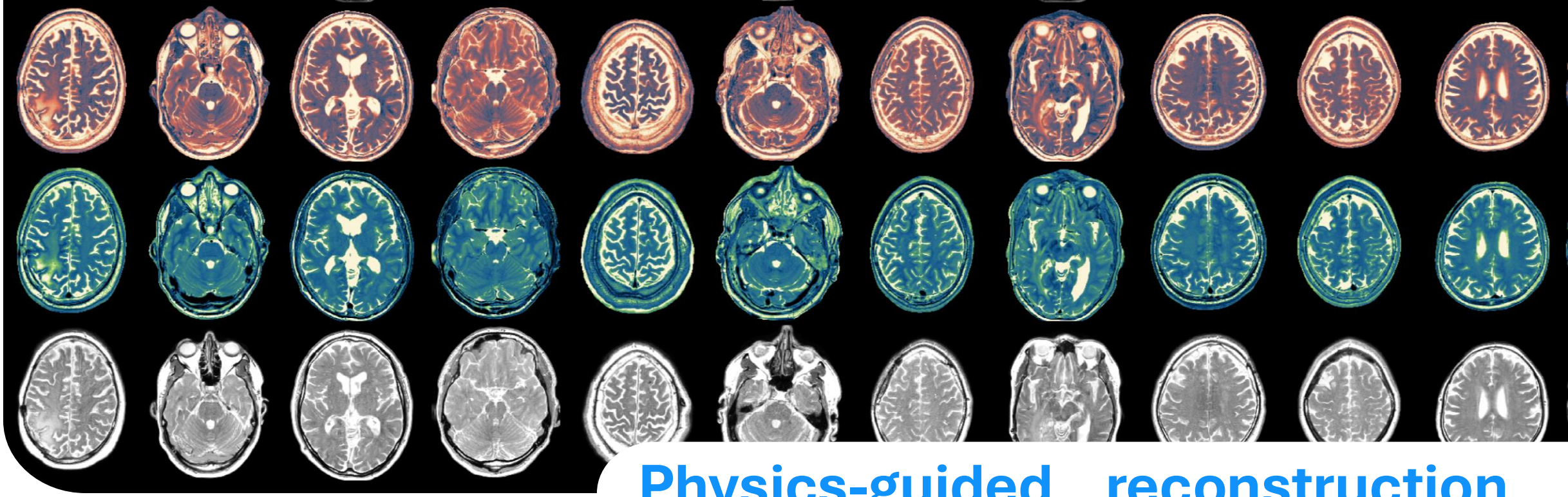

Physics-guided reconstruction of quantitative MRI from conventional contrasts by self-supervised deep learning

Applications to a large-scale, clinically heterogeneous dataset

Jelmer van Lune, Stefano Mandija, Oscar van der Heide, Matteo Maspero, Martin B. Schilder, Jan Willem Dankbaar, Cornelis A.T. van den Berg, and Alessandro Sbrizzi

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HANARTH FONDS

UMC Utrecht

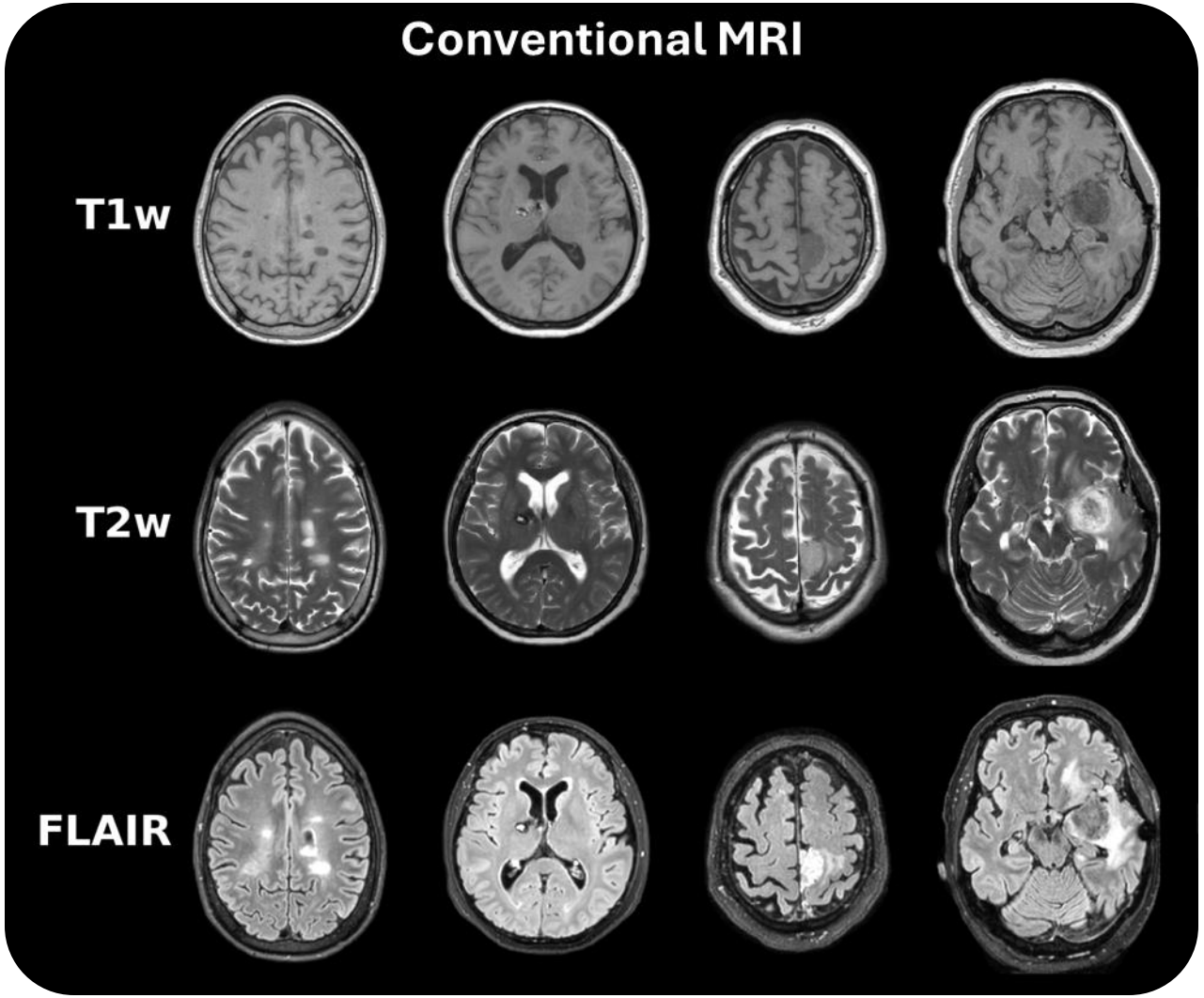
Symposium on AI and Reconstruction for Biomedical Imaging: March 9-10 2026, London

Introduction: Motivation

- **Conventional MRI in brain**
  - Detect, characterize, monitor neurological diseases

- **Signal Intensity**
  - **Intrinsic tissue parameters**
    - **PD** (proton-density)
    - **T1** (longitudinal relaxation)
    - **T2** (transversal relaxation)
  - **Extrinsic parameters**
    - Scanner hardware
    - Acquisition settings (TR, TE, TI, FA)

- **Limitations**
  - Objective biomarkers
  - Longitudinal analyses
  - Data-driven image analysis models



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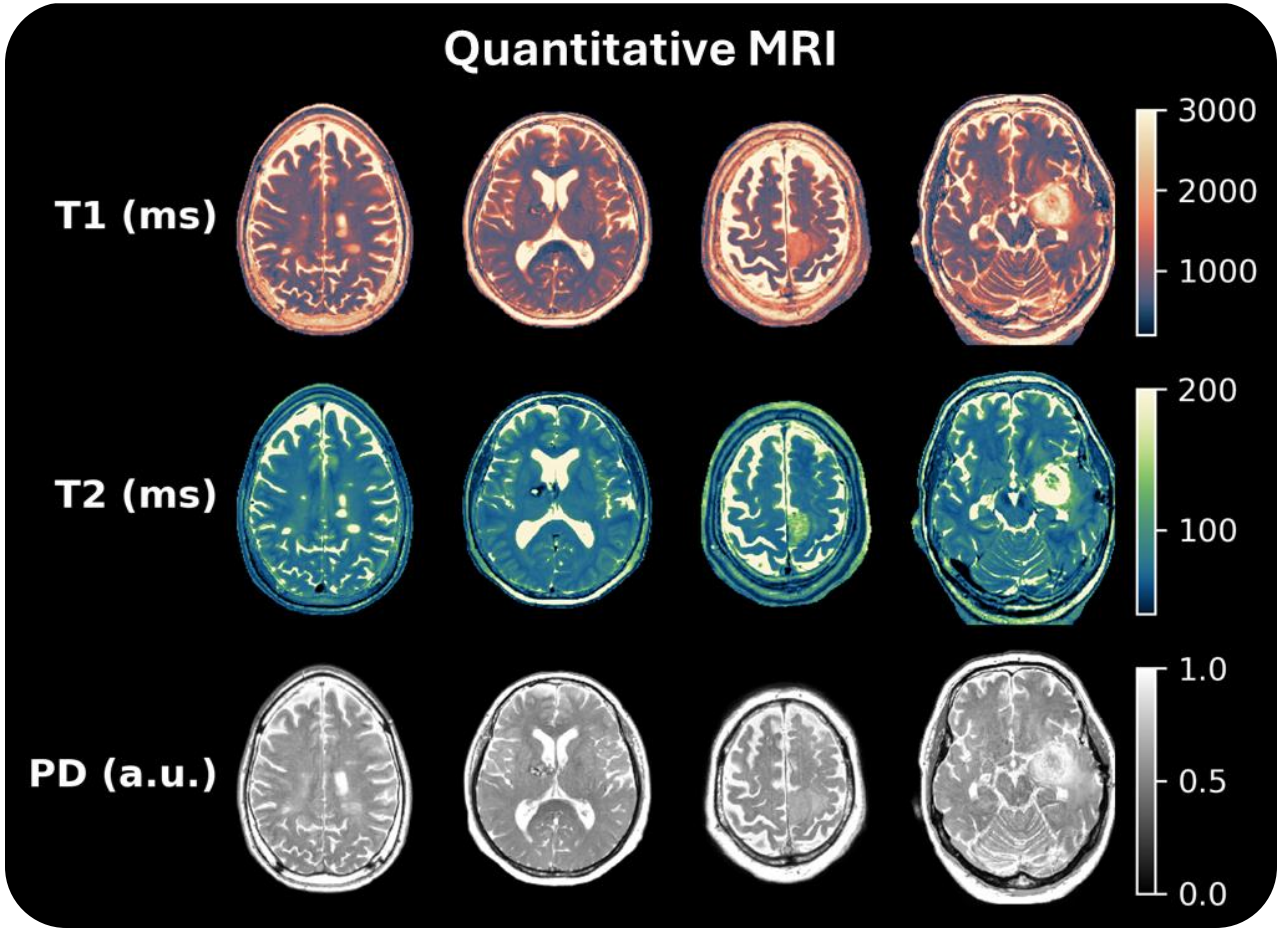
Introduction: Motivation

