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

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#0948

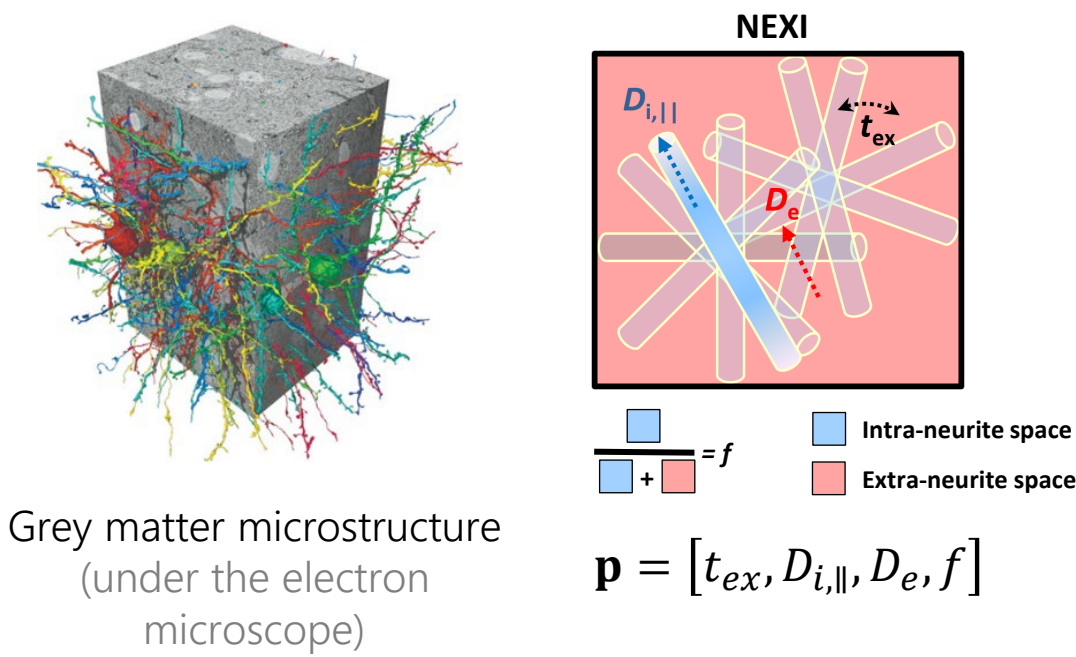ISMRM & ISMRT Annual Meeting & Exhibition 2023
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Declaration of
Financial Interests or Relationships

Speaker Name: Quentin Uhl

I have no financial interests or relationships to disclose with regard to the subject matter of this presentation.

The Neurite Exchange Imaging model

NEXI

$$\mathbf{p} = [t_{ex}, D_{i,\parallel}, D_e, f]$$

Grey matter microstructure
(under the electron microscope)

- Geometry different from white matter
- Little myelin : water exchange across the cell membrane
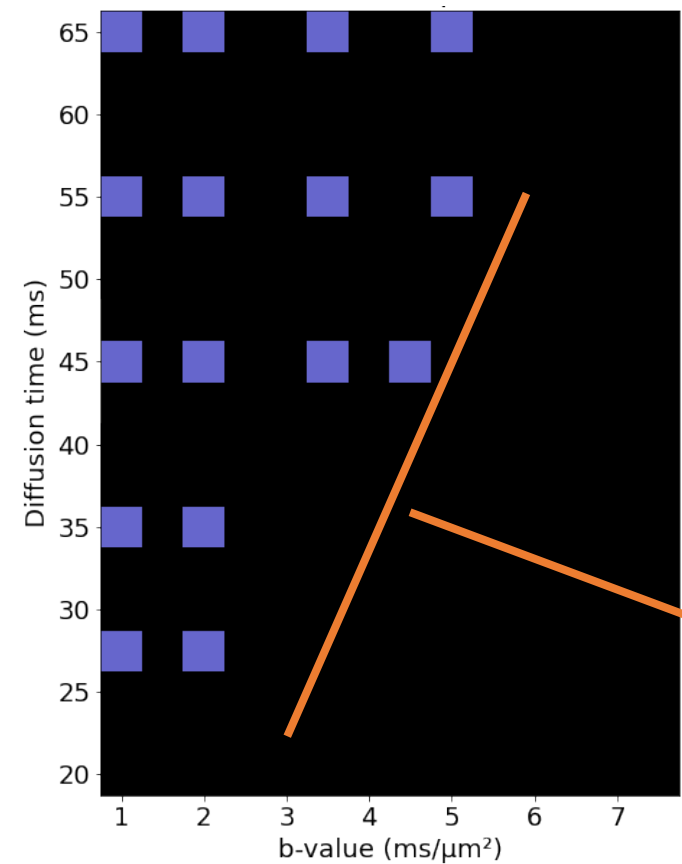
From the parameters to the signal

