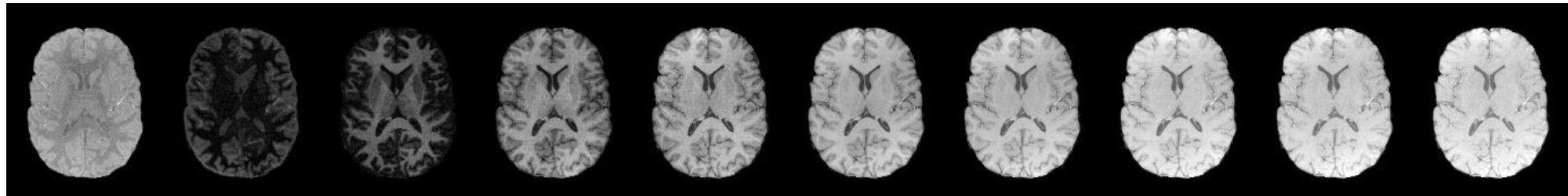


INR meets Multi-Contrast MRI Reconstruction

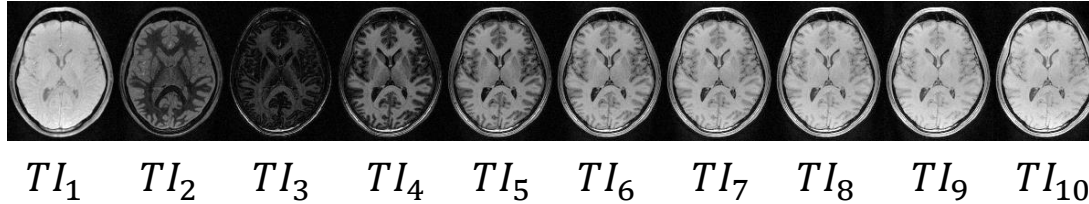
Natascha Niessen^{1,2}, Carolin M. Pirkel², Ana Beatriz Solana², Hannah Eichhorn^{1,3}, Veronika Spieker^{1,3}, Wenqi Huang¹, Tim Sprenger^{2,4}, Marion I. Menzel^{2,5,6}, and Julia A. Schnabel^{1,3,7}
on behalf of the PREDICTOM consortium



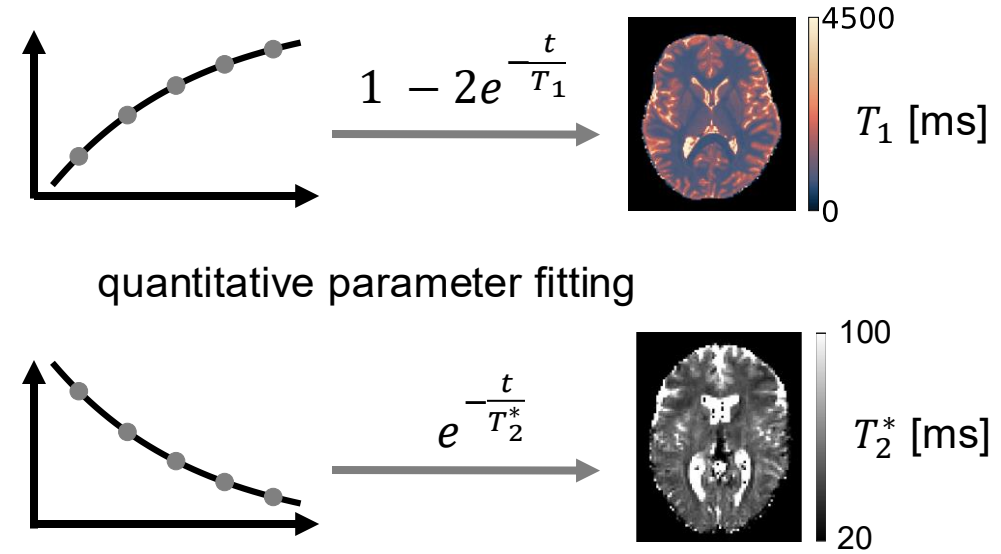
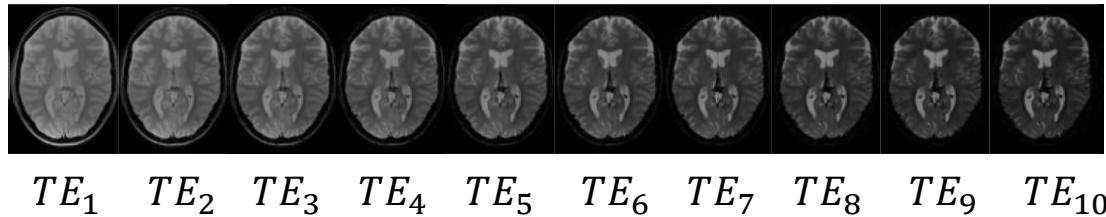
¹School of Computation, Information and Technology, Technical University of Munich, Munich, Germany; ²GE HealthCare, Munich, Germany; ³Institute of Machine Learning in Biomedical Imaging, Helmholtz Munich, Neuherberg, Germany; ⁴Department of Clinical Neuroscience, Karolinska Institutet, Stockholm, Sweden ⁵Technische Hochschule Ingolstadt, Ingolstadt, Germany; ⁶School of Natural Sciences, Technical University of Munich, Munich, Germany; ⁷King's College London, London, United Kingdom