- **Quantitative MRI (qMRI)**
  - Specialized sequences
  - Reconstruct quantitative intrinsic properties (**PD**, **T1**, and **T2**)
- **Absolute Interpretation**
  - Comparisons across subjects, time, etc.
- **Help to develop interpretable biomarkers**
  - Diagnosis, disease characterization, and treatment-response monitoring



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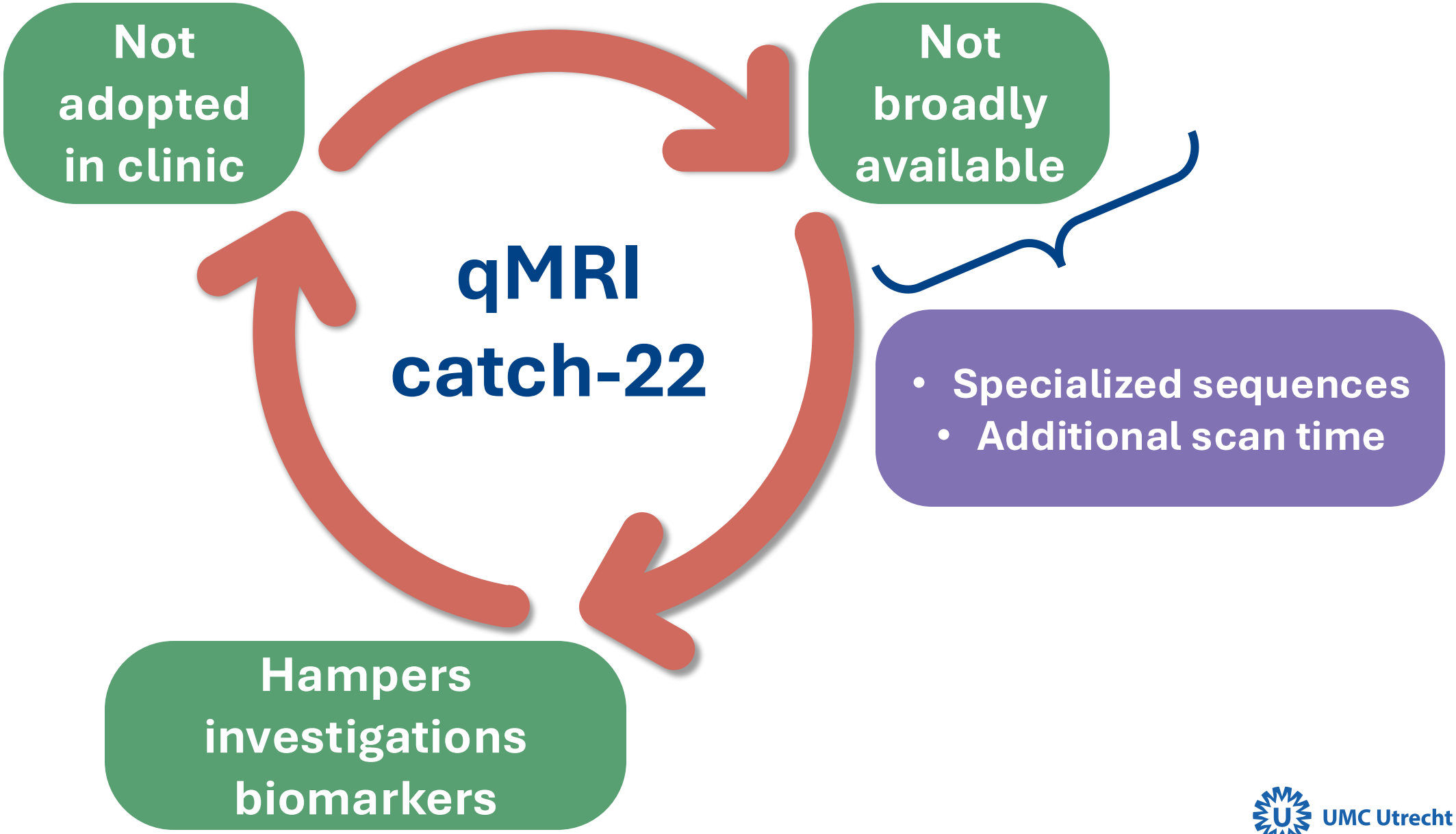
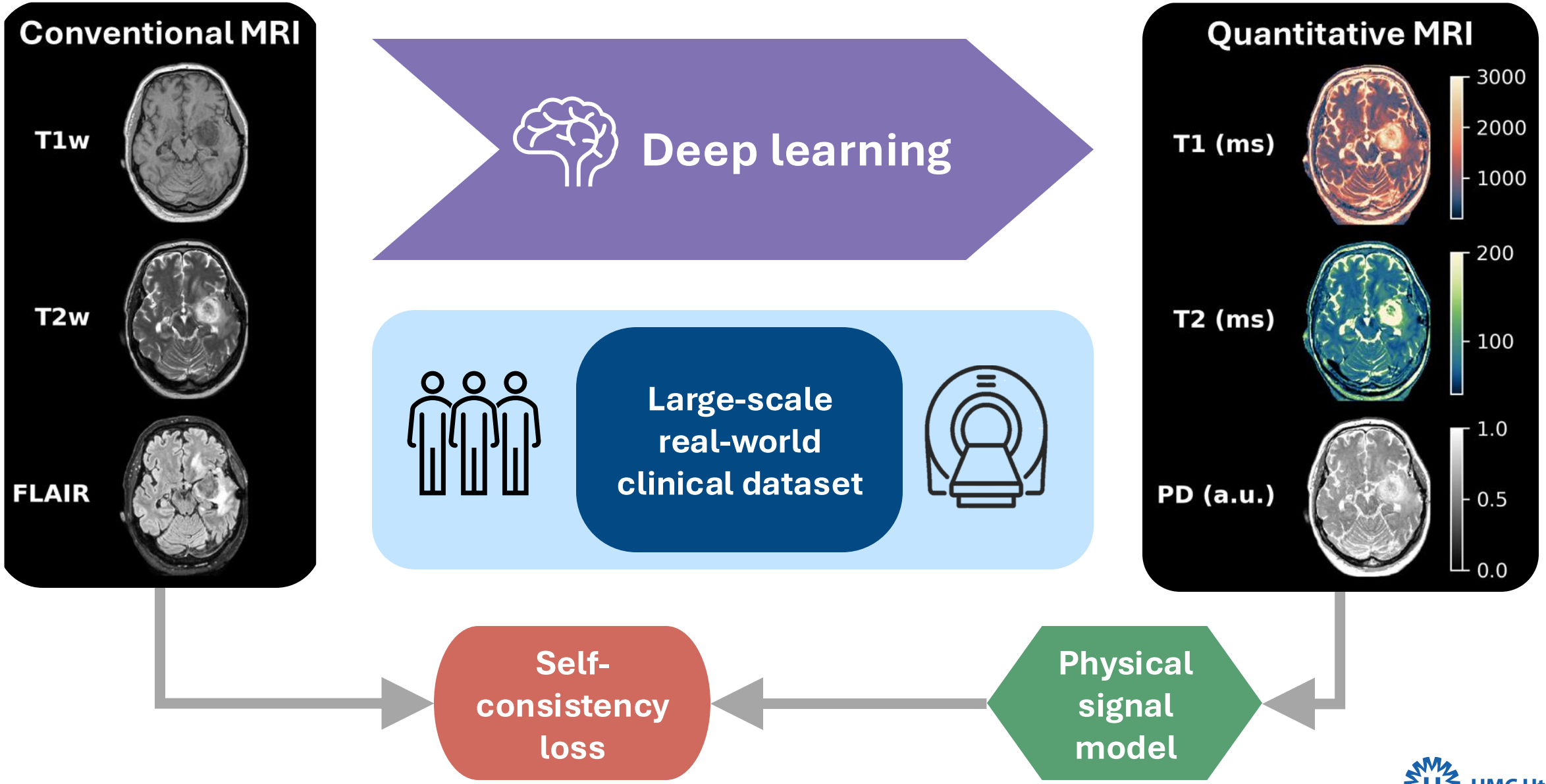
Introduction: Motivation



