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

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ISMRM Diffusion Workshop 2022 – October 12, 2022

UNIL | Université de Lausanne
Faculty of Biology and Medicine

Declaration of Financial Interests or Relationships

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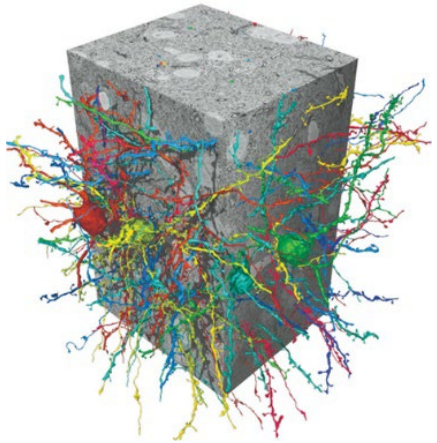
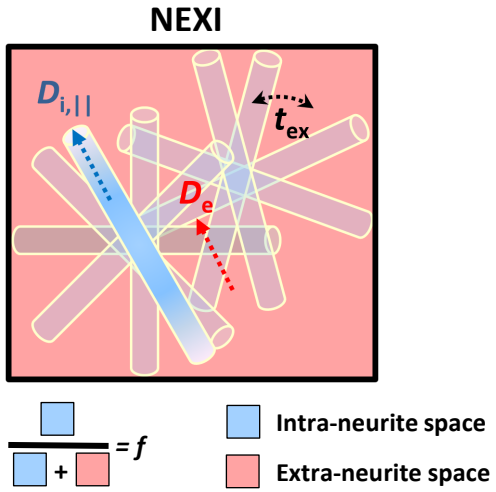
I have no financial interests or relationships to disclose with regard to the subject matter of this presentation.

The Neurite Exchange Imaging model



Grey matter microstructure
(under the electron microscope)



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

- 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):	$\bar{S}(\mathbf{p}, q, t) = S\big\|_{q=0} \cdot \int_0^1 \mathcal{K}(q,t,\mathbf{g}\cdot\mathbf{n};\mathbf{p}) d(\mathbf{g}\cdot\mathbf{n})$

