

GPU BASED MODELING PIPELINE TO EXTRACT BRAIN CELL MORPHOLOGY FROM IN VIVO DIFFUSION-WEIGHTED MR SPECTROSCOPY DATA

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# OUTLINE

 $\succ$  Introduction and Rationale;

Application 1: Brain cell's morphology extraction;

Application 2: finer cell's morphology characterization

Future Perspectives: applications to pathology



### MOLECULAR DIFFUSION MEASURED BY DIFFUSION-WEIGHTED MR

Possibility to investigate the apparent diffusion of endogenous molecules



<u>Non invasive</u>



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## INTRODUCTION

### MOLECULAR DIFFUSION MEASURED BY DIFFUSION-WEIGHTED MR

Possibility to investigate the apparent diffusion of endogenous molecules

### Diffusion-weighted MRI: water

Ischemic stroke Fiber tracking





High sensitivity

<u>**But</u>**: Diffusion of water = <u>**no specific**</u> (extra + intracellular space, crosses membranes)</u>



Brain intracellular metabolites are primarily localized and diffuse in cell fibers rather than in cell bodies<sup>1-4</sup>

(1) Marchadour C et al. Journal of Cerebral Blood Flow & Metabolism (2012) **32 (12)**: 2153-2160;

(2) Najac C et al. Neuroimage (2014) 90: 374-380;

(3) Najac C et al. Brain Structure and Function (2014) **221 (3)**: 1245-1254

(4) Ligneul C et al. Magnetic Resonance in Medicine (2016): DOI: 10.1002/mrm.26217



→ Interpretation and modeling of metabolite diffusion primarily based on cell geometry



Diffusion Weighted NMR



$$\rightarrow \mathbf{b} = \mathbf{q}^2 \mathbf{t}_{\mathbf{d}} \approx \mathbf{g}^2 \mathbf{t}_{\mathbf{d}}$$



**Diffusion Weighted NMR** 



 $\rightarrow$  b = q<sup>2</sup> t<sub>d</sub>  $\approx$  g<sup>2</sup> t<sub>d</sub>

 $\rightarrow$  S(b)  $\approx$  exp[-b ADC(t<sub>d</sub>)]; ADC=<r(t<sub>d</sub>)<sup>2</sup>>/d t<sub>d</sub>

$$d\phi_{j}(t) = \gamma g(t) \cdot x_{j}(t) \Delta t$$

$$\phi_{j} = \sum_{t=0}^{t_{seq}} d\phi_{j}(t)$$

$$ADC = -\frac{\ln(S/S_{0})}{b}$$

$$S = \left| \frac{1}{N} \sum_{j=1}^{N} e^{i\phi_{j}} \right|$$

$$b = \gamma^{2} \int^{eq} dt \left[ \int \tilde{g}(t') dt' \right]^{2}$$

### LONG DIFFUSION TIME EXPERIMENTS AND MODELING

METHODS







METHODS SIMULATION-FITTING PIPELINE





N particles =  $10^3$ ; N time step =  $10^4$ ; System replication = 50; Fitting iteration = 200 x 3; <u>Total iterations = ~  $10^{11}$ </u>

	1	2	3	4
Fitting free diffusion data	~ 17.5 minute	~ 5 minute	~ 3 minute	~ 0.1 minute
Fitting restricted diffusion data	~ 40 minute	~ 12 minute	~ 6 minute	~ 0.8 minute

FITTING STABILITY TO EXPERIMENTAL NOISE



RESULTS





**250 Monte-Carlo trials** Gaussian noise (15% relative SD) added to

a reference simulated ADC(t<sub>d</sub>) curve

Simulation-Fitting pipeline

250 sets of fitted morphological parameters

\$ Palombo M. et al. Proceedings of the 23rd ISMRM Annual Meeting 2015; Abstract # 2982

FITTING STABILITY TO EXPERIMENTAL NOISE

RESULTS



→ Fitting pipeline very stable (Bias and CV < 5%) with respect to experimental noise

Palombo M. et al. PNAS (2016); 113(24), 6671-6676

### LONG DIFFUSION TIME EXPERIMENTS AND MODELING

**RESULTS** 



### RESULTS

### RECONSTRUCTED ASTROCYTES AND COMPARISON WITH HISTOLOGY



Palombo M. et al. PNAS (2016); **113**(24), 6671-6676





A) Zoom and binarization of bitmap images

→ Reasonable values for cell morphology parameters in both mouse and macaque brain

→ Good match between Sholl based metrics measured by real and virtual histology



### Basic cell-graph model





- 1) Presence of very long processes/axons;
- 2) Presence of leaflets/spines;
- 3) Presence of vericosities.