Introduction: Research objective



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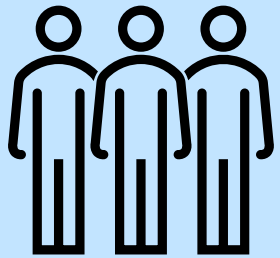
Methods: Dataset

Large-scale real-world clinically heterogenous dataset



- **4,000+** scan sessions
- **1,750+** subjects
- **6-year** period

- Conventional MRI: **T1w, T2w, FLAIR**
- Range of **acquisition settings**
  - TR, TE, TI, FA
- Different 3T **scanner hardware**

- **Diverse pathologies**
  - Oncology
  - Neurodegenerative
  - Epilepsy
  - Vascular

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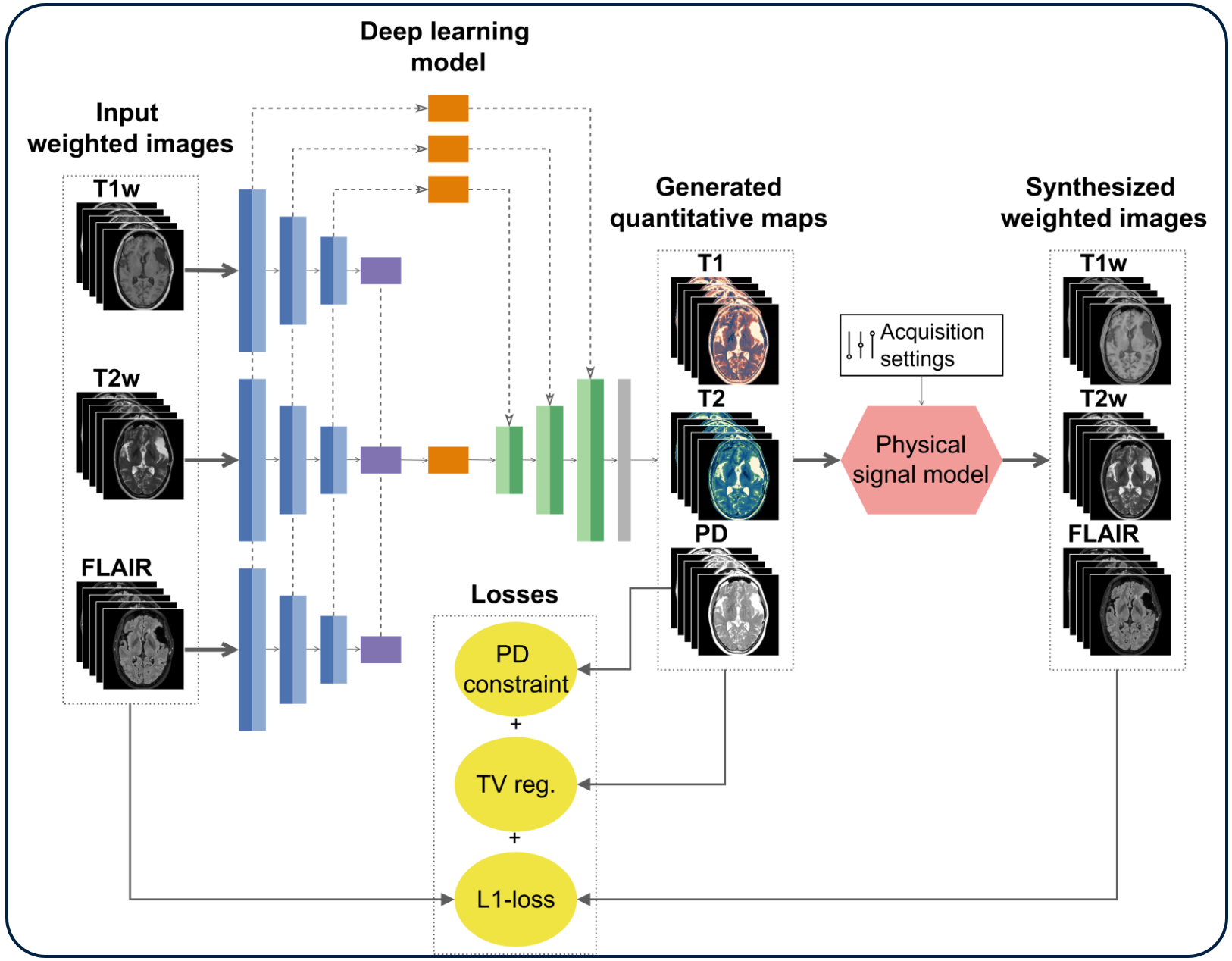
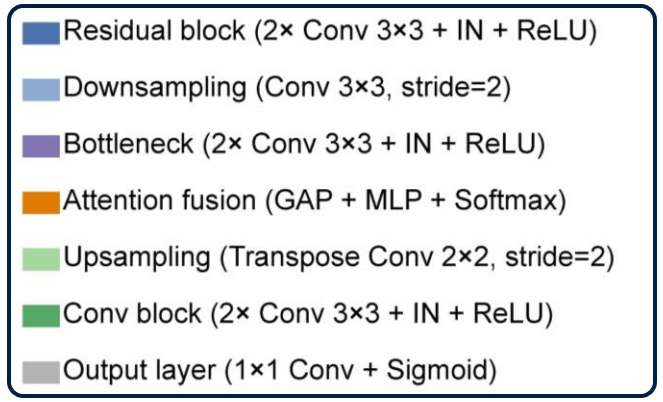
Methods: Physics-guided self-supervised framework





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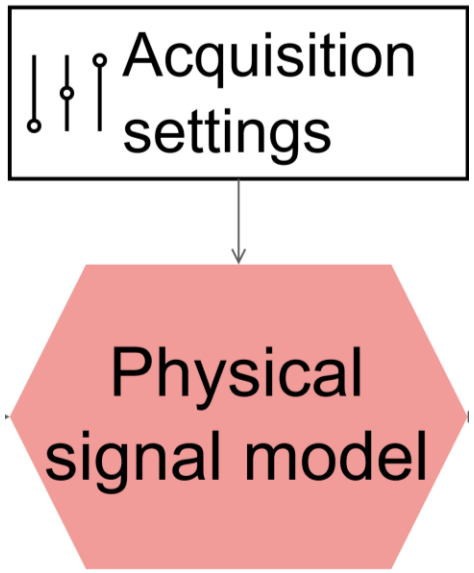
Established Bloch-based signal models



$$S_{\text{T1w GRE}} = PD \cdot \sin(FA) \cdot \frac{1 - \exp(-TR/T1)}{1 - \cos(FA) \cdot \exp(-TR/T1)} \cdot \exp(-TE/T2)$$

$$S_{\text{T2w TSE}} = PD \cdot (1 - \exp(-TR/T1)) \cdot \exp(-TE/T2)$$

$$S_{\text{FLAIR}} = |PD \cdot (1 - 2\exp(-TI/T1) + \exp(-TR/T1)) \cdot \exp(-TE/T2)|$$

Quantitative parameters
PD: Proton-density
T1: longitudinal relaxation time
T2: Transversal relaxation time

Acquisition settings
FA: Flip angle
TR: Repetition time
TE: Echo time
TI: Inversion time

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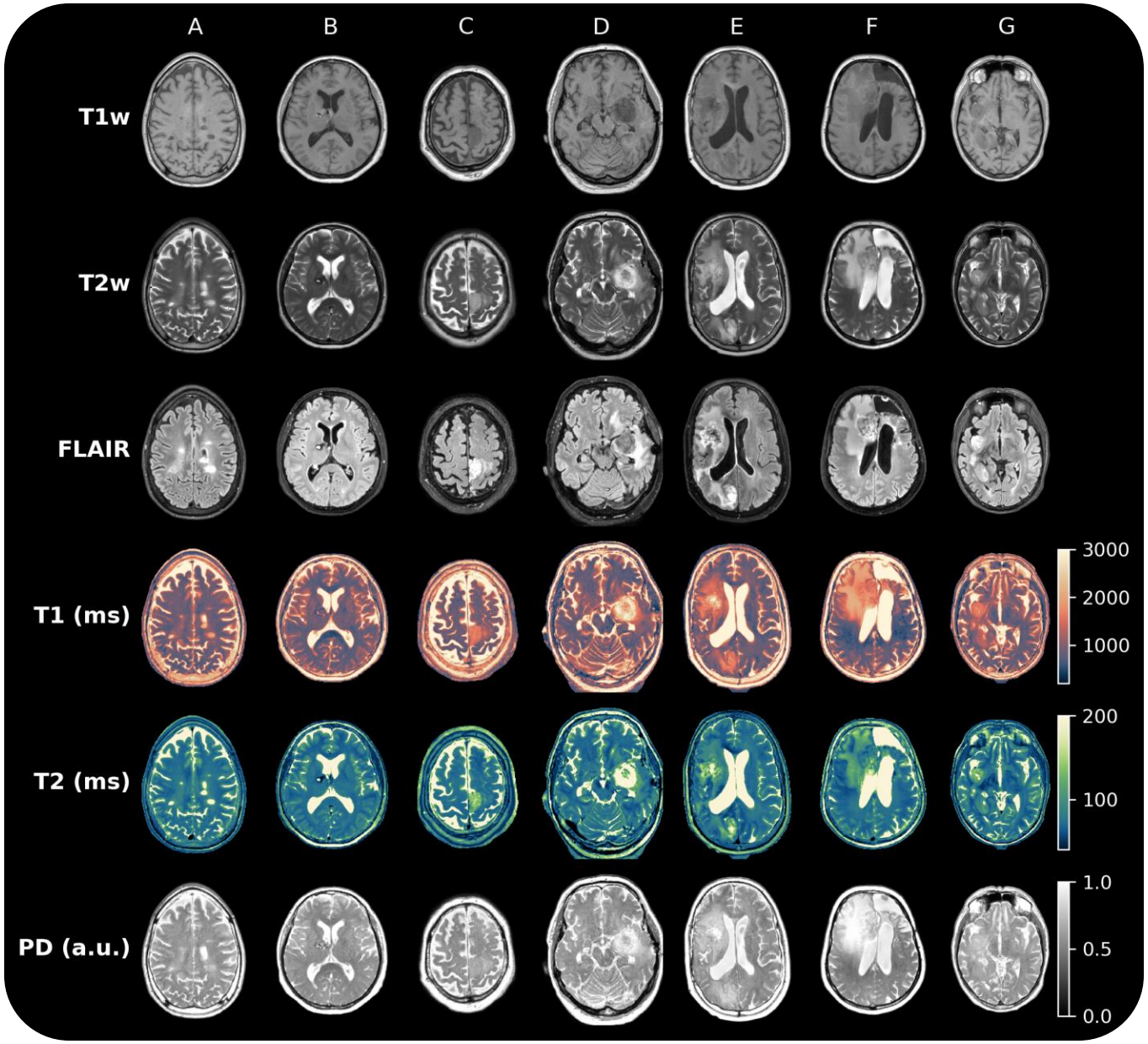
Results: Clinical test set



