5th MICCAI Workshop on

Domain Adaptation and Representation Transfer (DART)

MICCAI 2023 Vancouver CANADA

Domain adaptation of MRI scanners as an alternative to MRI harmonization

Rafsanjany Kushol[1], Richard Frayne[2], Simon J. Graham[3], Alan H. Wilman[4], Sanjay Kalra[1,5], and Yee-Hong Yang[1]

[1] Department of Computing Science, University of Alberta, Edmonton, Canada
[2] Department of Radiology, University of Calgary, Calgary, Canada
[3] Sunnybrook Health Sciences Centre, University of Toronto, Toronto, Canada
[4] Department of Radiology and Diagnostic Imaging, University of Alberta, Canada
[5] Department of Medicine, University of Alberta, Edmonton, Canada
kushol@ualberta.ca

Presented by

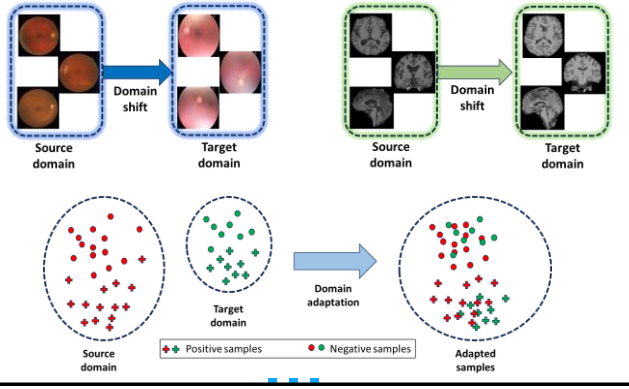
Rafsanjany Kushol

UNIVERSITY OF ALBERTA

CALSNIC Canadian ALS Neuroimaging Consortium

1

Introduction



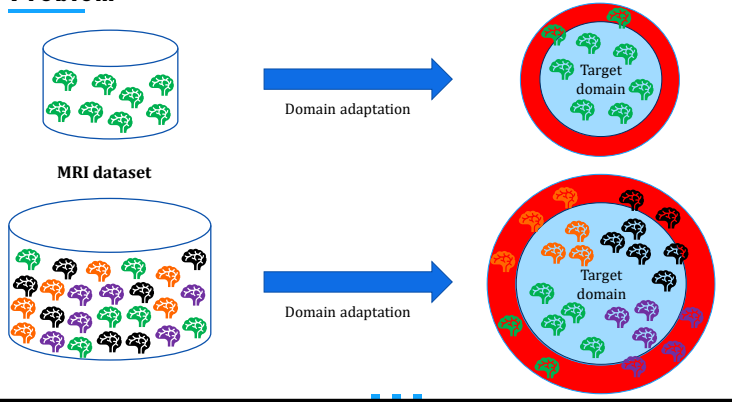
2

Problem

Training		Testing	Result
Source domain	Similar data distribution	Target domain	Higher accuracy
Source domain	Different data distribution	Target domain	Lower accuracy

3

Problem

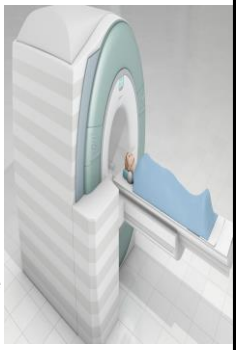


4

5

Domain shift in MRI

- Factors affecting MR imaging properties :
  - **Scanner manufacturer:** GE, Philips, Siemens
  - **Scanner model:** Symphony, Skyra, Verio, TrioTim, Prisma, Espree
  - **Acquisition orientation:** axial, sagittal, coronal
  - **Magnetic field strength (T):** 1.5, 3.0
  - **Coil configuration:** 8, 20, 32, 64 (number of channels per coil)
  - **Slice thickness (mm):** 176, 224
  - **Scan parameters:** flip angle, repetition time, echo time
  - **Image processing and reconstruction methods:** different software
  - **Hardware specific artifacts:** motion artifacts



5

6

Datasets

- **T1-weighted structural MRI**

	Classification task
• **ADNI1**: 925 (429 AD, 496 HC) • **ADNI2**: 852 (355 AD, 497 HC) • **AIBL**: 288 (73 AD, 215 HC) • **MIRIAD**: 69 (46 AD, 23 HC)	Alzheimer's Disease (AD) vs. Healthy Control (HC)
• **CALSNIC1**: 281 (135 ALS, 146 HC) • **CALSNIC2**: 546 (255 ALS, 291 HC)	Amyotrophic Lateral Sclerosis (ALS) vs. Healthy Control (HC)

