<b>0.83</b>	0.88 ± 0.12	0.93
		Registration	0.84 ± 0.16	0.89	0.67 ± 0.24	0.76	0.76 ± 0.15	0.79	0.79 ± 0.16	0.87
SEDD	Equal	Segmentation	0.79 ± 0.16	0.85	0.46 ± 0.28	0.53	0.77 ± 0.14	0.80	0.85 ± 0.12	0.91
		Registration	0.82 ± 0.16	0.87	0.66 ± 0.26	0.78	0.75 ± 0.15	0.79	0.78 ± 0.16	0.86
	Homoscedastic	Segmentation	0.84 ± 0.15	0.89	0.50 ± 0.28	0.58	0.76 ± 0.18	0.82	0.88 ± 0.13	0.94
		Registration	0.84 ± 0.16	0.88	0.68 ± 0.24	0.78	0.76 ± 0.15	0.80	0.79 ± 0.17	0.88
	DWA	Segmentation	0.83 ± 0.14	0.88	0.62 ± 0.27	0.74	0.78 ± 0.16	0.83	0.87 ± 0.14	0.94
		Registration	0.84 ± 0.15	0.88	0.67 ± 0.24	0.78	0.75 ± 0.15	0.79	0.78 ± 0.18	0.86
Cross-stitch	Equal	Segmentation	<b>0.84 ± 0.14</b>	<b>0.89</b>	0.61 ± 0.27	0.73	0.78 ± 0.14	0.81	0.88 ± 0.10	0.93
		Registration	0.84 ± 0.15	0.89	<b>0.68 ± 0.24</b>	<b>0.80</b>	0.77 ± 0.15	0.80	0.80 ± 0.16	0.87
	Homoscedastic	Segmentation	0.84 ± 0.13	0.87	0.65 ± 0.24	0.76	0.74 ± 0.18	0.80	<b>0.92 ± 0.08</b>	<b>0.95</b>
		Registration	0.84 ± 0.15	0.89	0.68 ± 0.24	0.79	0.75 ± 0.15	0.79	0.80 ± 0.17	0.87
	DWA	Segmentation	0.82 ± 0.14	0.86	0.66 ± 0.24	0.76	0.75 ± 0.18	0.79	0.92 ± 0.08	0.95
		Registration	0.84 ± 0.15	0.89	0.68 ± 0.23	0.79	0.75 ± 0.15	0.78	0.77 ± 0.17	0.83

Table 4: %95 HD (mm) values for the different networks and loss weighting methods for the HMC dataset. Lower values are better.