(A) Multiple sclerosis (MS)

(B) Cerebral cavernous venous malformation

(C) Meningioma

(D) Glioblastoma

(E) High-grade glioma progression

(F) Oligodendroglioma

(G) Multifocal high-grade glioma

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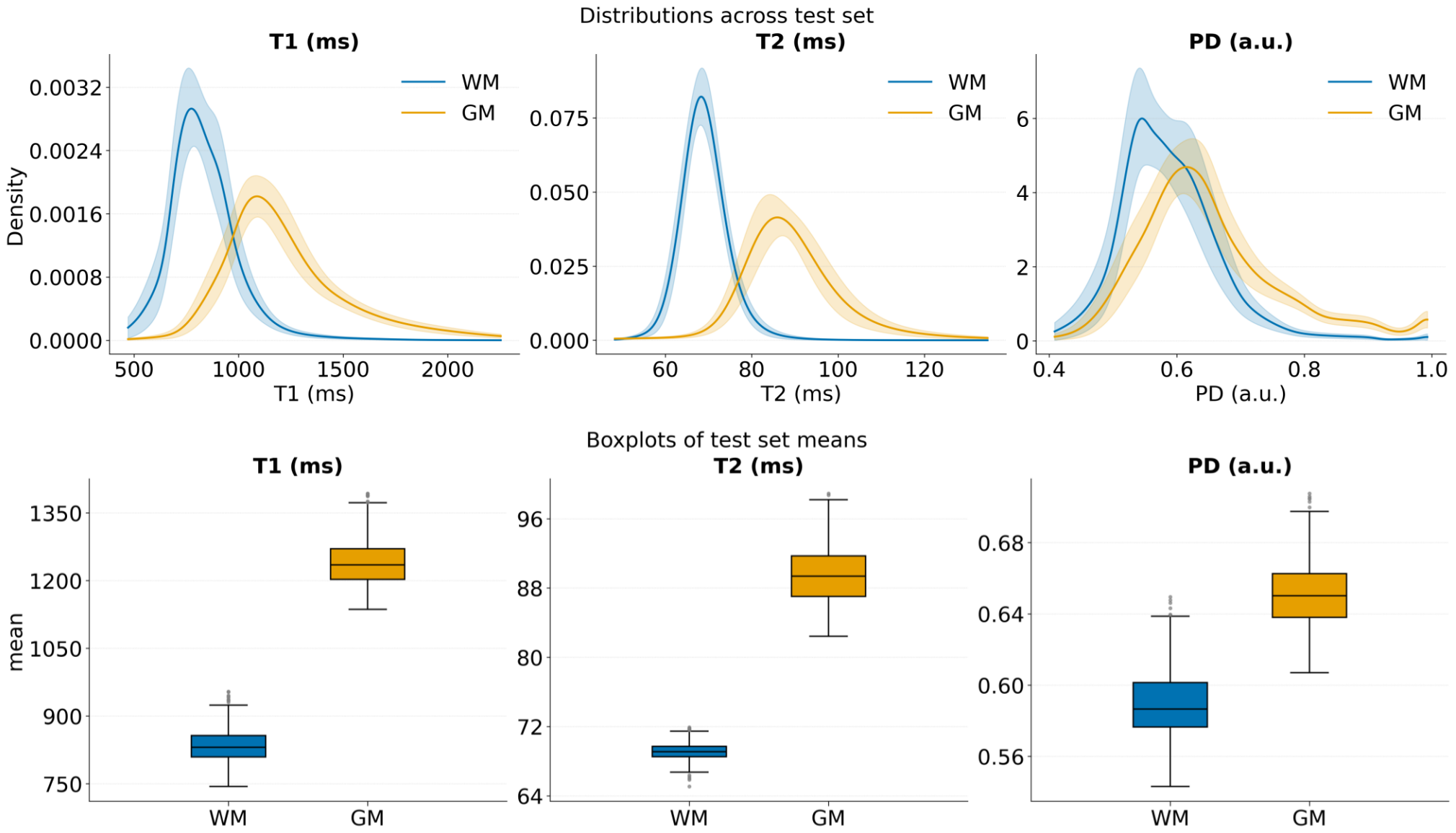
Results: Clinical test set (603 scan sessions)



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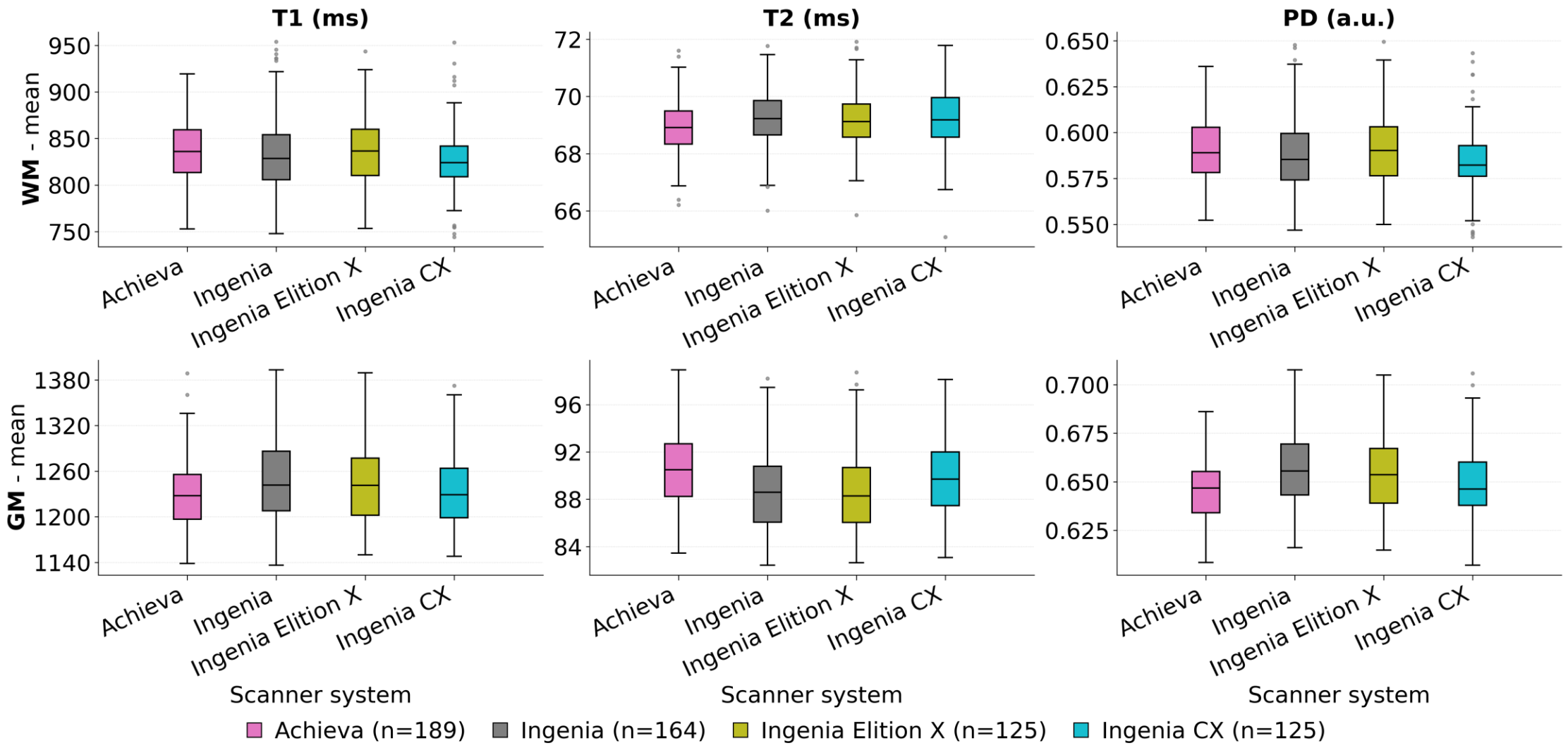
Results: Clinical test set (603 scan sessions)