Kernel:	$\mathcal{K}(q, t, \mathbf{g} \cdot \mathbf{n}; f, D_{i,\parallel}, D_e, t_{ex}) = f' e^{-q^2 t D_i'} + (1 - f') e^{-q^2 t D_e'}$
Where: "apparent" diffusivities	$D_{i/e}' = \frac{1}{2} \left\{ D_{i,\parallel}(\mathbf{g} \cdot \mathbf{n})^2 + D_e + \frac{1}{q^2 t_{ex}} \mp \left[\left[D_e - D_{i,\parallel}(\mathbf{g} \cdot \mathbf{n})^2 + \frac{2f - 1}{q^2 t_{ex}} \right]^2 + \frac{4f(1-f)}{q^4 t_{ex}^2} \right]^{\frac{1}{2}} \right\}$
"apparent" fraction	$f' = \frac{1}{D_i' - D_e'} \left[f D_{i,\parallel}(\mathbf{g} \cdot \mathbf{n})^2 + (1-f)D_e - D_e' \right]$
Powder average (over directions):	$\bar{S}(\mathbf{p}, q, t) = S\Big|_{q=0} \cdot \int_0^1 \mathcal{K}(q, t, \mathbf{g} \cdot \mathbf{n}; \mathbf{p}) d(\mathbf{g} \cdot \mathbf{n})$

$$b = q^2 t = (\gamma G \delta)^2 t$$

→ Objective: retrieve $\mathbf{p}$ from $\bar{S}(\mathbf{p}, b, t_d)$

multiple acquisition parameter combinations

Source :   Kärger 1985. Advances in Colloid and Interface Science
             Jelescu et al. 2022. NeuroImage

