

Optimizing the NEXI acquisition protocol for human gray matter microstructure mapping on a clinical MRI scanner using Explainable AI

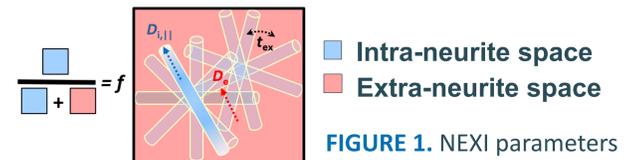
Quentin Uhl¹, Tommaso Pavan¹, Thorsten Feiweier², Erick Jorge Canales-Rodríguez³ and Ileana Jelescu¹

¹Dept. of Radiology, Lausanne University Hospital (CHUV) and University of Lausanne, Lausanne, Switzerland; ²Siemens Healthcare GmbH, Erlangen, Germany; ³Signal Processing Lab 5 (LTS5), École Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland.

AIMS & BACKGROUND

We aim to optimize the acquisition protocol for parameter estimation of the NEXI model of two exchanging compartments^{1,2} and demonstrate feasibility on a clinical 3T system.

The NEXI model is suited to characterize gray matter microstructure; its parameters are the **exchange time** t_{ex} , the **intra and extra-neurite apparent diffusivities** D_i and D_e and the **intra-neurite signal fraction** f .



METHODS

One healthy volunteer was scanned.

Acquisition:

- DWI acquired on a 3T Siemens Prisma system
- PGSE EPI sequence with N=16 (b, t) pairs among b=1, 2, 3.2, 4.44 and 5ms/ μm^2 , $\Delta=28.3, 36, 45, 55$ and 65ms, $\delta=16.5$ ms, 4 b=0 images per Δ , 340 total dwi, at 2-mm isotropic resolution, total scan time: 35min.

Preprocessing:

- Multi-shell multi-diffusion time data preprocessed jointly.
- Preprocessing steps : MP-PCA magnitude denoising⁴, Gibbs ringing correction⁵, distortion and eddy current correction⁶, average over all the directions and normalization by the mean value of the b=0 volumes.

Processing:

- Fitting the NEXI model using a Multi-Layer Perceptron (MLP) of 3 hidden layers and 500 neurons per layer trained on $2 \cdot 10^6$ random sets (NEXI parameter combinations) and applied to a test set of 10^4 examples.
- Segmentation of the cortical ribbon ROI on the anatomical MPRAGE image using FastSurfer⁷ and transformation into diffusion native space using linear registration⁸ of b=0 images to MPRAGE images.

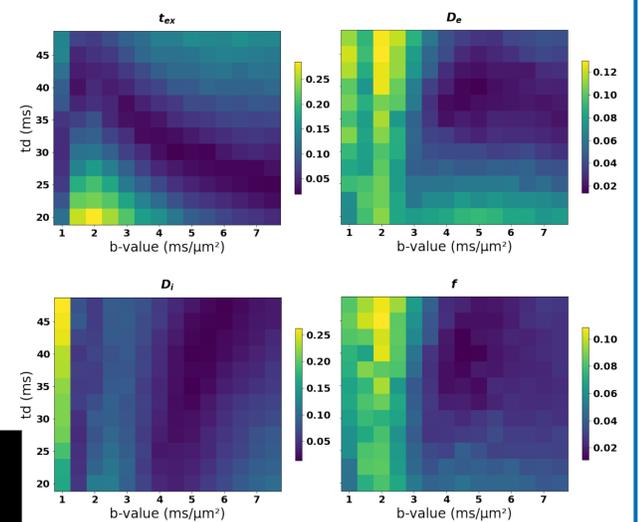
Explainable AI analysis:

- Extraction of Shapley values from an extended protocol of 12x14 (b, t) pairs using the SHAP framework⁹.
- Ranking of these values to produce an optimized protocol of N=16 (b, t) pairs.
- The RMSE obtained from the clinical protocol on each parameter, normalized by their limits, gave the number of optimal pairs selected from each parameter ranked SHAP values.

Protocol Optimization

FIGURE 3.

Mean absolute SHAP values of each NEXI parameter for each (b, t) pair in the Extended protocol.



- Based on the normalized RMSE on each parameter, we assigned **8 optimal pairs** for t_{ex} , 4 for D_i , 2 for D_e and 2 for f .

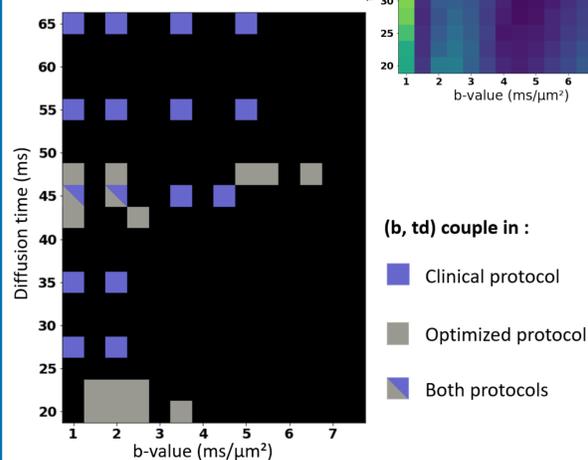


FIGURE 4. (b, t) pairs selected in the Clinical and Optimized protocols.

NEXI parametric maps

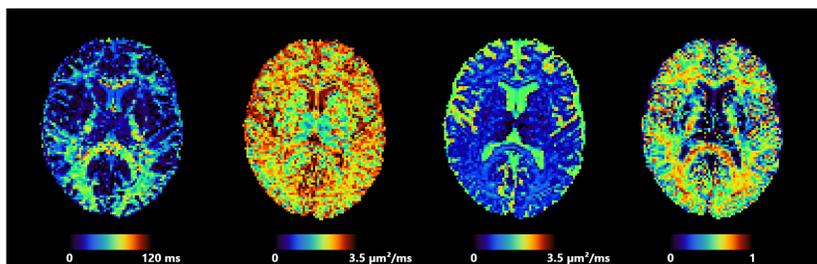


FIGURE 2. Axial slice of NEXI parametric maps in our subject with, below, the median and quartiles of the estimations on the cortical ribbon, showed on the right.

- These are the first microstructure maps of the NEXI model estimated in the **human brain** on a “standard” clinical scanner.
- Typical NEXI parameter values in the cortex are **consistent with previous estimates** in the **rat cortex**¹.

MLP Scores

	t_{ex} (ms)	D_i ($\mu\text{m}^2/\text{ms}$)	D_e ($\mu\text{m}^2/\text{ms}$)	f
Clinical Protocol MAE	27.457	0.423	0.351	0.083
Optimized Protocol MAE	25.496	0.419	0.330	0.076

TABLE 1. Mean Absolute Error of the MLP with each input protocol.

- These scores are very similar, we can note a **small improvement of 2ms** in t_{ex} MAE with the optimized protocol.
- This marginal reduction **does not allow us to prefer one protocol** over the other, especially as some pairs of the Optimized protocol are **difficult to achieve** on a clinical system, due to gradient limitations.

CONCLUSION

- We developed an **optimization method of MRI protocols** using Explainable AI.
- The limit on NEXI parameter estimation precision and accuracy is however largely **driven by the model** and the **type of measurements available**.
- Our clinical acquisition protocol feasible on a 3T system with 80 mT/m gradients **already yields reasonable NEXI microstructure maps** in the human brain.