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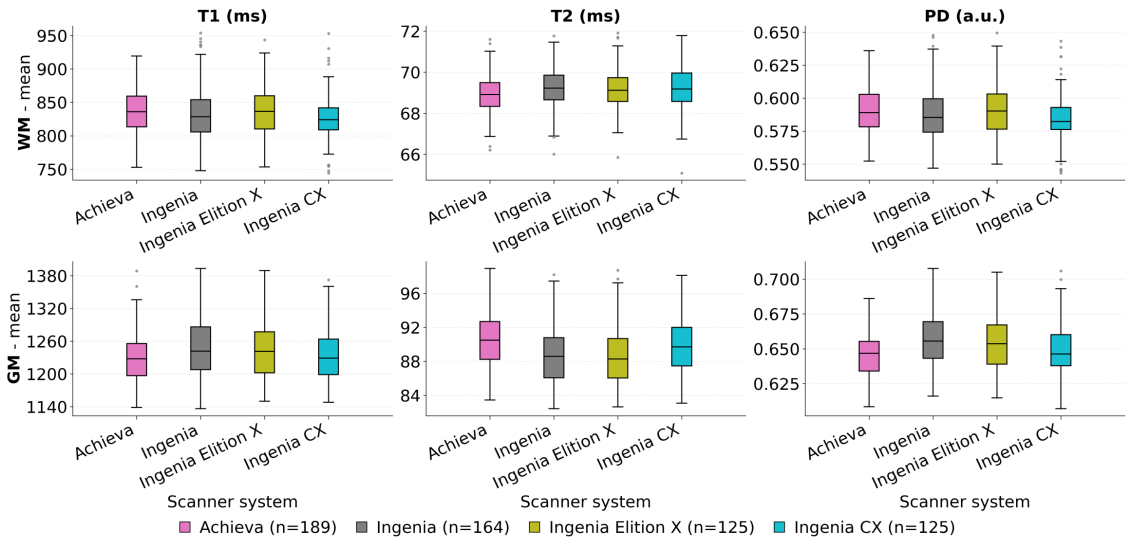
Results: Clinical test set (603 scan sessions)



Inter-group CV:

- **T1**
  - 0.57 % (WM) and 0.68 % (GM)
- **T2**
  - 0.22 % (WM) and 1.07 % (GM)
- **PD**
  - 0.54 % (WM) and 0.78 % (GM)

Quantitative maps **invariant** to **scanner system**

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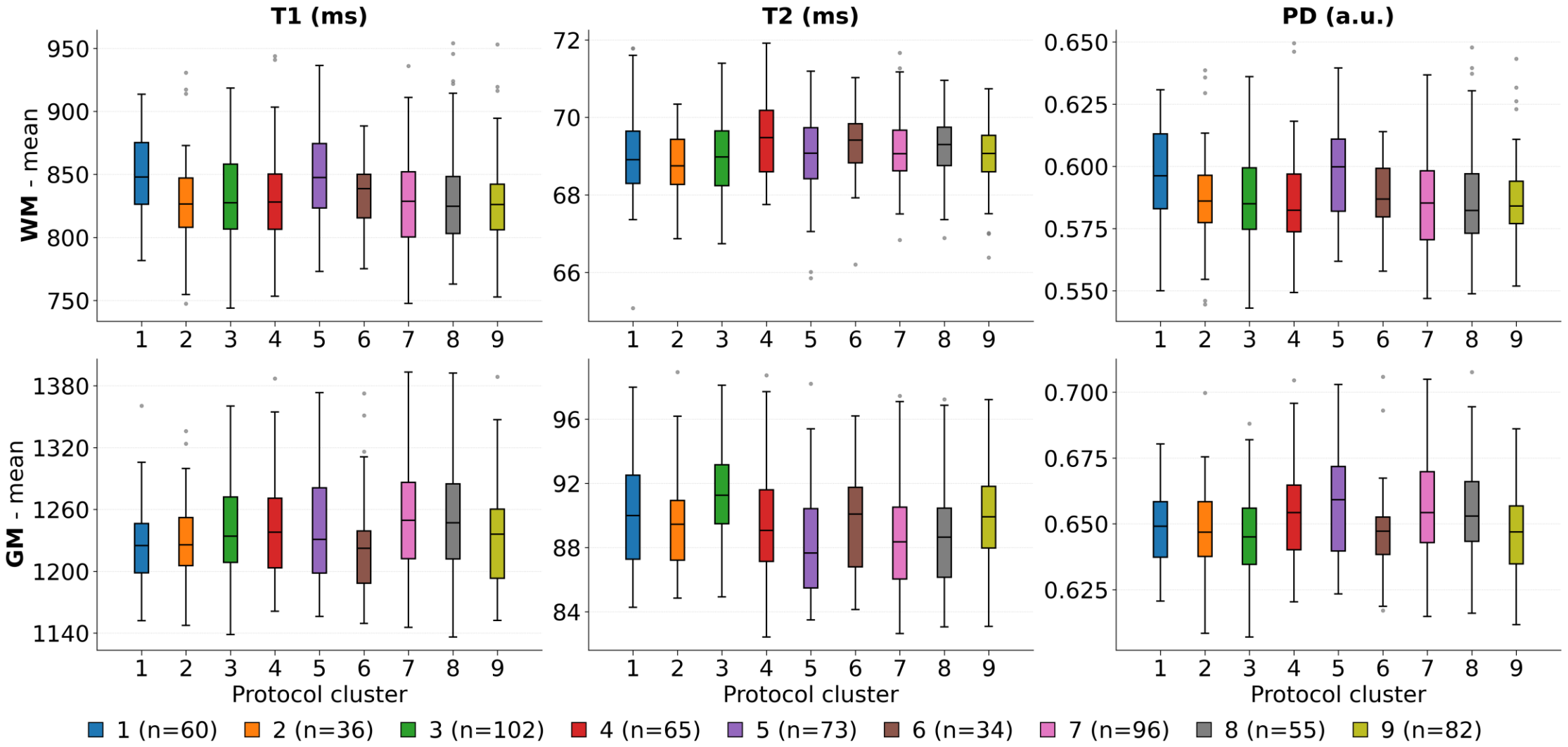
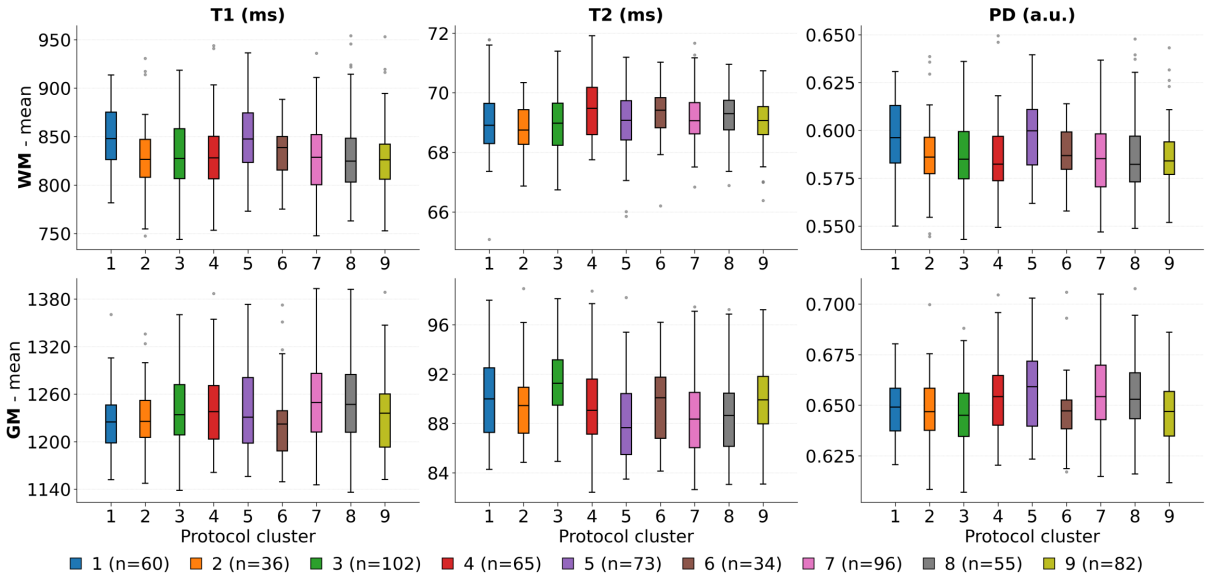
Results: Clinical test set (603 scan sessions)



Results: Clinical test set (603 scan sessions)



Inter-group CV:

- **T1**
  - 1.08% (WM) and 0.82 % (GM)
- **T2**
  - 0.31 % (WM) and 1.07 % (GM)
- **PD**
  - 0.84 % (WM) and 0.72 % (GM)