Our MRI Protocol on the clinical 3T Prisma Scanner

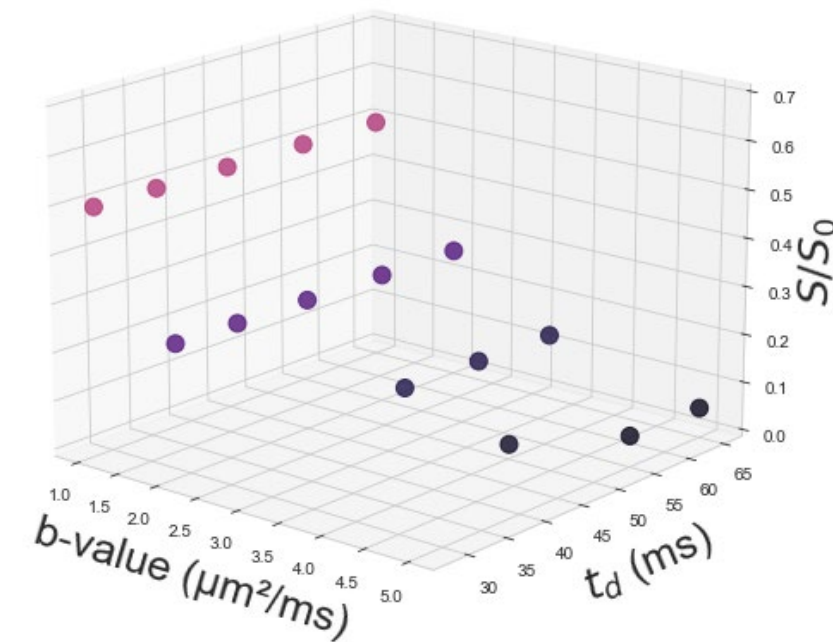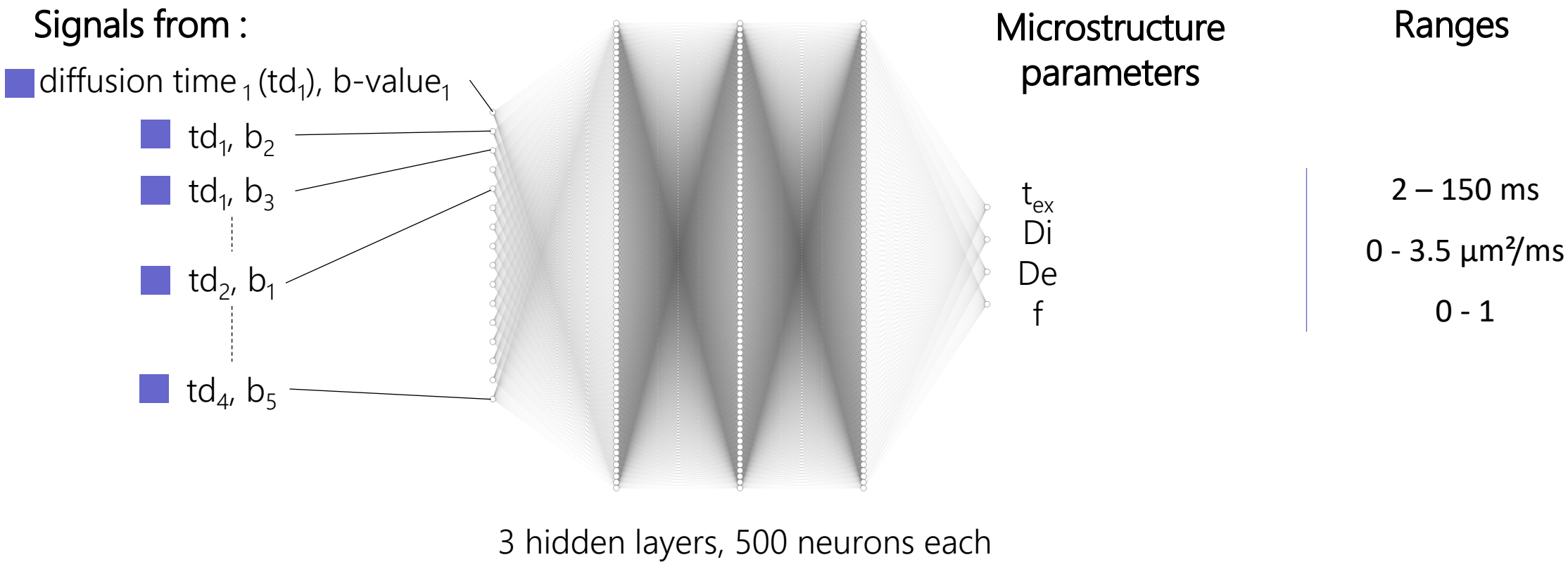**Additional information on the protocol**

Scan time: 35min

Image resolution : 2x2x2 mm^3

Gradient duration : 16.5ms

20 directions per shell

Echo time: 100ms

Gradient limitations (80mT/m)

Powder-averaged signal S depends on b and t_d

Retrieving parameters using a Multi-Layer Perceptron (MLP)

Signals from :