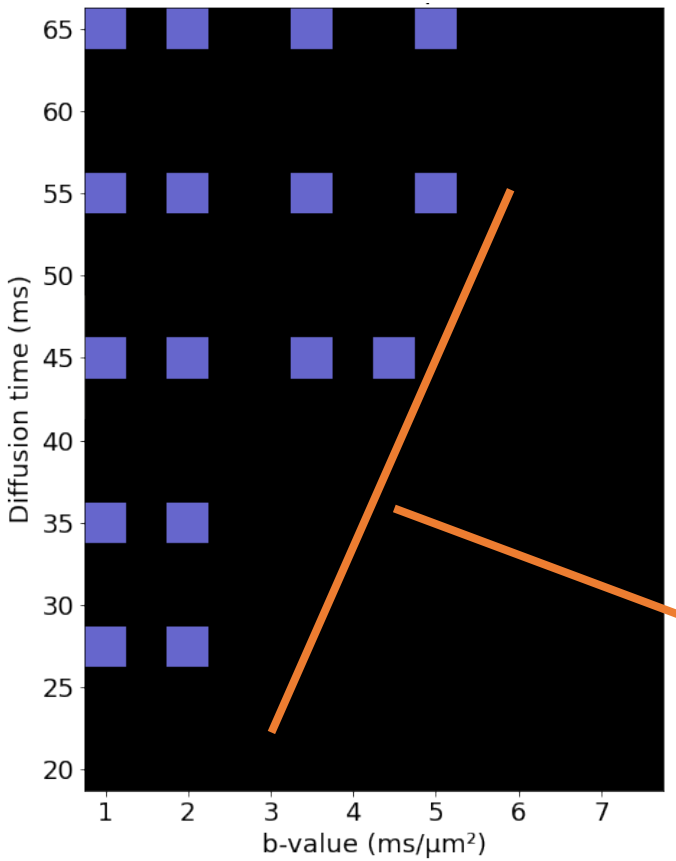
$$b = q^2 t = (\gamma G \delta)^2 t$$

→ 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

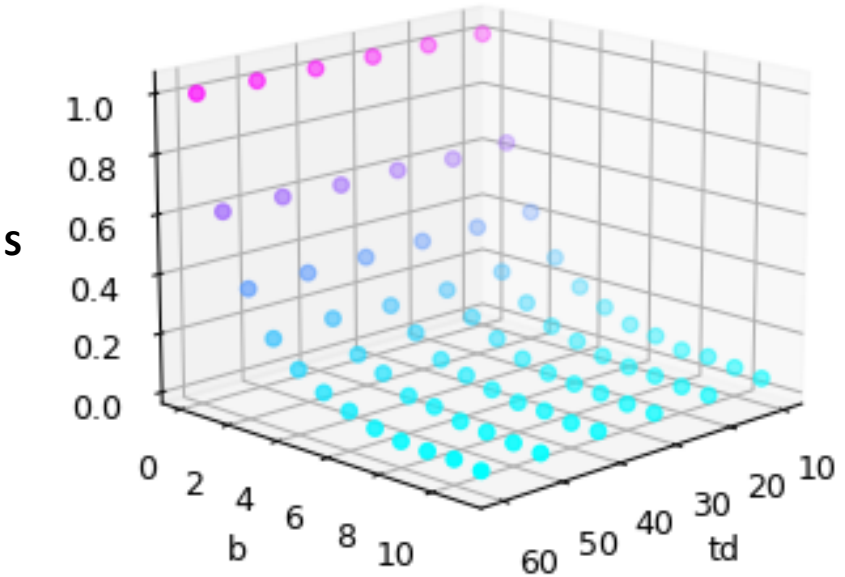
Our MRI Protocol on the clinical 3T Prisma Scanner



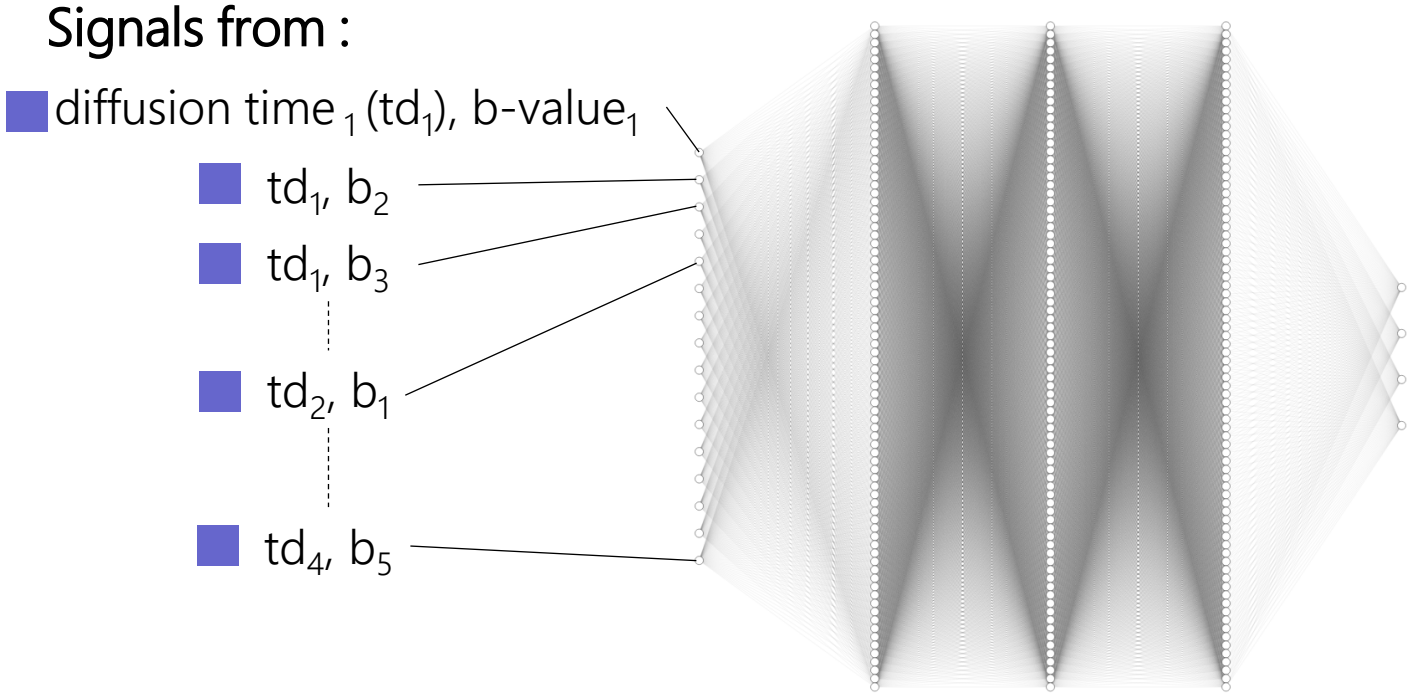
Gradient limitations (80mT/m)