Network	Weight	Output path	Prostate		Seminal vesicles		Rectum		Bladder	
			$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median
JRS-reg	Equal	Registration	5.2 ± 5.7	3.2	6.5 ± 7.1	4.0	12.6 ± 6.7	12.0	20.3 ± 14.0	18.6
	Homoscedastic	Registration	5.7 ± 5.9	3.7	6.2 ± 7.1	3.6	13.0 ± 7.3	<b>11.5</b>	18.5 ± 14.0	13.0
		DWA	Registration	5.7 ± 5.9	3.5	6.4 ± 6.8	3.7	13.2 ± 7.3	12.2	20.0 ± 13.2
Dense	Equal	Segmentation	5.7 ± 5.4	4.1	14.4 ± 17.2	6.8	16.8 ± 12.6	13.6	10.9 ± 10.9	5.5
		Registration	5.6 ± 5.6	4.0	6.6 ± 7.8	4.0	13.1 ± 6.7	13.0	19.6 ± 12.0	17.4
	Homoscedastic	Segmentation	5.8 ± 5.9	3.3	10.0 ± 11.6	5.1	17.1 ± 16.6	13.8	11.4 ± 11.3	5.9
		Registration	5.3 ± 5.7	3.0	6.4 ± 6.8	<b>3.2</b>	13.0 ± 6.5	12.6	19.2 ± 13.7	14.2
	DWA	Segmentation	5.4 ± 5.5	3.6	12.7 ± 17.0	5.9	16.2 ± 12.5	14.4	10.8 ± 10.7	6.2
		Registration	5.3 ± 5.6	3.5	<b>6.0 ± 6.6</b>	<b>3.3</b>	13.1 ± 7.2	13.0	19.4 ± 11.9	17.4
SEDD	Equal	Segmentation	8.5 ± 7.1	6.0	18.9 ± 19.5	8.6	16.7 ± 11.9	14.7	12.7 ± 11.0	8.5
		Registration	5.6 ± 5.8	3.6	6.7 ± 7.2	4.1	13.3 ± 7.0	12.0	19.0 ± 12.7	15.2
	Homoscedastic	Segmentation	5.7 ± 5.5	3.9	16.0 ± 16.3	10.6	18.8 ± 16.5	15.3	9.4 ± 9.9	4.1
		Registration	5.5 ± 5.6	3.3	6.3 ± 6.7	3.6	13.3 ± 7.3	13.0	18.8 ± 13.5	14.6
	DWA	Segmentation	6.2 ± 5.4	4.4	11.5 ± 14.0	5.0	16.8 ± 14.4	13.0	9.5 ± 10.8	4.4
		Registration	5.8 ± 5.7	4.0	6.4 ± 7.4	3.6	13.4 ± 7.5	12.5	21.9 ± 11.5	19.0
Cross-stitch	Equal	Segmentation	5.8 ± 5.4	4.0	12.2 ± 15.8	5.0	17.0 ± 14.7	14.0	10.8 ± 11.3	4.4
		Registration	<b>5.1 ± 5.5</b>	<b>3.2</b>	6.2 ± 8.6	3.3	<b>12.6 ± 6.7</b>	12.0	19.1 ± 12.5	16.2
	Homoscedastic	Segmentation	5.9 ± 5.4	4.1	7.8 ± 7.4	4.6	20.5 ± 18.9	14.7	7.8 ± 8.7	<b>3.1</b>
		Registration	6.2 ± 5.6	4.5	6.1 ± 7.2	3.2	13.5 ± 7.3	13.5	19.4 ± 12.3	16.3
	DWA	Segmentation	6.7 ± 5.8	4.2	7.6 ± 9.1	4.1	20.7 ± 18.6	14.9	<b>7.5 ± 8.8</b>	3.5
		Registration	6.0 ± 5.7	4.1	6.1 ± 6.8	3.4	13.5 ± 7.5	13.6	21.5 ± 11.6	20.1

Table 5: DSC values for the different networks on the validation set (HMC). Higher values are better.

Network	Output path	Prostate		Seminal vesicles		Rectum		Bladder	
		$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median
Seg	Segmentation	$0.84 \pm 0.03$	0.84	$0.60 \pm 0.14$	0.62	$0.75 \pm 0.10$	0.77	$0.90 \pm 0.07$	0.93
Reg	Registration	$0.85 \pm 0.06$	0.86	$0.62 \pm 0.18$	0.68	$0.79 \pm 0.08$	0.81	$0.82 \pm 0.10$	0.84
JRS-reg	Registration	$0.86 \pm 0.03$	0.87	$0.69 \pm 0.13$	0.73	$0.83 \pm 0.06$	0.84	$0.88 \pm 0.08$	0.92
Dense	Segmentation	$0.88 \pm 0.04$	<b>0.89</b>	$0.70 \pm 0.12$	0.73	$0.85 \pm 0.04$	0.86	$0.94 \pm 0.02$	0.94
	Registration	$0.87 \pm 0.04$	0.88	$0.68 \pm 0.15$	0.73	$0.82 \pm 0.06$	0.83	$0.87 \pm 0.08$	0.90
SEDD	Segmentation	$0.87 \pm 0.04$	0.88	$0.69 \pm 0.12$	0.72	$0.83 \pm 0.07$	0.84	$0.93 \pm 0.02$	0.94
	Registration	$0.86 \pm 0.04$	0.87	$0.69 \pm 0.13$	0.74	$0.82 \pm 0.06$	0.83	$0.88 \pm 0.08$	0.92
Cross-stitch	Segmentation	<b><math>0.88 \pm 0.04</math></b>	0.88	<b><math>0.70 \pm 0.11</math></b>	<b>0.74</b>	<b><math>0.86 \pm 0.05</math></b>	<b>0.88</b>	<b><math>0.94 \pm 0.02</math></b>	<b>0.95</b>
	Registration	$0.87 \pm 0.03$	0.88	$0.68 \pm 0.15$	0.73	$0.84 \pm 0.05$	0.85	$0.88 \pm 0.08$	0.91
Elastix [131]	Registration	$0.84 \pm 0.07$	0.86	$0.50 \pm 0.25$	0.53	$0.74 \pm 0.06$	0.74	$0.75 \pm 0.10$	0.76
Hybrid [23]	Registration	$0.88 \pm 0.04$	0.89	$0.70 \pm 0.14$	0.72	$0.85 \pm 0.06$	0.87	$0.91 \pm 0.08$	0.95
JRS-GAN [17]	Registration	$0.86 \pm 0.04$	0.87	$0.61 \pm 0.20$	0.67	$0.82 \pm 0.06$	0.83	$0.88 \pm 0.08$	0.92