Multi-Contrast MRI: infeasible scan times

inversion times



echo times



- Acquiring multiple image contrasts within a single scan
- Varying MR experimental parameters e.g. TI, TE

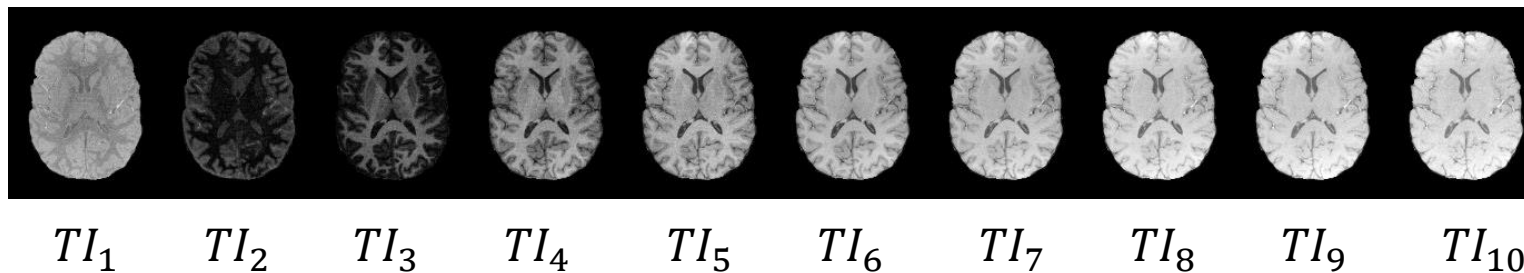
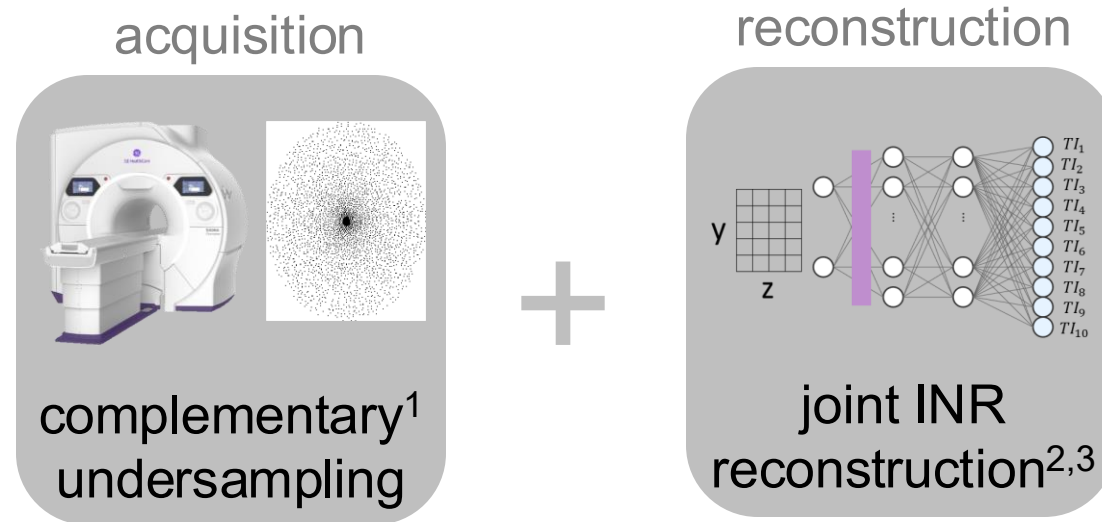
Long scan times limit clinical adoption of multi-contrast MRI