Additional information on the protocol
Scan time: 35min
Image resolution : 2x2x2 mm^3
Gradient duration : 16.5ms
20 directions per shell
Echo time: 100ms

Powder-averaged signal S depends on b and td



Retrieving parameters using a Multi-Layer Perceptron (MLP)



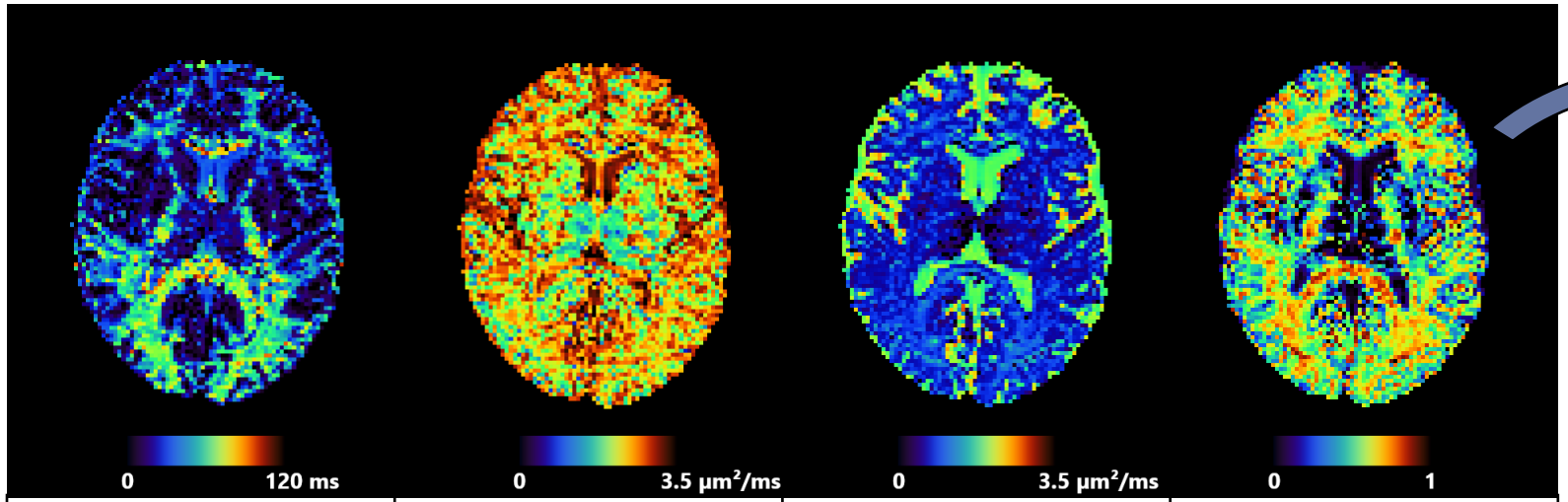
3 hidden layers, 500 neurons each

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



t_{ex} (ms)	Di (μm²/ms)	De (μm²/ms)	f
24 [12, 46]	**2.5** [2.1, 2.8]	**0.89** [0.70, 1.4]	**0.40** [0.26, 0.53]

