

## Identification of Gadolinium (Gd) contrast enhanced regions in MS lesions using brain tissue microstructure information obtained from diffusion and T2 relaxometry MRI

Sudhanya Chatterjee<sup>1</sup> Olivier Commowick<sup>1</sup> Onur Afacan<sup>2</sup> Simon K. Warfield<sup>2</sup> Christian Barillot<sup>1</sup>

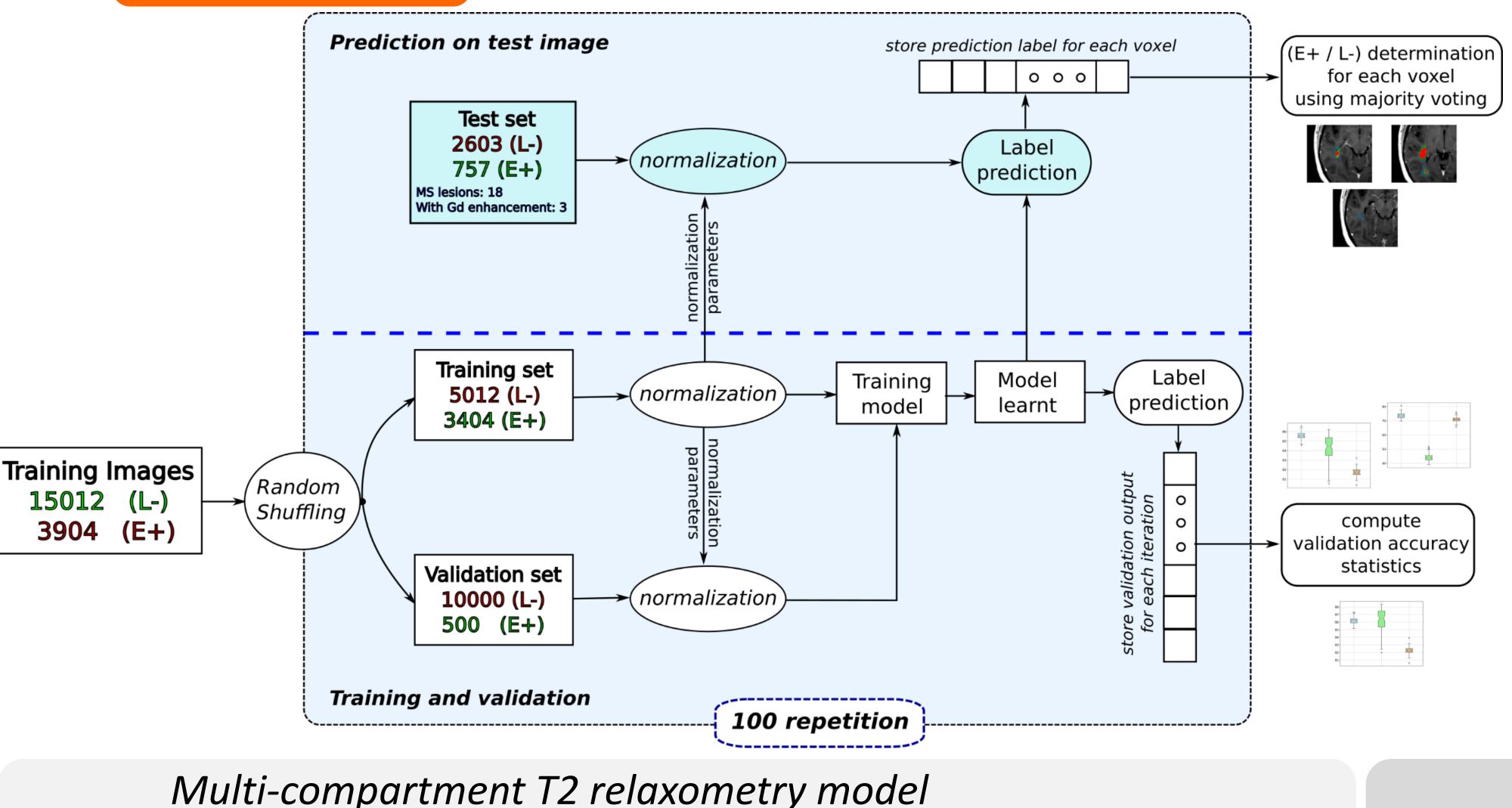
<sup>1</sup> VisAGeS U1228 INSERM/INRIA, IRISA UMR CNRS 6074, University of Rennes 1, France <sup>2</sup> Computational Radiology Laboratory, Boston Children's Hospital, Boston, MA, USA

## PURPOSE

- Suggestions insisting on greater debate before Gd based contrast agents (GBCA) administration has gained traction due to observed MRI signal changes in the brain tissues due to repeated GBCA administrations and other possible health issues.
- We evaluated the potential of tissue microstructure information obtained from diffusion and T2 relaxometry MRI to identify regions in MS lesions undergoing active blood brain barrier breakdown.
- Perform predictions on images acquired under clinical settings. Combined acquisition time for T2 relaxometry and diffusion MRI was around 12 minutes (with full brain coverage).



## **METHOD**



## Feature sets

•  $\mathcal{F}_R \in \mathbb{R}^3$ : It consists of water fractions corresponding to short, medium and high T2 tissue components in a voxel obtained from a multi-compartment T2 relaxometry model [1].

 $\mathcal{F}_{D} \in \mathbb{R}^{4}$ : Features are derived using a multi-compartment diffusion model [2]. A compartment wise weighted average of fraction anisotropy, apparent diffusion coefficient and axial diffusivity at each voxel is used. The weight of isotropic free water is also included in the feature set.