**Our method:**

- ✓ scan-specific
- ✓ self-supervised
- ✓ no training data required

3.25 min

Overview of our method



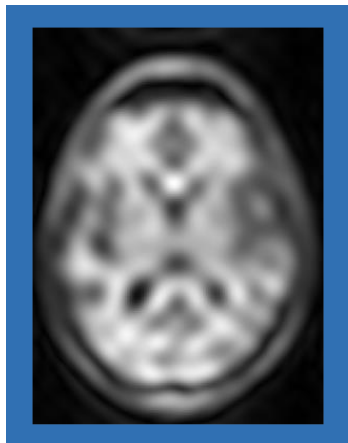
The **contrast changes**, BUT the **anatomy** remains **constant**

¹ Levine et al. (2017)

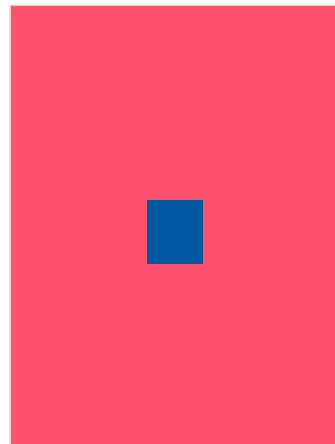
² Niessen. et al. MICCAI-RIME (2025)

³ Huang W. et al. IPMI (2025)

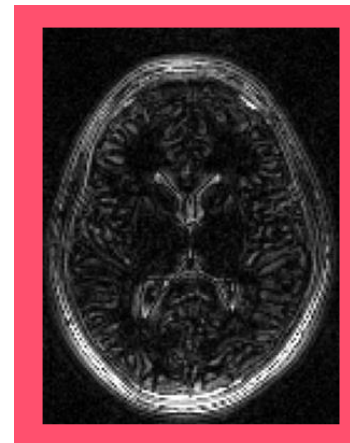
Complementary undersampling



contrast



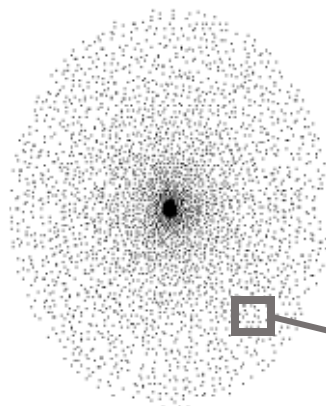
k-space



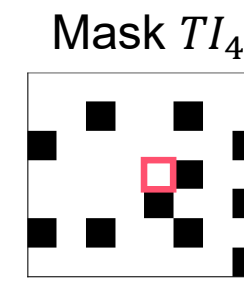
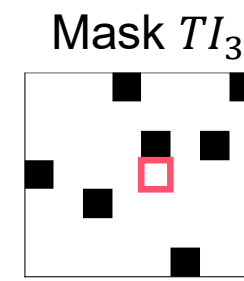
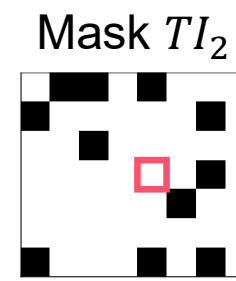
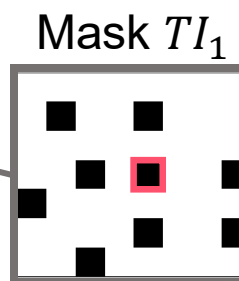
anatomical details