- **Pre-processing:**
  - Skull-stripping
  - Registration to MNI-152

6

7

Motivation

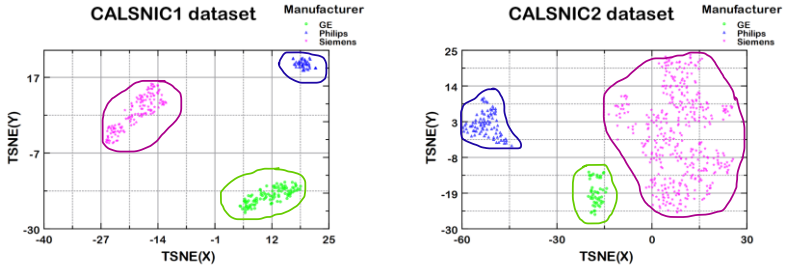


Figure: Graphs show the distribution of MRI data used in our study from CALSNIC1 and CALSNIC2 datasets generated by the features of MRQy using t-SNE. Three different colors indicate three different MRI scanner manufacturers' data which are separable from each other.

7

8

Motivation

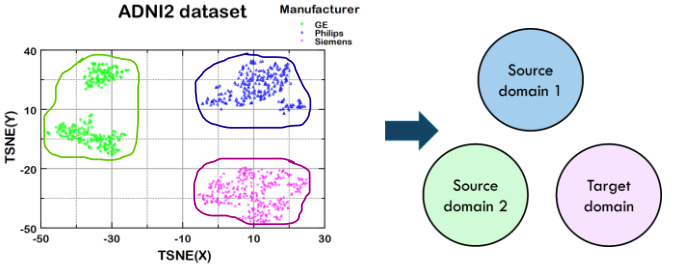


Figure: Graphs show the distribution of MRI data used in our study from the ADNI dataset generated by the features of MRQy using t-SNE. Three different colors indicate three different MRI scanner manufacturers' data which are separable from each other. The right panel shows that among three manufacturers, two can be regarded as source domains and the other as the target domain.

8

Motivation

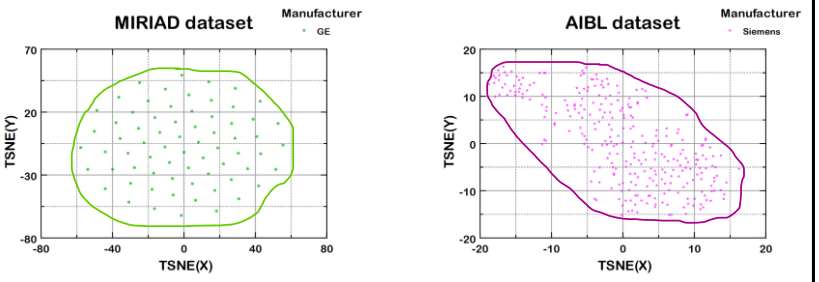


Figure: Graphs show the distribution of MRI data used in our study from the MIRIAD and AIBL datasets generated by the features of MRQy using t-SNE. Both AIBL and MIRIAD consist of MRI data from a single scanner manufacturer. Therefore, no significant clustering is noticeable in their data distribution.

9

Proposed network

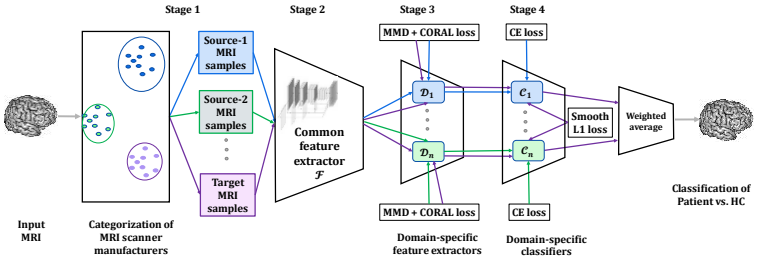


Figure: The architecture of the proposed framework. (MMD: Maximum Mean Discrepancy, CORAL: Correlation Alignment, CE: Cross-entropy, HC: Healthy control)