Table 6: % 95 HD (mm) values for the different networks on the validation set (HMC). Lower values are better.

Network	Output path	Prostate		Seminal vesicles		Rectum		Bladder	
		$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median
Seg	Segmentation	$4.4 \pm 1.0$	4.4	$8.6 \pm 8.6$	7.3	$16.5 \pm 11.0$	13.3	$6.9 \pm 6.6$	4.0
Reg	Registration	$5.5 \pm 4.5$	4.0	$5.6 \pm 4.1$	4.3	$11.0 \pm 6.4$	9.4	$15.7 \pm 9.6$	12.1
JRS-reg	Registration	$3.8 \pm 1.3$	3.2	$4.1 \pm 2.8$	3.2	$9.9 \pm 6.2$	8.4	$11.7 \pm 10.3$	9.2
Dense	Segmentation	$3.2 \pm 1.0$	3.0	$5.8 \pm 7.6$	3.9	$9.6 \pm 5.8$	8.0	$3.8 \pm 3.9$	<b>2.8</b>
	Registration	$3.4 \pm 1.1$	3.2	$4.4 \pm 3.0$	3.2	$10.5 \pm 6.0$	9.0	$12.6 \pm 9.2$	10.2
SEDD	Segmentation	$3.5 \pm 1.1$	3.3	$5.2 \pm 5.2$	4.0	$10.5 \pm 5.5$	9.7	<b><math>3.3 \pm 1.3</math></b>	3.0
	Registration	$3.6 \pm 1.2$	3.2	$4.1 \pm 2.6$	3.1	$10.4 \pm 6.3$	9.5	$11.7 \pm 9.9$	8.7
Cross-stitch	Segmentation	$3.0 \pm 1.0$	3.0	$4.3 \pm 1.7$	3.9	$9.5 \pm 6.2$	7.2	$3.3 \pm 2.9$	2.3
	Registration	$3.2 \pm 0.9$	3.0	$4.5 \pm 3.3$	3.6	$9.8 \pm 6.3$	8.6	$12.2 \pm 10.1$	9.7
Elastix [131]	Registration	$4.0 \pm 1.7$	3.7	$6.0 \pm 3.4$	5.6	$10.9 \pm 5.2$	9.8	$15.3 \pm 8.3$	13.6
Hybrid [23]	Registration	<b><math>2.9 \pm 0.9</math></b>	<b>2.8</b>	<b><math>3.8 \pm 2.2</math></b>	<b>3.1</b>	<b><math>7.7 \pm 4.5</math></b>	<b>6.1</b>	$5.7 \pm 4.6$	3.3
JRS-GAN [17]	Registration	$3.4 \pm 1.2$	3.0	$5.3 \pm 3.0$	4.6	$10.1 \pm 6.1$	8.4	$11.0 \pm 9.6$	7.6

Table 7: DSC values for the different networks on the independent test set (EMC). Higher values are better.