■ diffusion time $_1$ (td$_1$), b-value$_1$

■ td$_1$, b$_2$

■ td$_1$, b$_3$

■ td$_2$, b$_1$

■ td$_4$, b$_5$

Microstructure parameters

t_{ex}
Di
De
f

Ranges

2 – 150 ms

0 - 3.5 µm²/ms

0 - 1

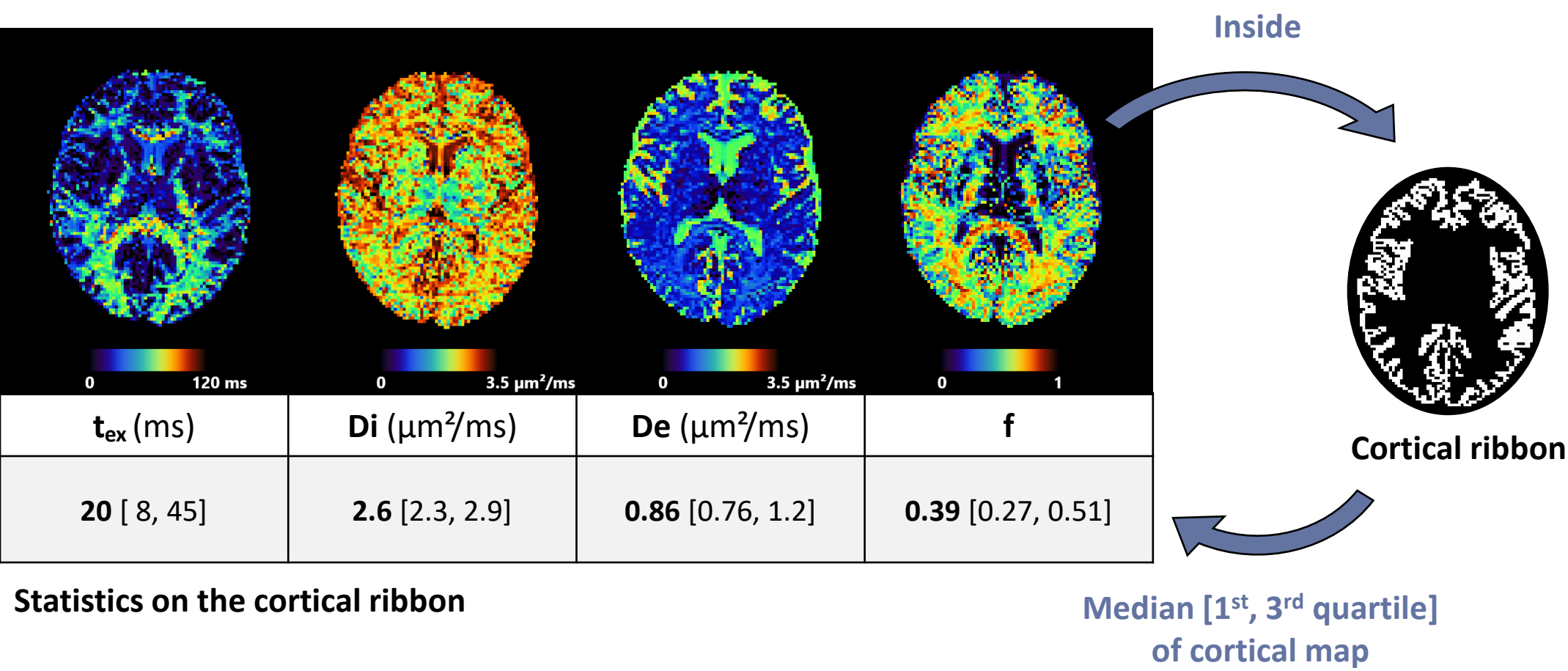3 hidden layers, 500 neurons each

Retrieving parameters using a Multi-Layer Perceptron (MLP)