10

Multi-center intra-study classification results

Study	Source domain	Classification accuracy on source domain	Target domain	Classification accuracy w/o domain adaptation	Classification accuracy with proposed method
ADNI1	GE+Siemens	0.90	Philips	0.80	0.88
	GE+Philips	0.91	Siemens	0.80	0.91
	Siemens+Philips	0.89	GE	0.81	0.87
ADNI2	GE+Siemens	0.89	Philips	0.79	0.89
	GE+Philips	0.92	Siemens	0.81	0.88
	Siemens+Philips	0.92	GE	0.82	0.92
CALSNIC 1	GE+Siemens	0.75	Philips	0.56	0.68
	GE+Philips	0.75	Siemens	0.65	0.77
	Siemens+Philips	0.77	GE	0.60	0.68
CALSNIC 2	GE+Siemens	0.77	Philips	0.60	0.74
	GE+Philips	0.69	Siemens	0.54	0.65
	Siemens+Philips	0.75	GE	0.68	0.80

~ 10 % ↓ ~ 9 % ↑ ~ 13 % ↓ ~ 10 % ↑

11

Multi-center intra-study classification results

Study	Source domain	Target domain	Classification accuracy with MMD	Classification accuracy with CORAL	Classification accuracy with proposed method	Classification accuracy with M3SDA	Classification accuracy with MFSAN
ADNI1	GE+Siemens	Philips	0.83	0.86	**0.88**	0.82	0.82
	GE+Philips	Siemens	0.90	**0.91**	**0.91**	0.85	0.87
	Siemens+Philips	GE	**0.87**	0.85	**0.87**	0.84	0.85
ADNI2	GE+Siemens	Philips	**0.89**	0.87	**0.89**	0.86	0.87
	GE+Philips	Siemens	0.87	0.87	**0.88**	0.84	0.87
	Siemens+Philips	GE	0.91	0.90	**0.92**	0.87	0.86
CALSNIC 1	GE+Siemens	Philips	0.64	0.62	**0.68**	0.63	0.64
	GE+Philips	Siemens	**0.77**	**0.77**	**0.77**	0.72	0.73
	Siemens+Philips	GE	0.65	0.66	**0.68**	0.63	0.63
CALSNIC 2	GE+Siemens	Philips	0.73	0.72	**0.74**	0.71	0.70
	GE+Philips	Siemens	0.59	**0.65**	**0.65**	0.62	0.59
	Siemens+Philips	GE	**0.80**	0.76	**0.80**	0.71	0.76

12

13

Multi-center inter-study classification results

Source domain	Classification accuracy on source domain	Target domain	Classification accuracy w/o domain adaptation	Classification accuracy with proposed method
ADNI1	0.89	ADNI2	0.81	0.90
		AIBL	0.75 ~10 %	0.84
		MIRIAD	0.78	0.88 ~9 %
ADNI2	0.91	ADNI1	0.79	0.88
		AIBL	0.74	0.82
		MIRIAD	0.75	0.87
CALSNIC1	0.75	CALSNIC2	0.61 ~12 %	0.73 ~12 %
CALSNIC2	0.73	CALSNIC1	0.64	0.77

13

14

Multi-center inter-study classification results

Source domain	Target domain	Classification accuracy with w/o TDH	Classification accuracy with MMD	Classification accuracy with CORAL	Classification accuracy with proposed method	Classification accuracy with M3SDA	Classification accuracy with MFSAN
ADNI1	ADNI2	0.83	0.88	0.89	**0.90**	0.87	0.87
	AIBL	**0.84**	0.83	0.82	**0.84**	0.80	0.83
	MIRIAD	**0.88**	**0.88**	0.85	**0.88**	0.85	**0.88**
ADNI2	ADNI1	0.84	0.87	0.87	**0.88**	0.84	0.85
	AIBL	**0.82**	**0.82**	**0.82**	**0.82**	0.80	0.81
	MIRIAD	**0.87**	**0.87**	**0.85**	**0.87**	0.82	**0.87**
CALSNIC1	CALSNIC2	0.69	0.70	0.73	**0.73**	0.68	0.69
CALSNIC2	CALSNIC1	0.72	0.76	0.74	**0.77**	0.71	0.73

14

15

Conclusion

- Techniques in neuroscience research are required to be robust, efficient and reliable.
- They must be sensitive to biological factors but resistant to non-biological sources.
- This study proposes a new perspective in solving the domain shift issue for MRI data by identifying and addressing the dominant factor causing heterogeneity in MRI dataset.

15

16

Acknowledgements

Dataset participants and their caregivers

ADNI Alzheimer's Disease Neuroimaging Initiative

CALSNIC

aibl The Australian Imaging, Biomarkers and Lifestyle Flagship Study of Ageing

SCAN ME

Funding

CIHR IRSC

Brain Canada Foundation

ALS SLA CANADA

NSERC CRSNG

16