Quantitative maps **invariant** to **sequence parameters**

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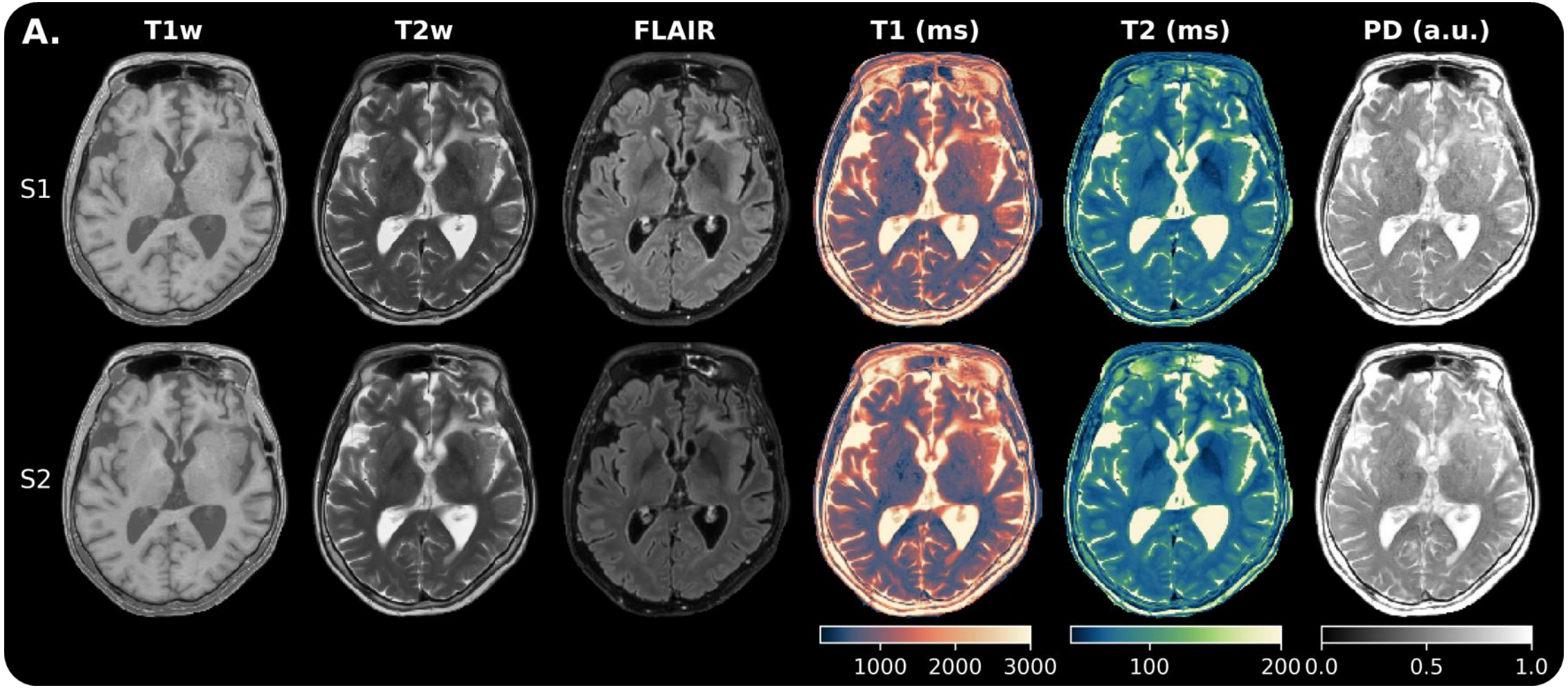
Results: Retrospective reproducibility

Patient scanned **twice** within three months



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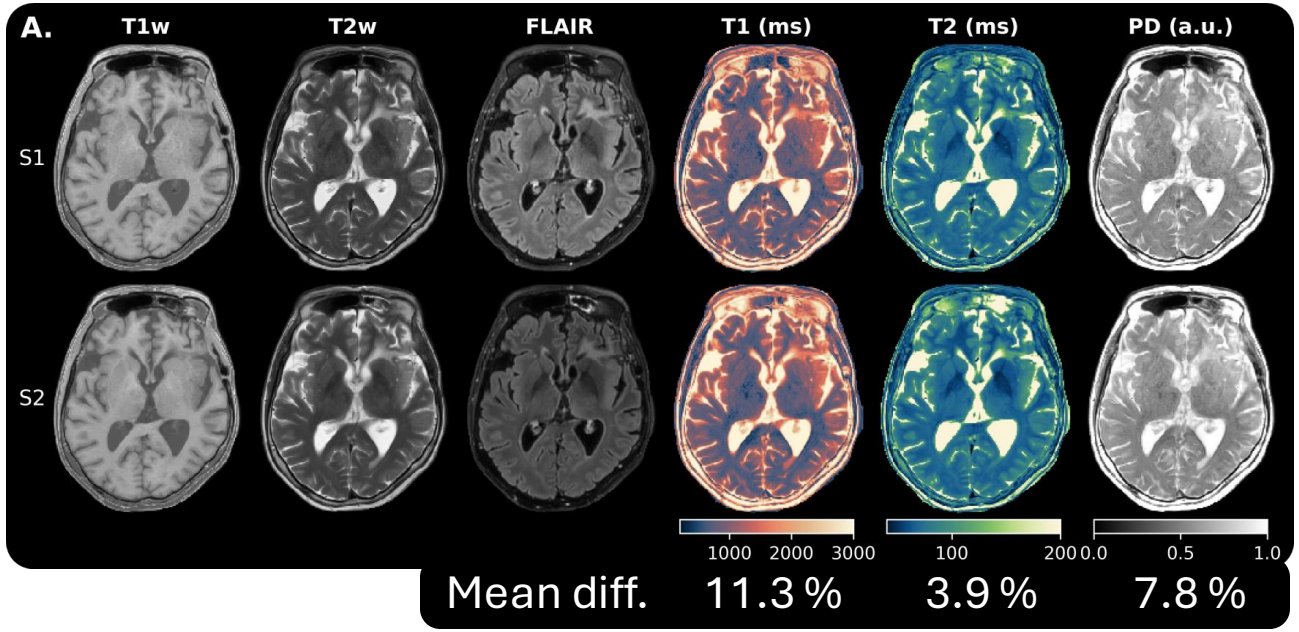
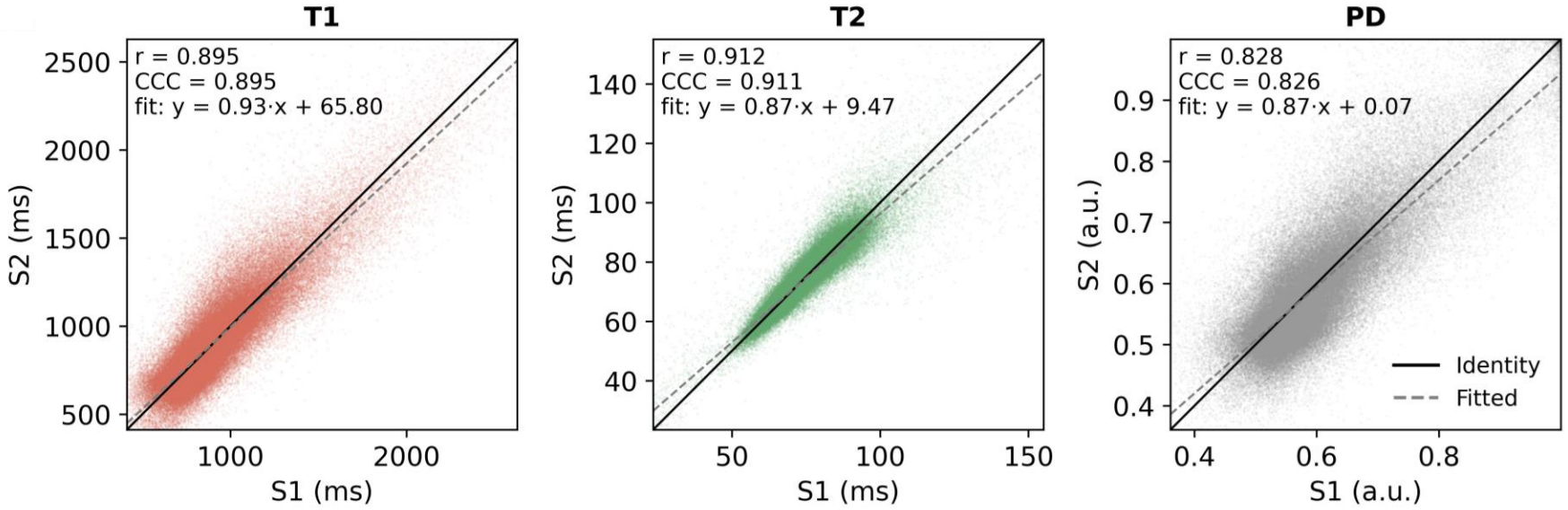
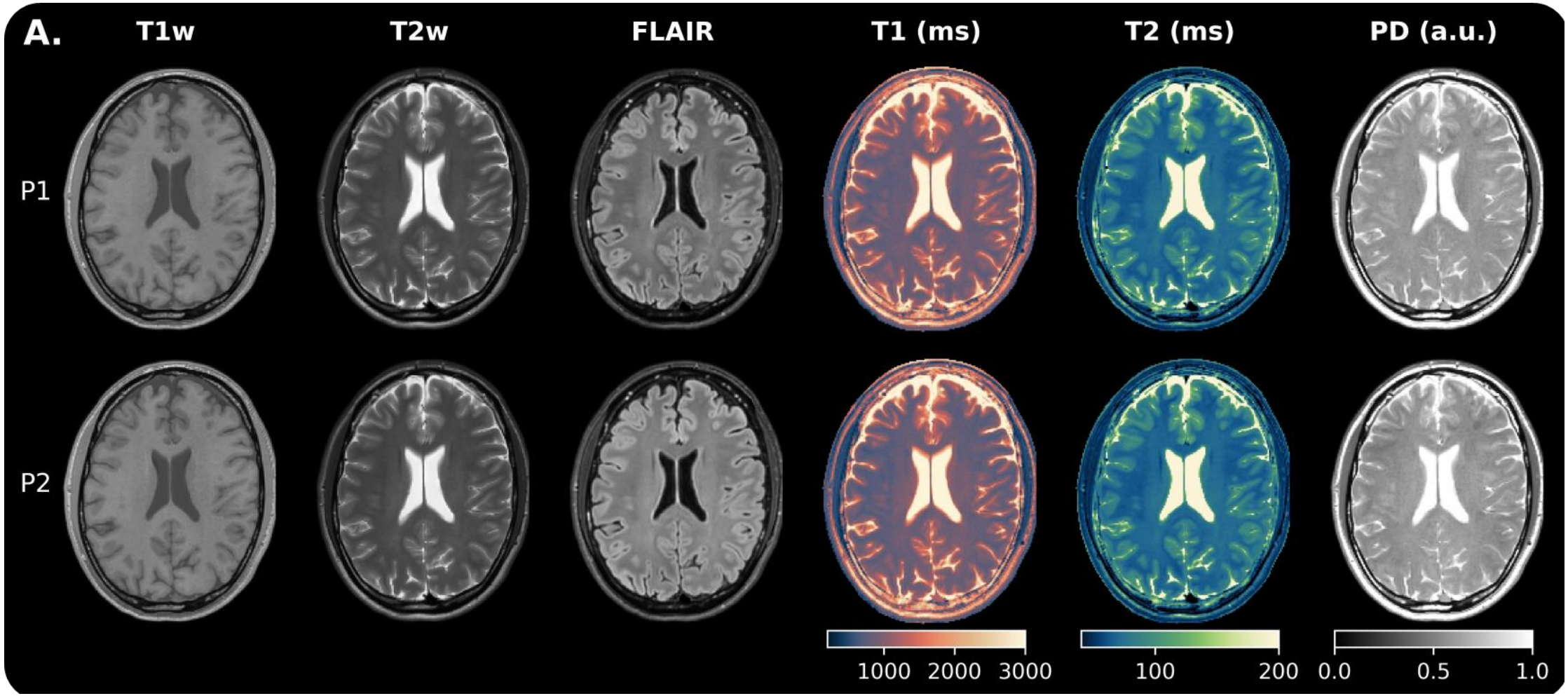
Results: Retrospective reproducibility