Training set : 2 000 000 examples
Test set :   10 000 examples
SNR : 80-120
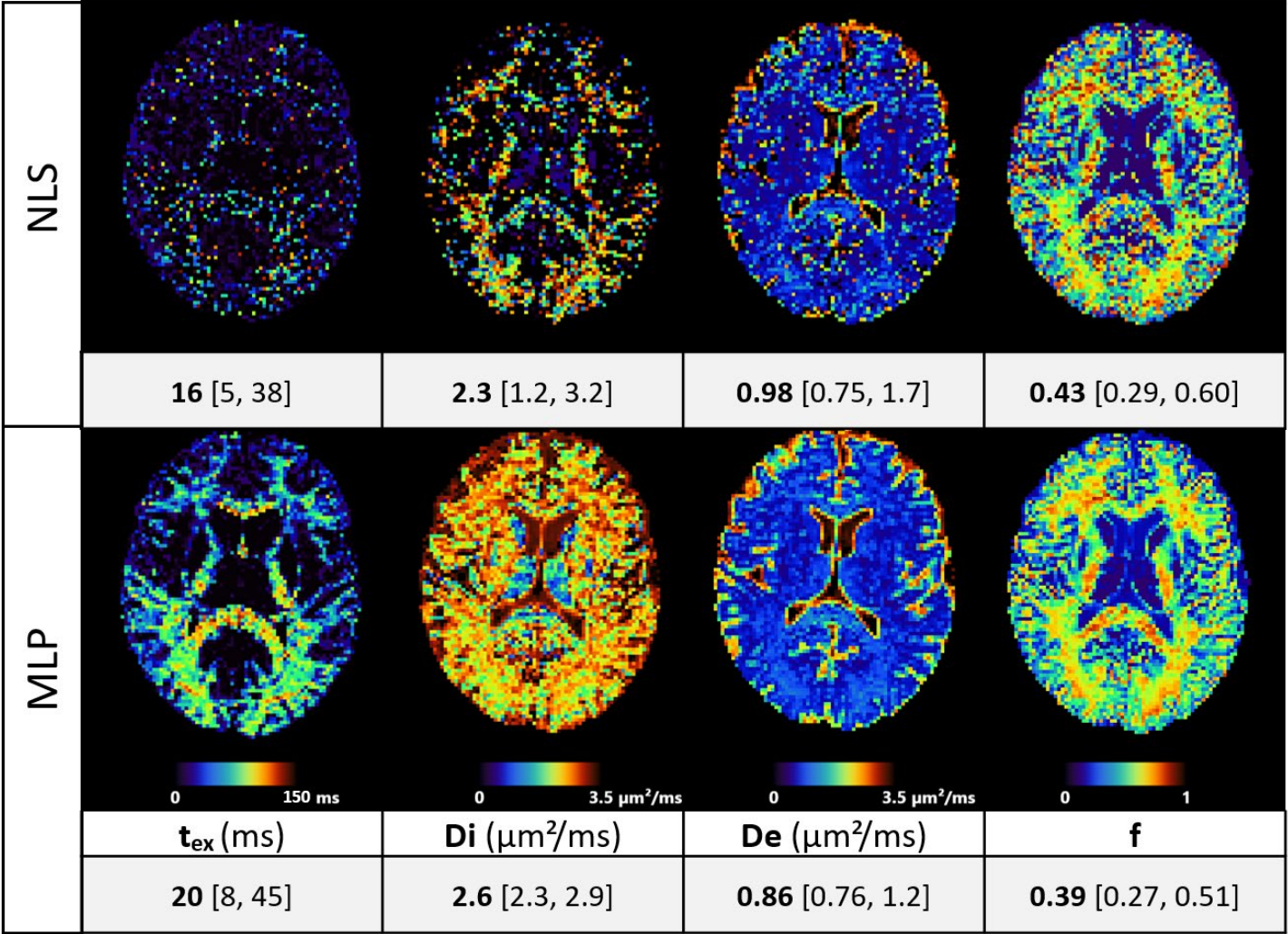
	t_{ex} (ms)	Di (µm²/ms)	De (µm²/ms)	f
Clinical Protocol Mean Absolute Error (MAE)	27.457	0.423	0.351	0.083