k-space center:
densely sampled

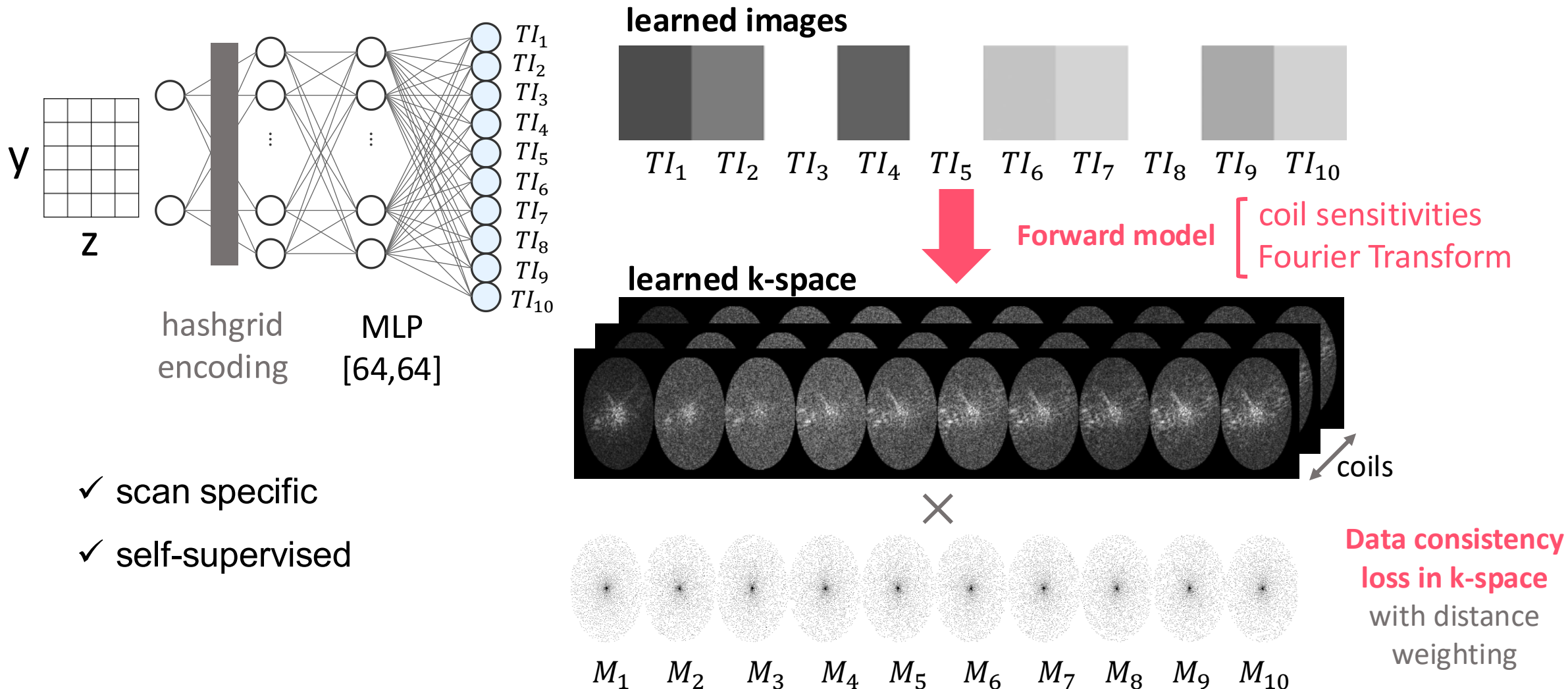
high frequencies:
sampled sparsely & **complementary** across contrasts