Results: Prospective reproducibility

Volunteer scanned **twice** with different **acquisition settings**



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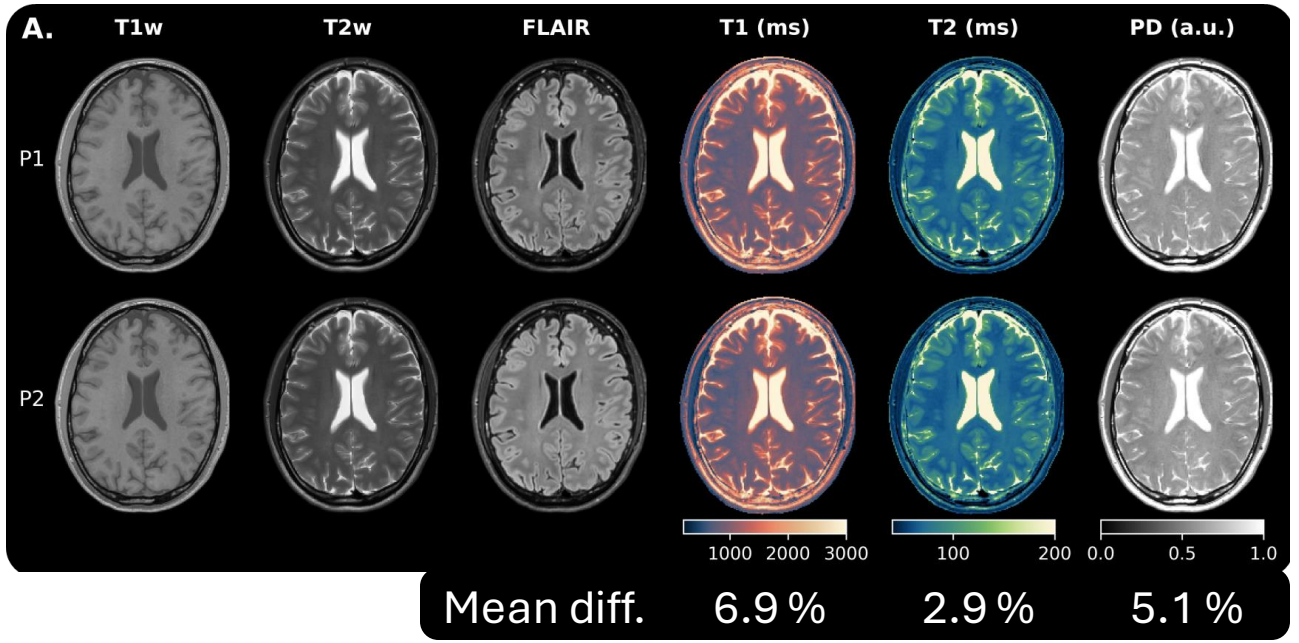
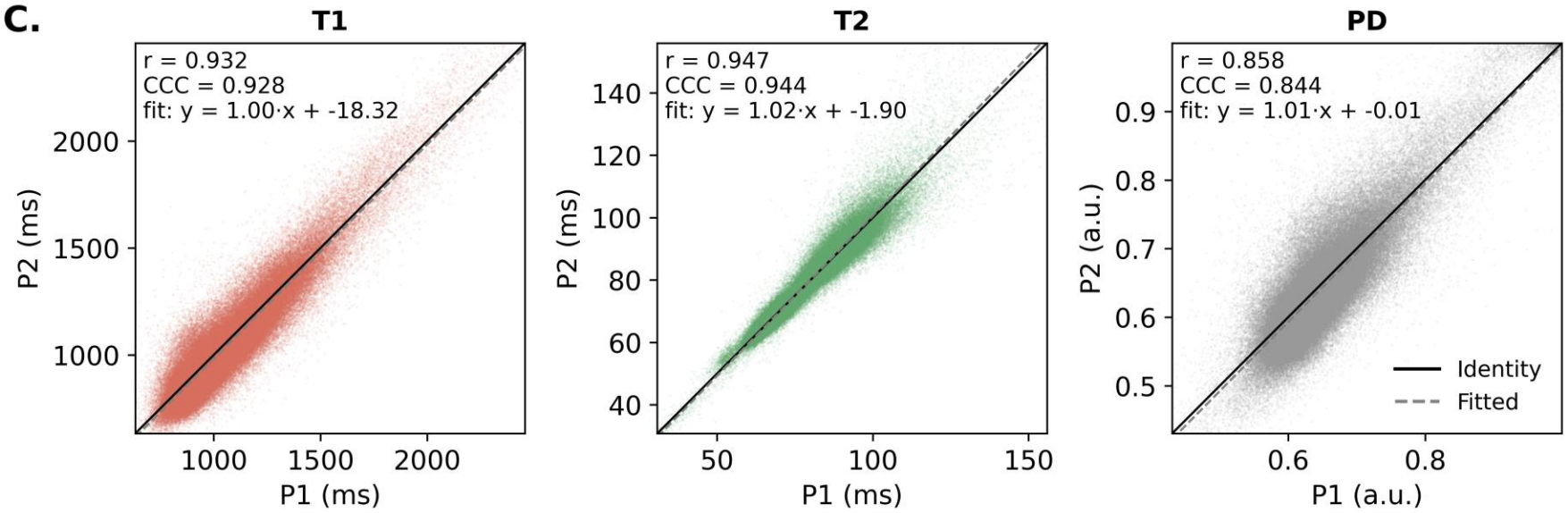
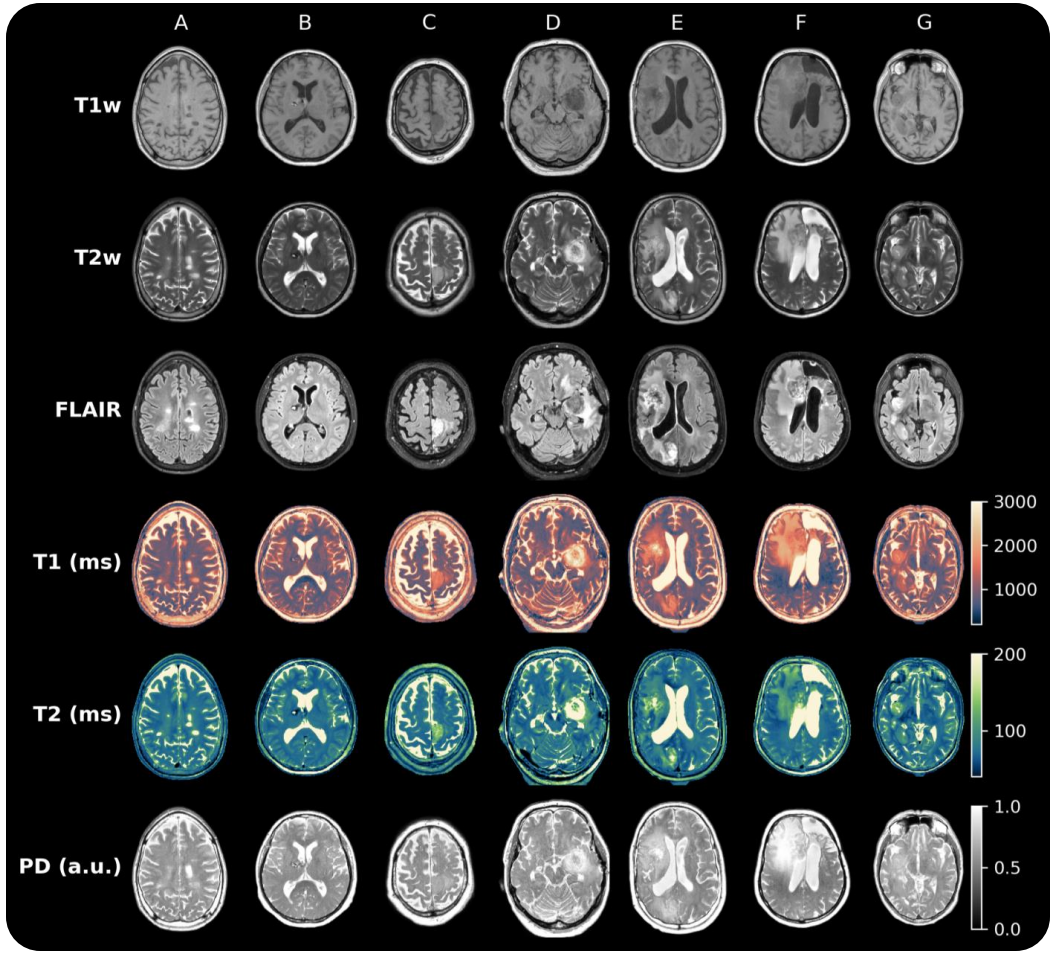
Results: Prospective reproducibility