Network	Output path	Prostate		Seminal vesicles		Rectum		Bladder	
		$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median
Seg	Segmentation	$0.73 \pm 0.11$	0.77	$0.37 \pm 0.30$	0.28	$0.67 \pm 0.10$	0.68	<b><math>0.91 \pm 0.07</math></b>	0.93
Reg	Registration	$0.83 \pm 0.16$	0.88	$0.64 \pm 0.26$	0.74	$0.72 \pm 0.16$	0.77	$0.75 \pm 0.19$	0.82
JRS-reg	Registration	$0.84 \pm 0.16$	0.89	$0.68 \pm 0.25$	0.77	$0.76 \pm 0.15$	0.80	$0.80 \pm 0.18$	0.89
Dense	Segmentation	$0.84 \pm 0.16$	0.89	$0.63 \pm 0.27$	0.75	$0.79 \pm 0.16$	0.82	$0.87 \pm 0.13$	0.93
	Registration	$0.84 \pm 0.16$	0.88	$0.68 \pm 0.25$	0.78	$0.77 \pm 0.14$	0.80	$0.78 \pm 0.17$	0.86
SEDD	Segmentation	$0.84 \pm 0.15$	0.89	$0.50 \pm 0.28$	0.58	$0.76 \pm 0.18$	0.82	$0.88 \pm 0.13$	<b>0.94</b>
	Registration	$0.84 \pm 0.16$	0.88	$0.68 \pm 0.24$	0.78	$0.76 \pm 0.15$	0.80	$0.79 \pm 0.17$	0.88
Cross-stitch	Segmentation	$0.84 \pm 0.14$	0.89	$0.61 \pm 0.27$	0.73	$0.78 \pm 0.14$	0.81	$0.88 \pm 0.10$	0.93
	Registration	$0.84 \pm 0.15$	0.89	$0.68 \pm 0.24$	0.80	$0.77 \pm 0.15$	0.80	$0.80 \pm 0.16$	0.87
Elastix [131]	Registration	<b><math>0.89 \pm 0.05</math></b>	<b>0.91</b>	$0.72 \pm 0.24$	<b>0.82</b>	$0.75 \pm 0.12$	0.76	$0.79 \pm 0.18$	0.87
Hybrid [23]	Registration	$0.88 \pm 0.04$	0.89	<b><math>0.77 \pm 0.15</math></b>	0.81	<b><math>0.80 \pm 0.10</math></b>	<b>0.82</b>	$0.85 \pm 0.13$	0.90

Table 8: %95 HD (mm) values for the different networks on the independent test set (EMC). Lower values are better.

Network	Output path	Prostate		Seminal vesicles		Rectum		Bladder	
		$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median	$\mu \pm \sigma$	median
Seg	Segmentation	10.7 ± 5.4	9.3	21.4 ± 17.9	15.4	30.5 ± 12.9	29.0	11.2 ± 8.5	10.0
Reg	Registration	6.7 ± 5.9	4.2	7.5 ± 8.6	4.3	13.1 ± 6.9	12.0	22.7 ± 14.0	20.2
JRS-reg	Registration	5.7 ± 5.9	3.7	6.2 ± 7.1	3.6	13.0 ± 7.3	11.5	18.5 ± 14.0	13.0
Dense	Segmentation	5.8 ± 5.9	3.3	10.0 ± 11.6	5.1	17.1 ± 16.6	13.8	11.4 ± 11.3	5.9
	Registration	5.3 ± 5.7	3.0	6.4 ± 6.8	3.2	13.0 ± 6.5	12.6	19.2 ± 13.7	14.2
SEDD	Segmentation	5.7 ± 5.5	3.9	16.0 ± 16.3	10.6	18.8 ± 16.5	15.3	<b>9.4 ± 9.9</b>	<b>4.1</b>
	Registration	5.5 ± 5.6	3.3	6.3 ± 6.7	3.6	13.3 ± 7.3	13.0	18.8 ± 13.5	14.6
Cross-stitch	Segmentation	5.8 ± 5.4	4.0	12.2 ± 15.8	5.0	17.0 ± 14.7	14.0	10.8 ± 11.3	4.4
	Registration	5.1 ± 5.5	3.2	6.2 ± 8.6	3.3	12.6 ± 6.7	12.0	19.1 ± 12.5	16.2
Elastix [131]	Registration	<b>3.6 ± 2.0</b>	<b>2.9</b>	<b>4.6 ± 4.4</b>	3.2	11.3 ± 6.0	11.3	16.1 ± 14.8	10.4
Hybrid [23]	Registration	3.9 ± 1.9	3.4	4.8 ± 4.7	<b>3.1</b>	<b>10.3 ± 6.8</b>	<b>8.6</b>	11.1 ± 10.6	6.6