variable density
Poisson disk sampling



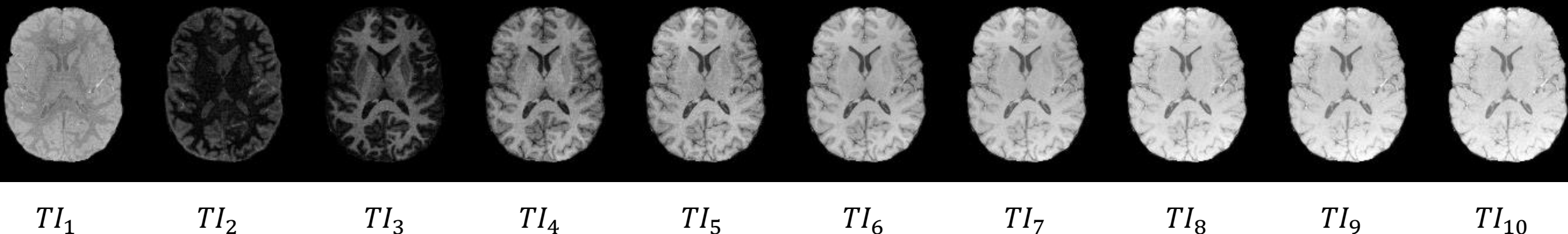
Joint reconstruction with Implicit Neural Representation (INR)



MPnRAGE: multiple inversion time (TI) contrasts

- 3D acquisitions on **3T DISCOVERY™** (GE HealthCare) scanner
- Scan time for 10 TI contrasts:

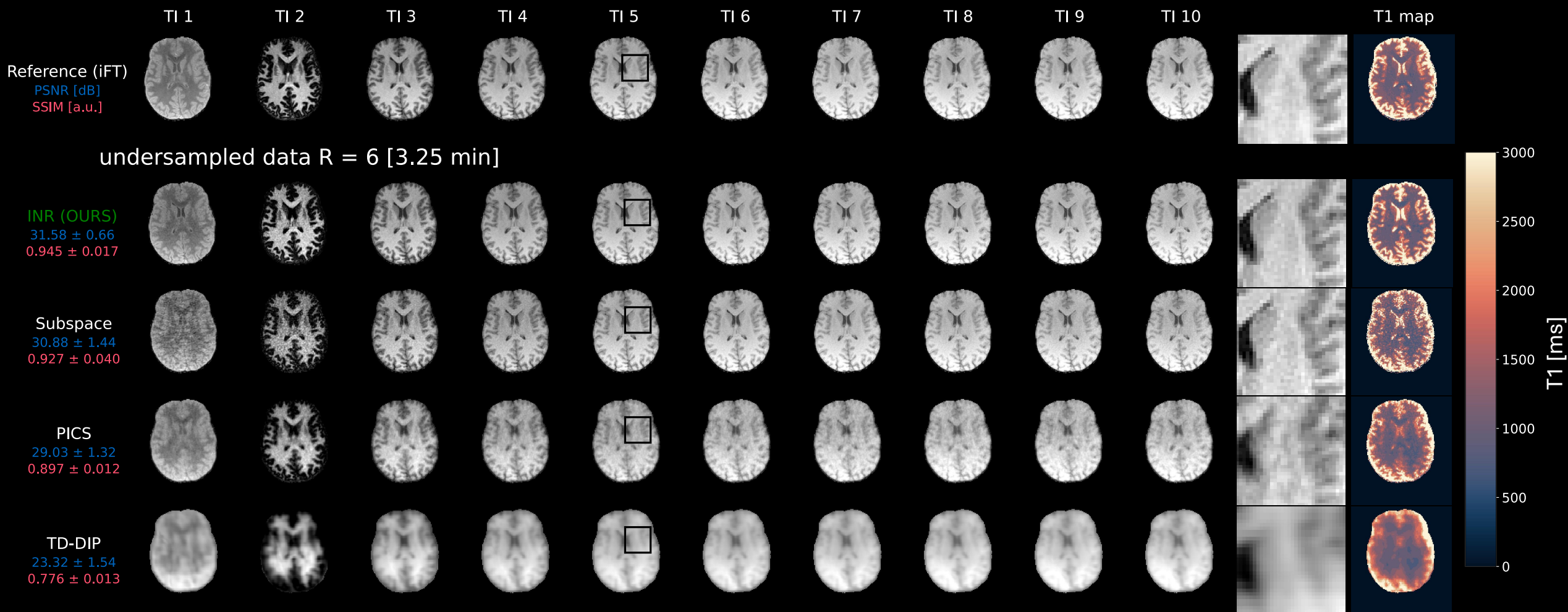
1.5 mm resolution	fully sampled	22 min	
	undersampled R=6	3.25 min	
1 mm resolution	fullysampled	1.45 hours	
	undersampled R=20	4.22 min	
- INR reconstruction was performed per slice (1.2 seconds), keeping the same hyperparameters