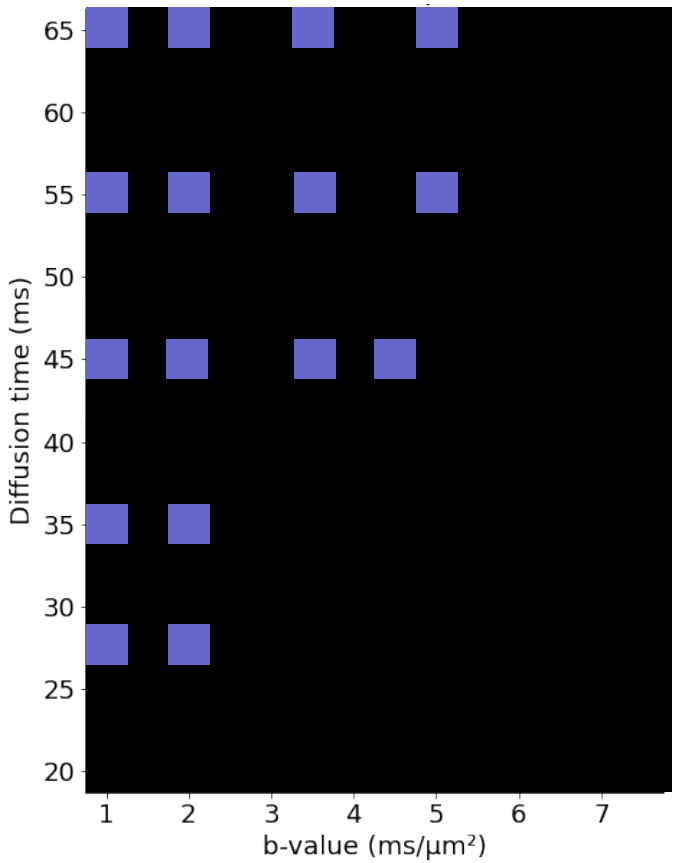
Statistics on the cortical ribbon

Inside

Cortical ribbon

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

Could we improve our protocol ?



	t_{ex} (ms)	Di (μm²/ms)	De (μm²/ms)	f
Clinical Protocol MAE	27.457	0.423	0.351	0.083

↓

	t_{ex} (ms)	Di (μm²/ms)	De (μm²/ms)	f
New Protocol MAE	?	?	?	?