MLP estimates on an axial slice of the human brain

Inside

t_{ex} (ms)	Di (µm²/ms)	De (µm²/ms)	f
20 [8, 45]	2.6 [2.3, 2.9]	0.86 [0.76, 1.2]	0.39 [0.27, 0.51]

Statistics on the cortical ribbon
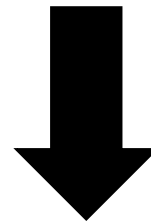
Cortical ribbon

**Median [1st, 3rd quartile]
of cortical map**

Comparison with the Non-linear Least Squares estimates

How to improve this protocol to get lower errors ?

Explainable AI

Shapley value of input i   ~   its contribution to the output

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Mapping Lab

# Explainable AI using Shapley values
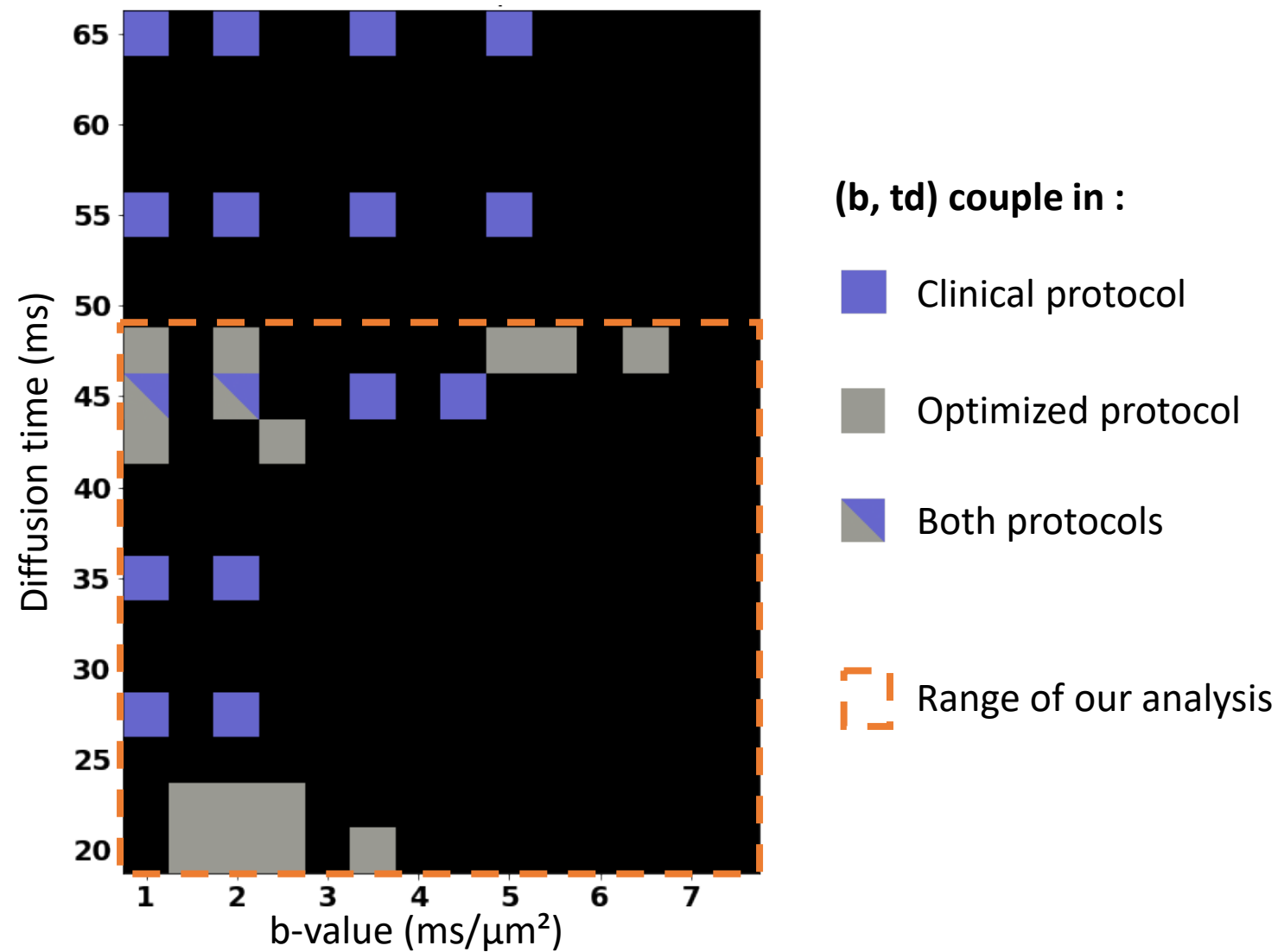
Shapley value of player i ~ his/her contribution to the game:

$$\varphi_i = \frac{1}{\#\ of\ players} \sum_{coalitions\ excluding\ i} \frac{marginal\ contribution\ of\ i\ to\ coalition}{\#\ of\ coalitions\ excluding\ i\ of\ this\ size}$$

the score of the team with the player
− the score of the team without the player

Looking for an optimized protocol

The two protocols

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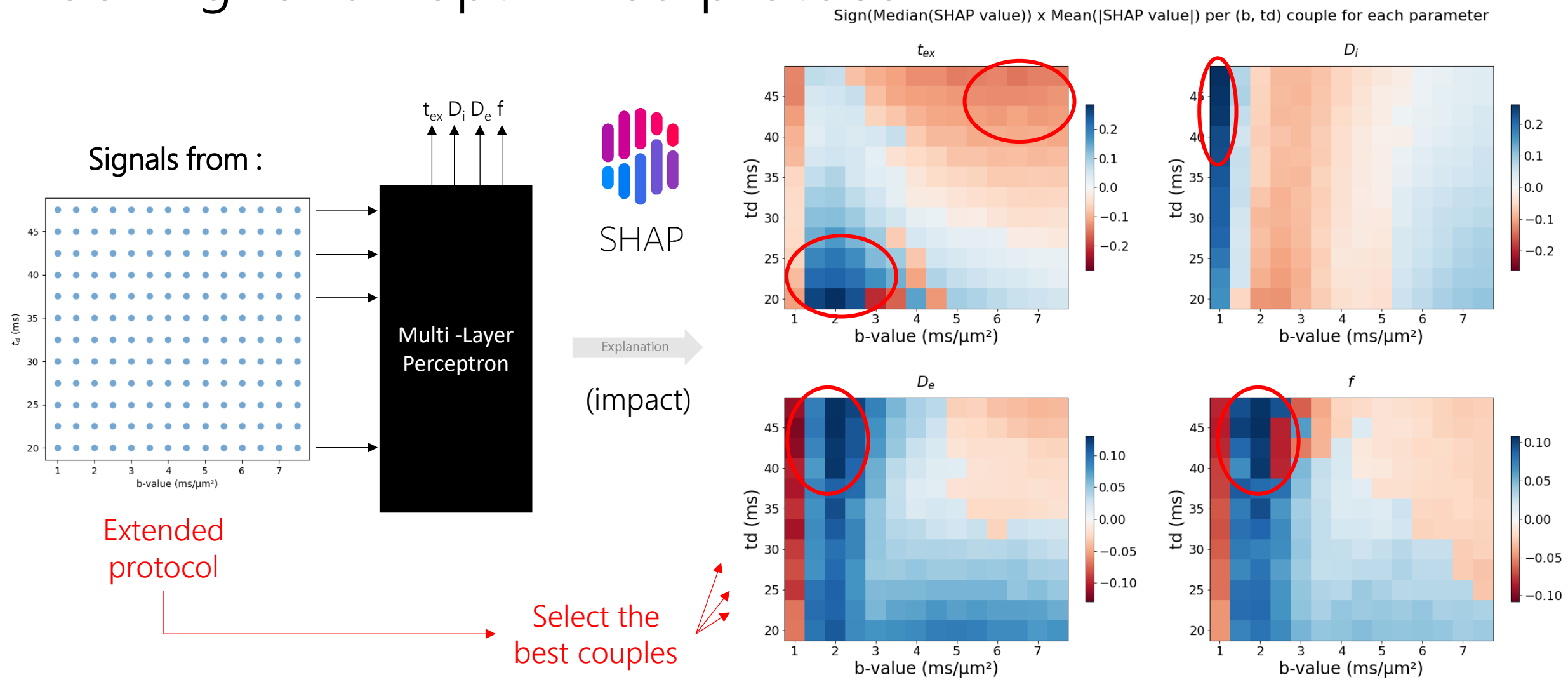
Is this new protocol really better ?