Highly accelerated MPnRAGE

1.5 mm resolution

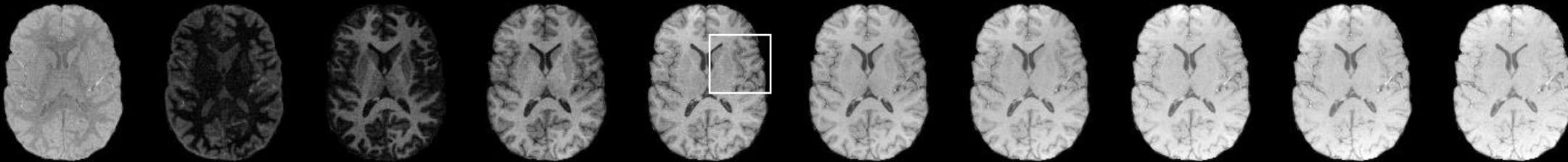
fully sampled data [21.52 min]



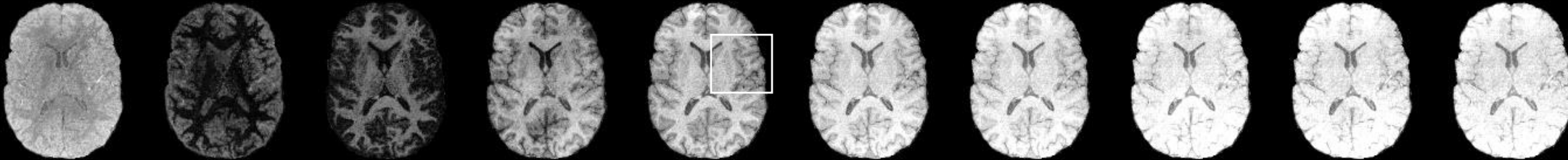
Highly accelerated MPnRAGE

1 mm resolution

R = 8 [10.54 min]



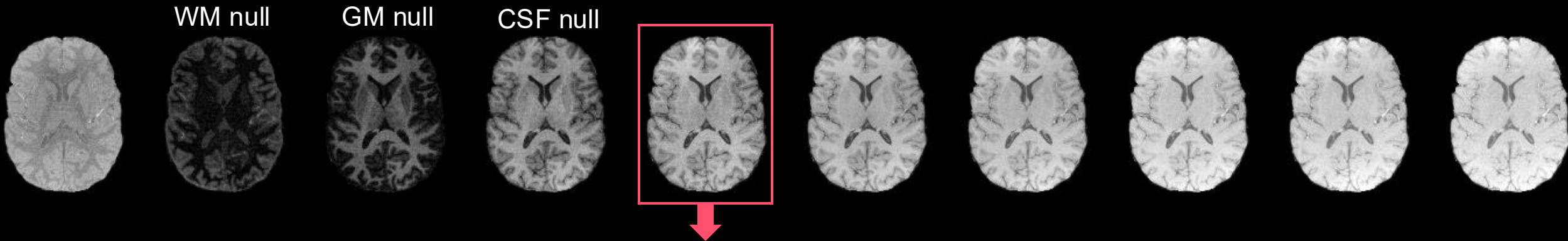
R = 20 [4.22 min]



What can MPnRAGE be used for?