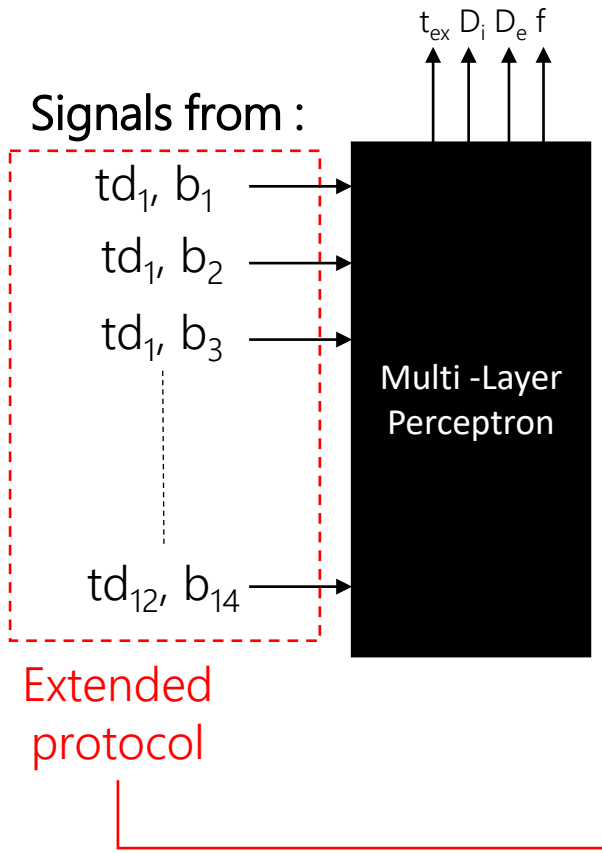
Explainable AI using Shapley values

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

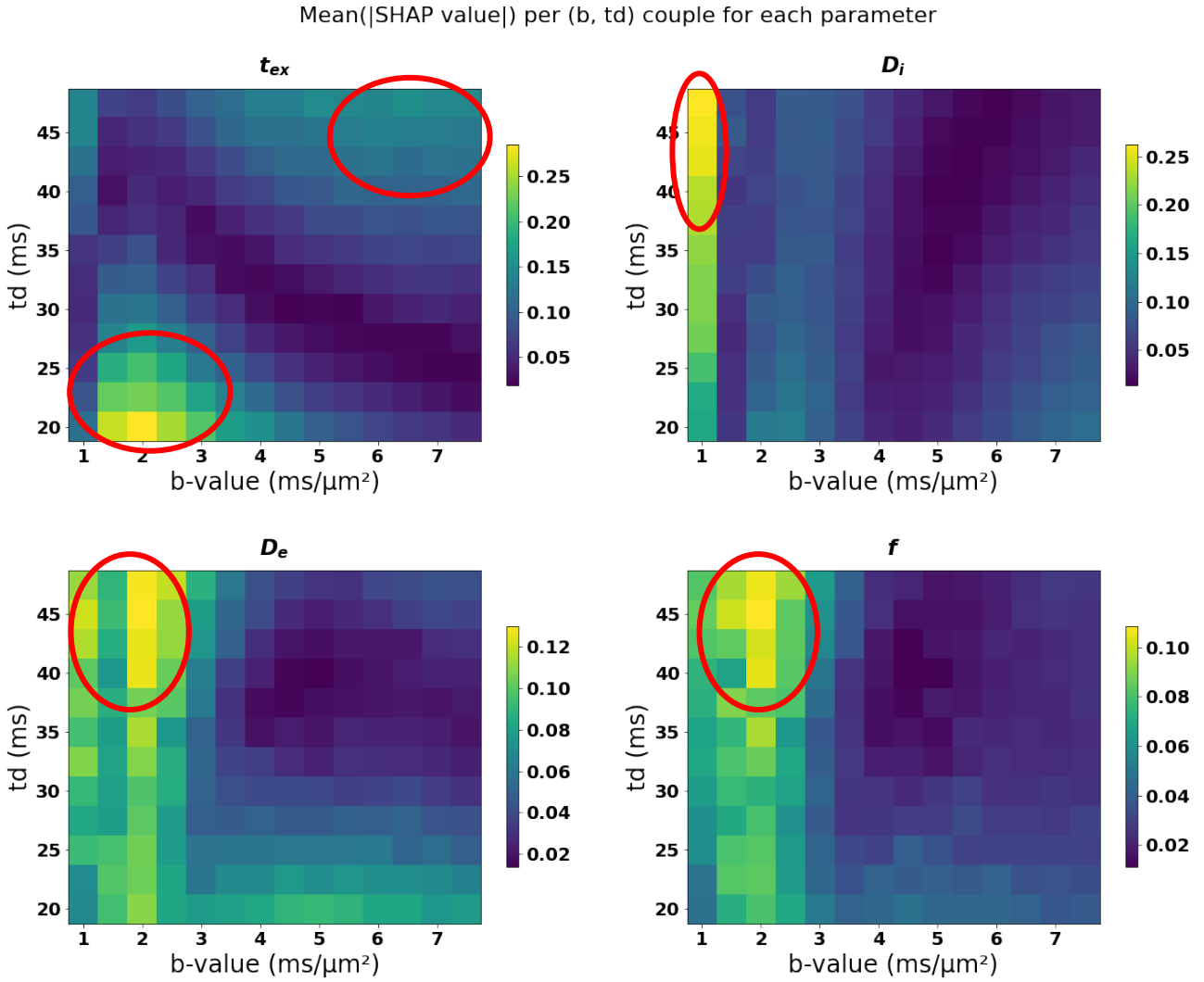
Looking for an optimized protocol



Explanation