|	t_{ex} (ms)	Di (µm²/ms)	De (µm²/ms)	f
Clinical Protocol MAE	27.457	0.423	0.351	0.083
Optimized Protocol MAE	25.496	0.419	0.330	0.076
	-1.961	-0.004	-0.021	-0.007

⚠ Still dependent on the training & test sets

Is this new protocol really better ?

To compare protocols, we set side by side their associated **Cramer-Rao Lower Bound (CRLB)** on some sets of microstructure parameters.

⚠️ Depends on the parameters **p** (4D)

Around [24, 2.5, 0.89, 0.4]

t_{ex} D_i D_e f

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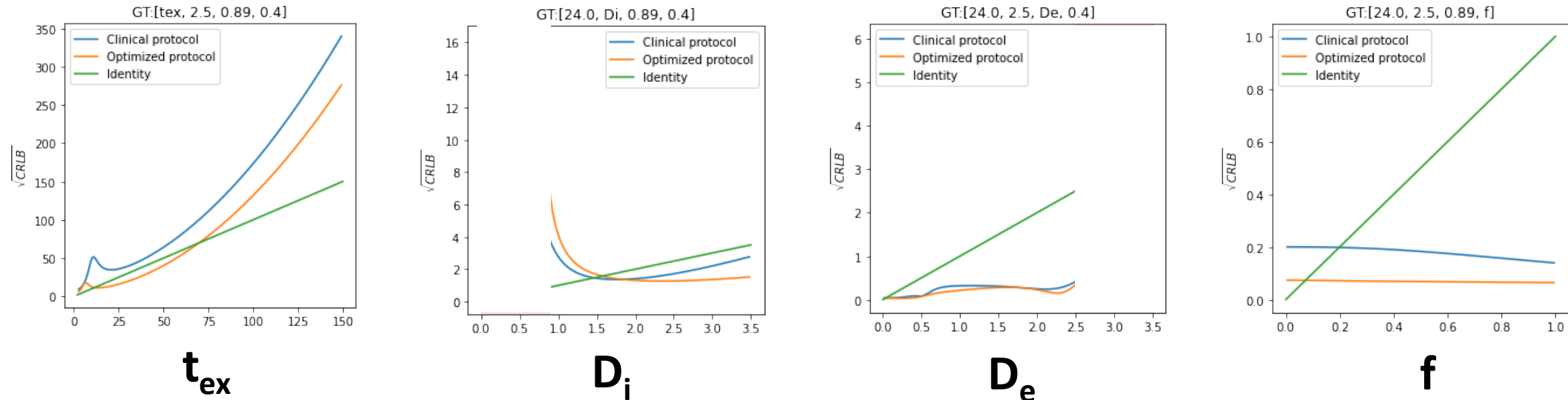
Summary & Perspectives

➢ We succeeded in estimating NEXI parameters on the human brain on a clinical scanner.

➢ A naïve protocol seems to already hold reasonable results.

➢ Next, we will identify a new protocol with this method within a range adapted to the Prisma gradient limitations, implement it experimentally and compare the maps.

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