Multitask radiological modality invariant landmark localization using deep reinforcement learning

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Motivation

- Automatic anatomical localization is an integral part of an AI radiology framework.
- Anatomical localization has diverse applicability across multiple applications such as image segmentation, registration, and classification.
- Deep reinforcement learning (RL) has emerged as the best technique for landmark localization in recent years.

- Currently, the models developed using deep RL for landmark localization have been limited to a single application.
 - Example: Landmark localization within a predefined anatomical environment (e.g. brain MRI) acquired using specific imaging parameters (e.g. T1-weighted MRI).

Multitask Modality Invariant Deep RL model

- We extend deep RL techniques and developed a **multitask deep RL model (MIDRL)** with single and multiple agents.
- MIRDL: A single model for simultaneous localization of a diverse set of landmarks across:
 - Different regions in the body (e.g. heart, breast, prostate, etc.)
 - Different imaging parameters (e.g. T1-weighted imaging, Dynamic contrast enhanced imaging, Diffusion Weighted Imaging)
 - Different imaging orientations (e.g. Axial, Sagittal, Coronal)



Reinforcement Learning (RL) Framework

• Environment: Radiological image



- State: Sequence of areas within the image (bounding box)
- Actions: move bounding box in one direction $(\pm x \text{ or } \pm y \text{ or } \pm z)$
- Reward: change in Euclidean distance to landmark
 - Positive if moved closer to landmark, negative if moved away
 - Clipped between -1 and 1
- Q-learning with experience replay

Reinforcement Learning Models

- 2D MIDRL model
 - Single agent
 - Evaluated on individual 2D slices

- 3D MIDRL model
 - Multi-agent (4 agents)
 - Each agent locates its assigned landmark
 - Evaluated on 3D whole body volumes



2D DQN (single agent)



- Input: bounding box regions from last 4 time steps
- Output: Q-value for each action (x++, x--, y++, y--)

- Input (for each agent): bounding box regions from last 4 time steps
- Output (for each agent): Q-value for each action (x++, x--, y++, y--, z++, z--)
- 3D DQN: analogous to 2D

3D DQN

- Convolutional layers are shared among all agents
- Each agent has its own separate final fully connected layers



Multiparametric MRI (mpMRI)







Clinical Dataset

- 25 whole body mpMRI (2D and 3D)
- 24 breast mpMRI (2D)
- 8 prostate mpMRI (2D)

Imaging Parameter	Heart	Kidney	Trochanter (pelvis)	Knee	Nipple	Prostate
T1WI	✓	✓	✓	✓	✓	
T2WI	✓	✓	✓	~	✓	✓
Dixon in	✓	✓	✓	~		
Dixon opp	✓	✓	✓	~		
Dixon fat	✓	✓	✓	✓		
Dixon water	✓	✓	✓	~		
Post DCE					✓	
Pre DCE					✓	
Sub DCE					✓	
ADC						~

2D MIDRL model locating landmarks

Target bounding box: red

Agent's bounding box: yellow

Multi-scale search

Nipple

Prostate

Heart

3D MIDRL model locating landmarks

Target bounding box: red

Agent's bounding box: yellow

Multi-scale search

Kidney

Trochanter

Heart

Knee



2D Single Agent IoU

	Heart	Kidney	Trochanter	Knee	Breast	Prostate
T1WI	0.75 ± 0.20	0.70 ± 0.35	0.74 ± 0.23	0.88 ± 0.06	0.78 ± 0.16	
T2WI	0.58 ± 0.21	0.59 ± 0.20	0.29 ± 0.36	0.68 ± 0.11	0.51 ± 0.29	0.48 ± 0.42
Dixon in	0.79 ± 0.12	0.62 ± 0.25	0.85 ± 0.06	0.88 ± 0.05		
Dixon opp	0.77 ± 0.27	0.74 ± 0.17	0.83 ± 0.09	0.87 ± 0.08		
Dixon F	0.78 ± 0.11	0.69 ± 0.33	0.78 ± 0.14	0.87 ± 0.03		
Dixon W	0.82 ± 0.14	0.70 ± 0.35	0.75 ± 0.18	0.91 ± 0.03		
Post DCE					0.20 ± 0.32	
Pre DCE					0.50 ± 0.42	
Sub DCE					0.12 ± 0.24	
ADC						0.34 ± 0.36
All parameters	0.76 ± 0.19	0.68 ± 0.28	0.73 ± 0.25	0.86 ± 0.09	0.47 ± 0.37	0.41 ± 0.36