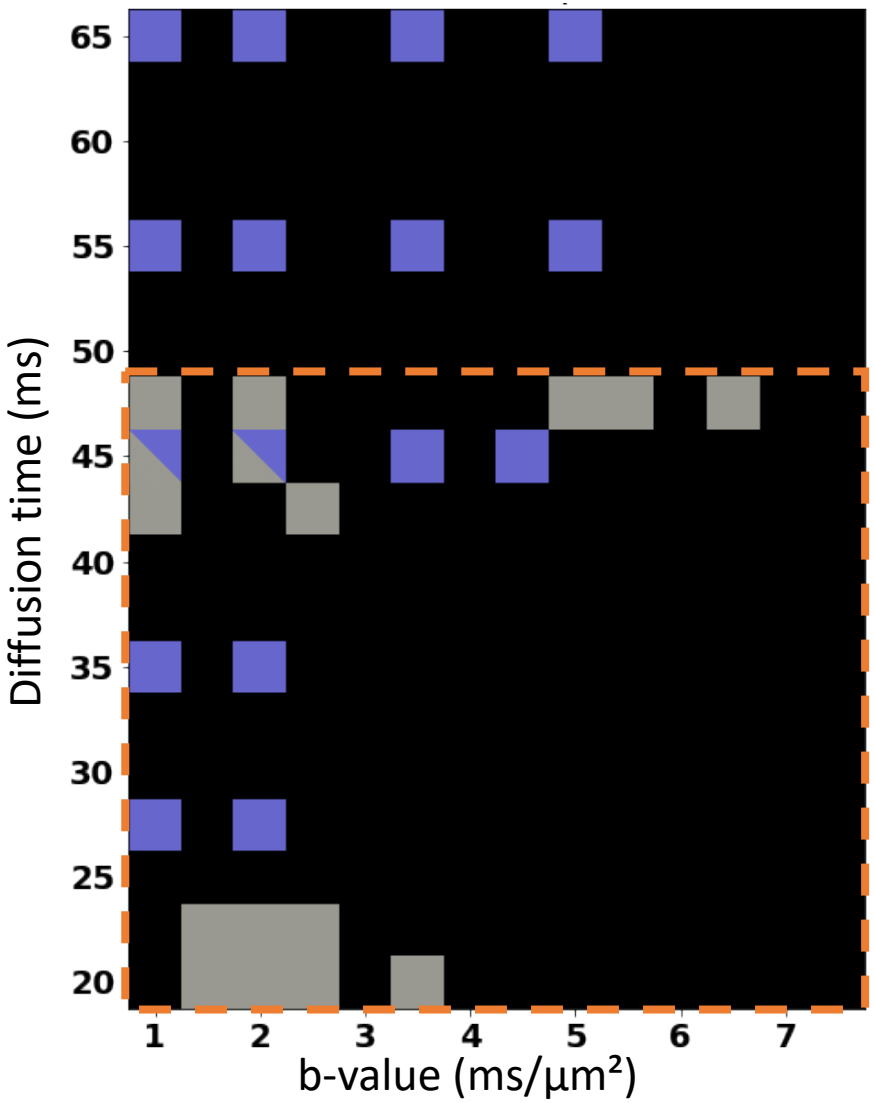
(absolute impact)

Select the best couples



Source : SHAP, Scott Lundberg

The two protocols



(b, td) couple in :

- Clinical protocol
- Optimized protocol
- Both protocols
- Range of our analysis