# Publications

## Journal articles

**Elmahdy, Mohamed S**, T. Jagt, R. T. Zinkstok, Y. Qiao, R. Shahzad, H. Sokooti, S. Yousefi, L. Incrocci, C. Marijnen, M. Hoogeman, et al. “Robust contour propagation using deep learning and image registration for online adaptive proton therapy of prostate cancer”. In: *Medical Physics* 46.8 (2019), pages 3329–3343

N. Pezzotti, S. Yousefi, **Elmahdy, Mohamed S**, J. H. F. Van Gemert, C. Schuelke, M. Doneva, T. Nielsen, S. Kastruyulin, B. P. Lelieveldt, M. J. Van Osch, et al. “An Adaptive Intelligence Algorithm for Undersampled Knee MRI Reconstruction”. In: *IEEE Access* 8 (2020), pages 204825–204838

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S. Yousefi, H. Sokooti, **Elmahdy, Mohamed S**, I. M. Lips, M. T. M. Shalmani, R. T. Zinkstok, F. J. Dankers, and M. Staring. “Esophageal Tumor Segmentation in CT Images Using a Dilated Dense Attention Unet (DDAUnet)”. In: *IEEE Access* 9 (2021), pages 99235–99248

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**Elmahdy, Mohamed S**, T. Jagt, S. Yousefi, H. Sokooti, R. Zinkstok, M. Hoogeman, and M. Staring. “Evaluation of multi-metric registration for online adaptive proton therapy of prostate cancer”. In: *International Workshop on Biomedical Image Registration*. Springer. 2018, pages 94–104

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**Elmahdy, Mohamed S**, T. Ahuja, U. A. van der Heide, and M. Staring. “Patient-Specific Finetuning of Deep Learning Models for Adaptive Radiotherapy in Prostate CT”. in: *2020 IEEE 17th International Symposium on Biomedical Imaging (ISBI)*. IEEE. 2020, pages 577–580

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Y. Li, **Elmahdy, Mohamed S**, M. S. Lew, and M. Staring. “Transformation-Consistent Semi-Supervised Learning for Prostate CT Radiotherapy”. In: *SPIE Medical Imaging: Image Processing*. Proceedings of SPIE. San Diego, CA, USA, 2022

## Code Repository

**Mohamed S. Elmahdy**, JRS-GAN, *GitHub*, [github.com/moelmahdy/JRS-GAN](https://github.com/moelmahdy/JRS-GAN)

**Mohamed S. Elmahdy**, JRS-MTL, *GitHub*, [github.com/moelmahdy/JRS-MTL](https://github.com/moelmahdy/JRS-MTL)

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# Curriculum Vitae

Mohamed S. Elmahdy was born in Cairo, Egypt. He received his BSc in biomedical engineering from Cairo University in 2013. In his BSc project, he designed an early prototype of a low-cost high-performance hand-held CAD system for early diagnosis of abnormalities in mammography. He obtained his MSc degree in biomedical engineering from the same university in 2017, where he developed an end-to-end deep learning framework for subvocal speech recognition via close-talk microphone and surface electromyogram.

From August 2017, he started his PhD study in the Division of Image Processing (LKEB) under the Department of Radiology at Leiden University Medical Center in the Netherlands. His PhD project mainly focuses on developing deep learning algorithms for online adaptive radiotherapy.

Starting from March 2021, he works as a post-doctoral researcher in LKEB, on a project of cardiac MR analysis using deep learning.