Discussion: Summary

- **Physics-guided self-supervised** deep learning framework
  - For **quantitative mapping** from conventional MRI



- Retrospectively **transform** widely available conventional MRI into qMRI
- Uses routine acquisitions (T1w, T2w, FLAIR) with **no added scan time.**

Limitation: Only homogeneous sequence types

- **Invariant** to:
  - Scanner hardware
  - Acquisition settings

Limitation: Analysis only in WM and GM

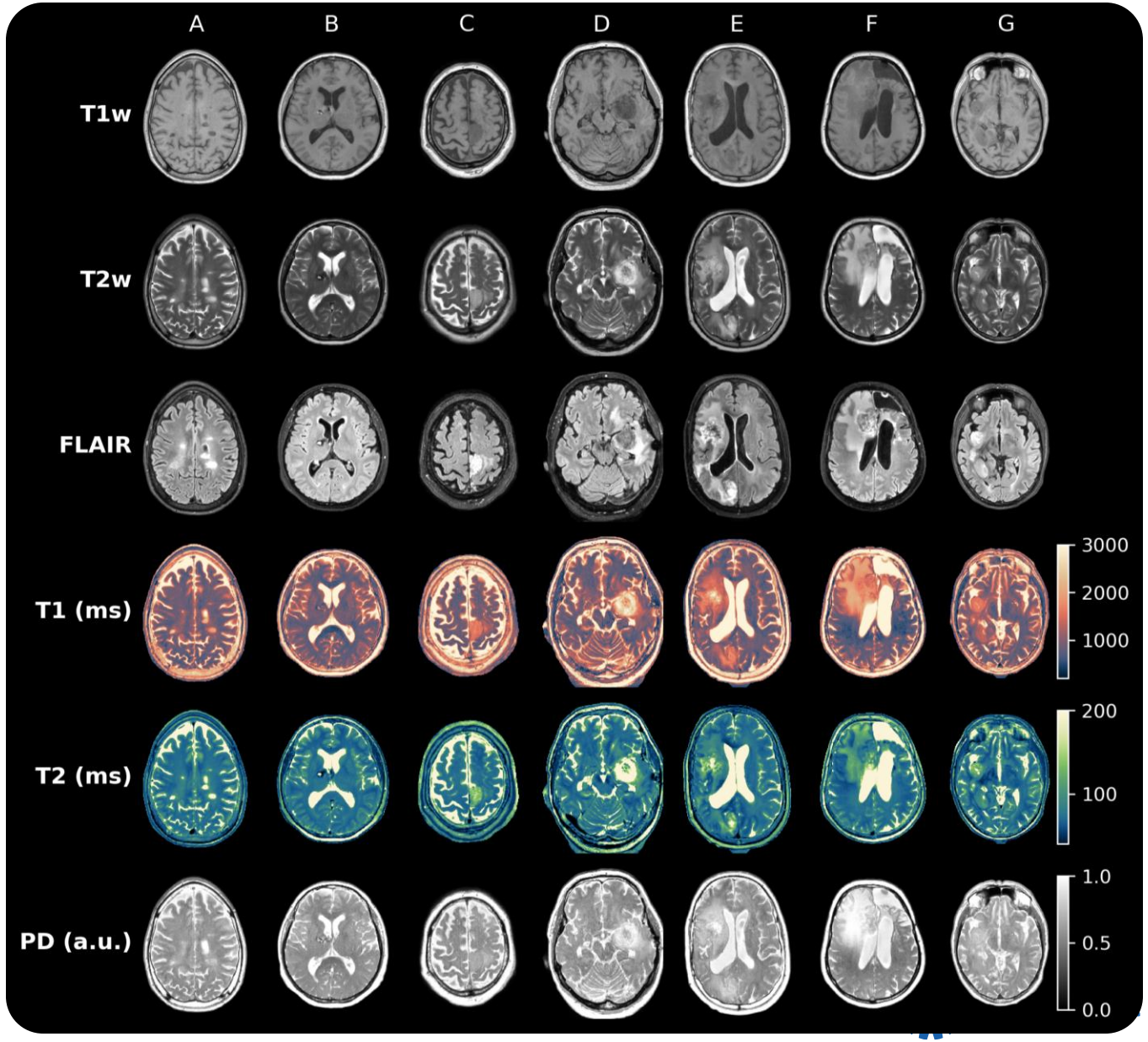
- Excellent **voxel-wise reproducibility**
  - Retrospective
  - Prospective

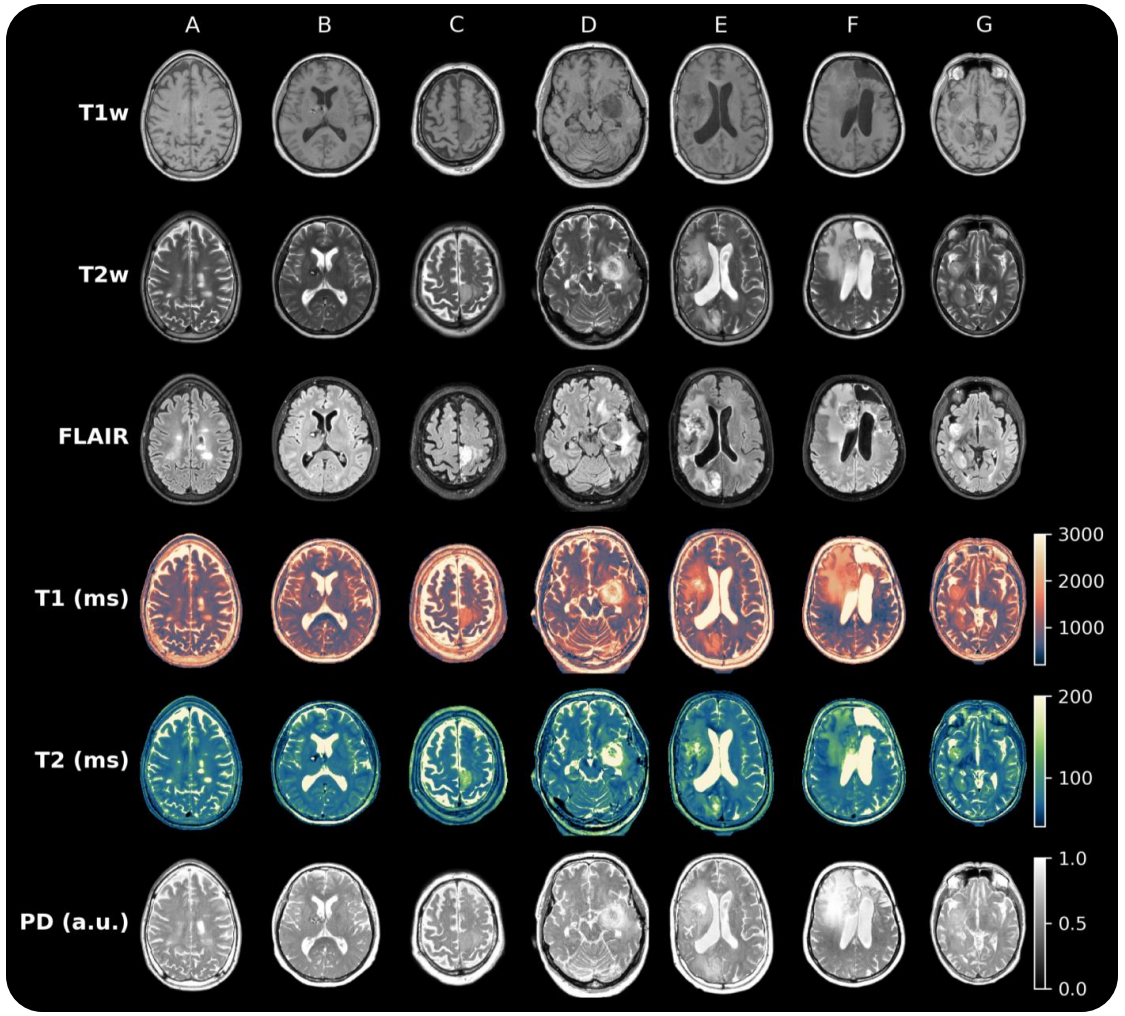
Discussion: Outlook

- Opens the door to **large-scale quantitative biomarker investigations**

- **Harmonizes** data across scanner hardware and sequence parameters
  - Improve **generalizability** of downstream deep learning models

- **Adaptable** beyond the brain (e.g. prostate)





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Link to arXiv preprint

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