 $\mathcal{F}_{RD} \in \mathbb{R}^7$ : Use both  $\mathcal{F}_R$  and  $\mathcal{F}_D$ .

Multi-compartment Diffusion Model N=3

 $s(t_i) = \sum_{j=1}^{\infty} \alpha_j \int_{\Omega} f_j(T_2; \mathbf{p_j}) EPG(T_2, \triangle TE, i, B_1) dT_2$ 

 $\infty$ 

- $j = \{1, 2, 3\}$ : Three compartments namely short T2, medium T2 and high T2 each represented by a fixed Gaussian PDF:  $f_i(\cdot)$
- $EPG(\cdot)$ : Account for stimulated echoes using the extended phase graph method.

Estimated parameters:

- { $\alpha_1, \alpha_2, \alpha_3$ }: Weights of the PDF corresponding to each compartment.
- $B_1$ : The inhomogeneity scale factor required to compute  $EPG(\cdot)$ Final weights are obtained as:

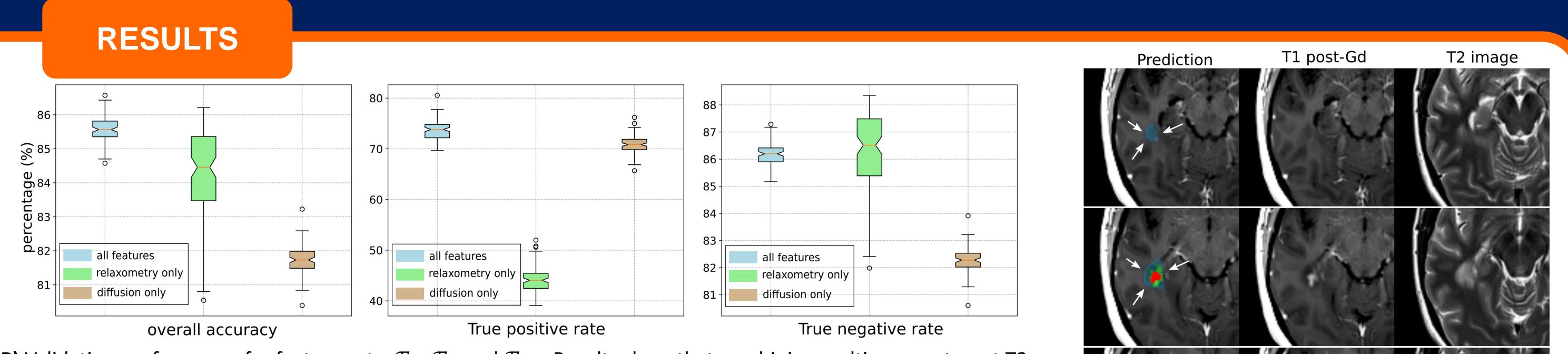
 $\{a_j/(\alpha_1 + \alpha_2 + \alpha_3)\}_{j=1,2,3}$ 

 $p(x) = f_w p_{FW}(x) + \sum a_i p_i(x) \quad \text{where} \quad f_w + \sum_i a_i = 1$ 

- $p_{FW}$ : isotropic Gaussian PDF for free water ( $\sigma^2 = 3.0 \times 10^{-3} mm^2 . s^{-1}$ )
- $p_i(\cdot)$ : *i*-th fascicle compartment PDF defined as a stick model [2].
- Ball and stick model was chosen taking into account the clinical data used for this work.
- Estimation was performed using the method proposed by Aymeric Stamm et al. [3].

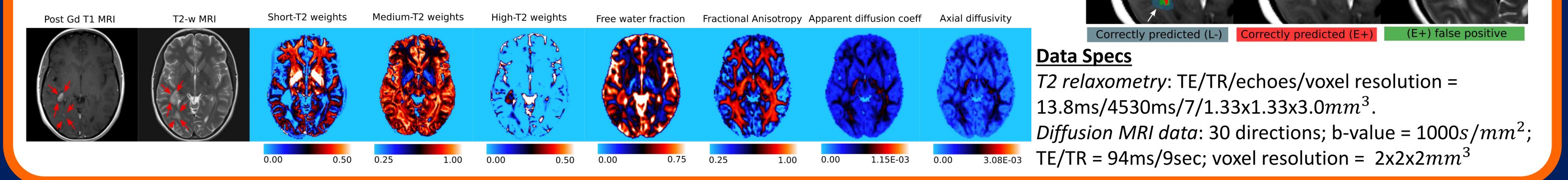
Multi-compartment T2 relaxometry and diffusion models can

be found at: https://github.com/Inria-Visages/Anima-Public



(TOP) Validation performance for feature sets:  $\mathcal{F}_R$ ,  $\mathcal{F}_D$  and  $\mathcal{F}_{RD}$ . Results show that combining multi-compartment T2 relaxometry and dMRI derived features improves the prediction performance. Hence there is added value in using them together over use of any of them standalone. (BELOW) An example of the features is shown for a case. (RIGHT) Results of prediction on a test case is shown. Dice score for E+ and L- voxel prediction was 0.64 and 0.86 respectively.

Children's Hospital Boston



<u>**References:</u>** [1] Chatterjee S., et al., "A 3-year follow-up study of enhancing multiple sclerosis (MS) lesions in MS patients demonstrating</u> clinically isolated syndrome (CIS) using a multi-compartment T2 relaxometry (MCT2) model," ISMRM, 2018. [2] Panagiotaki E., et al., "Compartment models" of the diffusion MR signal in brain white matter: A taxonomy and comparison," Neuroimage, 2012. [4] Stamm A. et al., "Comprehensive Maximum Likelihood Estimation of Diffusion Compartment Models Towards Reliable Mapping of Brain Microstructure", MICCAI, 2016.

CINIS