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

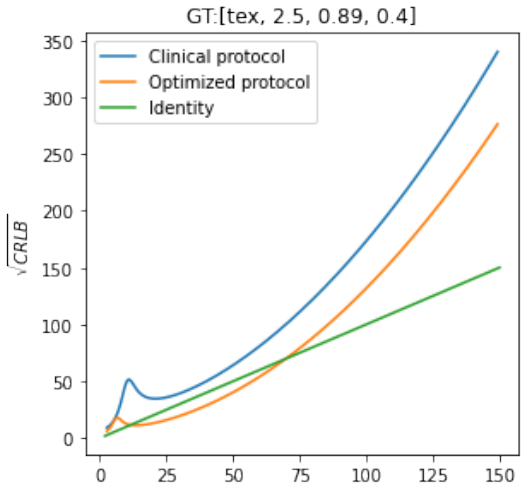
⚠ Still dependent on the training & test sets

Is this new protocol really better ?

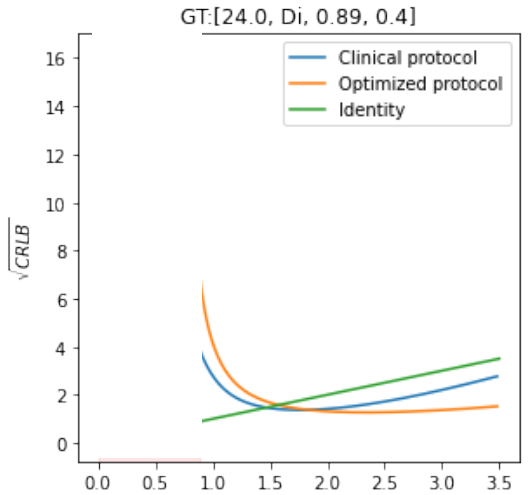
To compare protocols, we set side by side their associated **Cramer-Rao Lower Bound (CRLB)** on some sets of microstructure parameters.

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

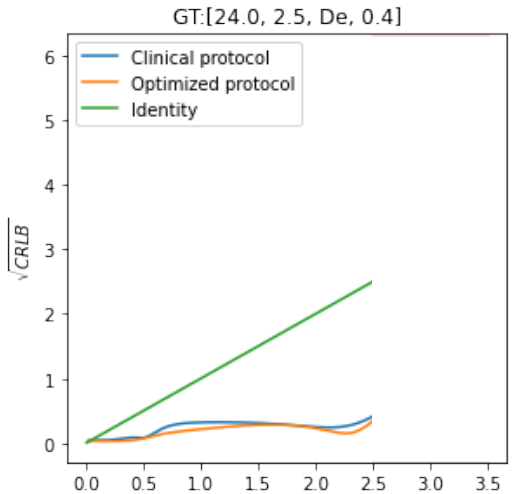
Around [24, 2.5, 0.89, 0.4]



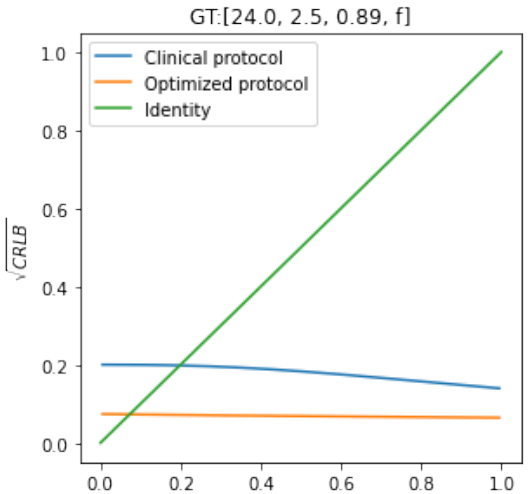
t_{ex}



D_i



D_e



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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.

Acknowledgments

The Mic-Map team & collaborators

Microstructure Mapping Lab

Thorsten Feiweier

SIEMENS Healthineers

Funding

Swiss National Science Foundation

PCEFP2_194260
PZ00P2_185814

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