2D Single Agent Distance Errors (mm)

	Heart	Kidney	Trochanter	Knee	Breast	Prostate
T1WI	9.8 ± 10.4	23.1 ± 46.2	9.6 ± 10.2	3.5 ± 2.4	3.1 ± 3.4	
T2WI	22.3 ± 17.7	19.0 ± 12.7	68.2 ± 51.8	13.4 ± 5.3	9.5 ± 7.4	20.6 ± 21.2
Dixon in	7.0 ± 4.3	15.1 ± 13.8	5.5 ± 2.2	3.6 ± 1.2		
Dixon opp	10.1 ± 16.8	11.6 ± 12.1	6.4 ± 3.2	3.8 ± 2.7		
Dixon F	7.4 ± 4.8	17.7 ± 30.0	7.9 ± 4.7	3.8 ± 0.7		
Dixon W	6.2 ± 5.6	15.6 ± 24.6	9.8 ± 8.5	2.3 ± 0.7		
Post DCE					30.0 ± 29.5	
Pre DCE					3.3 ± 2.8	
Sub DCE					38.6 ± 28.7	
ADC						16.7 ± 24.8
All parameters	10.0 ± 11.5	16.9 ± 25.5	15.7 ± 27.5	4.5 ± 3.9	16.9 ± 22.9	18.7 ± 20.7

(mean ± std dev)

3D Multi-Agent IoU

	Heart	Kidney	Trochanter	Knee
T1WI	0.62 ± 0.21	0.66 ± 0.19	0.78 ± 0.10	0.43 ± 0.34
T2WI	0.47 ± 0.14	0.44 ± 0.32	0.34 ± 0.26	0.35 ± 0.37
Dixon in	0.71 ± 0.14	0.54 ± 0.23	0.81 ± 0.10	0.45 ± 0.39
Dixon opp	0.62 ± 0.19	0.71 ± 0.14	0.74 ± 0.13	0.51 ± 0.42
Dixon F	0.48 ± 0.29	0.51 ± 0.29	0.85 ± 0.10	0.69 ± 0.29
Dixon W	0.65 ± 0.13	0.75 ± 0.14	0.60 ± 0.25	0.49 ± 0.41
All parameters	0.60 ± 0.20	0.61 ± 0.24	0.70 ± 0.23	0.49 ± 0.37

3D Multi-Agent Distance Errors (mm)

	Heart	Kidney	Trochanter	Knee
T1WI	12.6 ± 9.4	10.2 ± 6.5	6.4 ± 2.7	22.9 ± 20.4
T2WI	18.0 ± 7.6	29.3 ± 33.2	27.6 ± 17.1	91.7 ± 126.2
Dixon in	8.1 ± 4.7	18.3 ± 21.8	5.5 ± 2.6	51.6 ± 64.0
Dixon opp	11.4 ± 6.5	8.5 ± 4.5	7.0 ± 3.2	57.4 ± 78.5
Dixon F	21.7 ± 17.9	39.2 ± 72.0	4.2 ± 2.4	32.3 ± 75.9
Dixon W	10.1 ± 4.8	6.9 ± 4.0	15.9 ± 14.5	68.7 ± 92.6
All parameters	13.5 ± 10.3	18.3 ± 34.1	10.4 ± 11.4	52.5 ± 78.4

Conclusion

- One model for locating multiple landmarks in many different imaging environments
- More computationally efficient than one model per environment

Acknowledgements





Paul Bottomley Peter Barker David A. Bluemke Roisin Connolly Leisha Emens **Riham El Khouli** Susan Harvey Ihab Kamel **Doris Leung** Katarzyna Macura Meiyappan Solaiyappan **Vered Stearns** Katharyn Wagner **Antonio Wolff Atif Zaheer**





Funding

5P30CA006973 (IRAT), R01 CA190299, U01CA140204, and GPU equipment from NVidia.