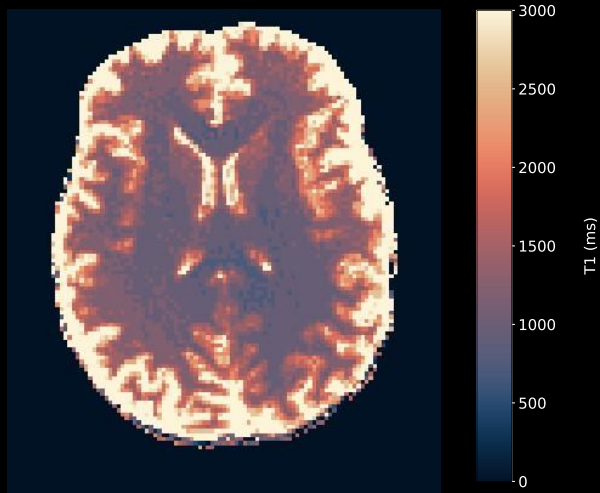
1. Tissue nulling

→ Biomarker discovery

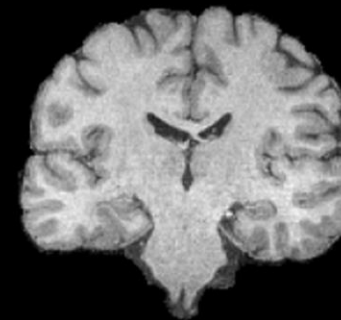


2. Quantitative T1 maps

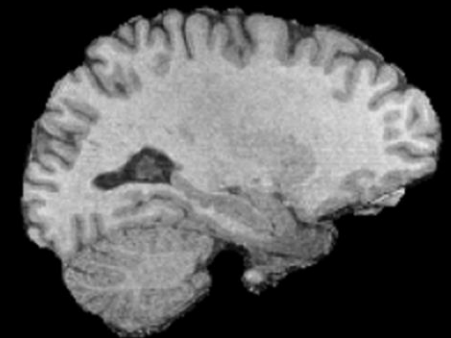
3. Synthesized clinical T1w contrast (MPRAGE) in 3D



axial



coronal



sagittal

Highly accelerated multi-contrast MRI

- ✓ Complementary undersampling and joint INR reconstruction leverage shared anatomical information

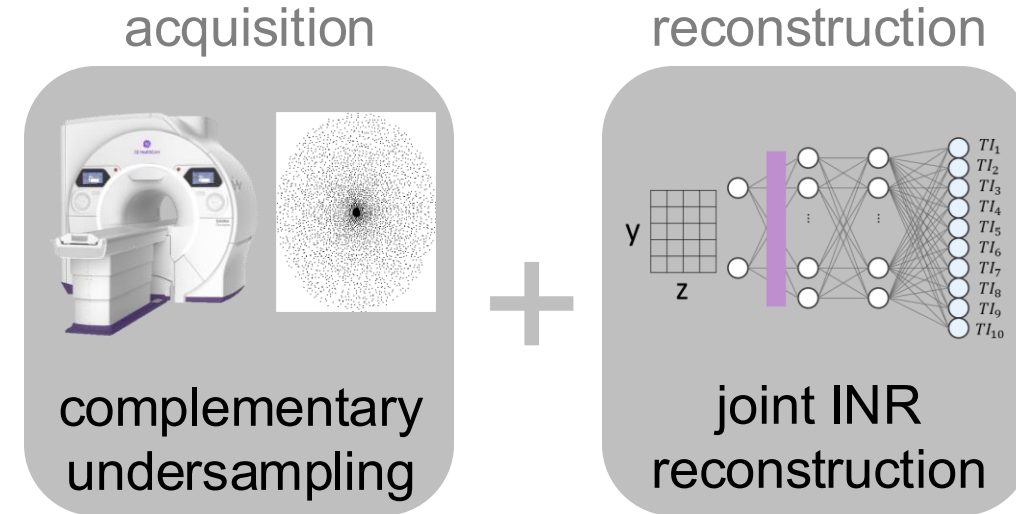
- ✓ Self-supervised & scan-specific

- ✓ Prospective accelerations up to $R=20$ yield promising image quality
→ allowing for clinically feasible scan times (e.g. MPnRAGE 4.22 min)



→ Next steps:

- Acquire MPnRAGE dataset as part of



Acknowledgments

Arxiv:



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