### Basic cell-graph model





### Basic cell-graph model



▶ It affects the estimation of D<sub>free</sub> only, inducing overestimation of it.



### Basic cell-graph model





- 1) Presence of very long processes/axons;
- 2) Presence of leaflets/spines;
- 3) Presence of varicosities.

#### Basic cell-graph model





Real Simulated





1) Presence of very long processes/axons;

2) Presence of leaflets/spines;

3) Presence of varicosities.

n=12

n=40



# High b-value DW-MRS signal simulations from realistic dendritic geometries



# High b-value DW-MRS signal simulations from realistic dendritic geometries



# High b-value DW-MRS signal simulations from realistic dendritic geometries





Spines/leaflets density

$$\frac{D_{\text{intra}}^{eff}}{D_0} = (2.4\phi^{0.35})^{-1.3} + [1 - (2.4\phi^{0.35})^{-1.3}]e^{-\phi}$$

$$r^{eff} = r_0 + 1.7(1 - e^{-0.6\phi})$$

#### Spines/leaflets length

$$\frac{D_{\text{intra}}^{\text{eff}}}{D_0} = [1.1(0.85l)^{0.065}]^{-1.4} + \left[1 - [1.1(0.85l)^{0.065}]^{-1.4}\right] e^{-0.85l}$$

$$r^{eff} = r_0 + 1.2(1 - e^{-0.25l})$$

Varicosities size

$$\frac{D_{\text{int}ra}^{eff}}{D_0} = e^{-\frac{A}{1-A}}$$

 $r^{eff} = r_0 e^{0.86\frac{A}{1-A}}$ 

| PAGE 26 Palombo M. et al. *Submitted (2016)* 





Metabolite	D <sub>intra</sub> <sup>cyl</sup> (μm²/ms)	a (µm)
NAA	0.339	0.62
Glutamate	0.440	0.90
Creatine	0.375	1.59
Taurine	0.436	1.30
Choline	0.308	1.33
Myo-Inositol	0.325	1.67

### **Neurons (D**<sub>0</sub> from ultra short t<sub>d</sub>)

NAA:  $\Phi = 0.19$  spine/ $\mu$ m;  $R_0 = 0.45 \mu$ m;  $I = 0.95 \mu$ m ( $D_0 = 0.454 \mu$ m<sup>2</sup>/ms) Glu:  $\Phi = 0.23$  spine/ $\mu$ m;  $R_0 = 0.52 \mu$ m;  $I = 1.05 \mu$ m ( $D_0 = 0.476 \mu$ m<sup>2</sup>/ms)

From histology:  $\Phi < 0.50$  spine/ $\mu$ m; R<sub>0</sub> ~ 0.50  $\mu$ m; I ~ 1.00  $\mu$ m

**Astrocytes (D**<sub>0</sub> from ultra short t<sub>d</sub>)

tCho:  $\Phi = 0.70$  leaflets/µm;  $R_0 = 0.75$  µm; I = 2.65 µm ( $D_0 = 0.370$  µm²/ms) Ins:  $\Phi = 0.73$  leaflets/µm;  $R_0 = 1.07$  µm; I = 2.79 µm ( $D_0 = 0.393$  µm²/ms)

From histology:  $\Phi \sim 1.00$  leaflets/µm; R<sub>0</sub> ~ 1.00 µm; I > 2.50 µm

### Merging structural information from high b-values / long t<sub>d</sub>



12 µm

Astrocyte and leaflets









14 µm

### Virtual Astrocyte



### **Real Astrocyte**

In CEA/MIRCen, Paris (France)

07

*Injury and inflammation* → *Astrocytes reactivity* 



Astrocyte

'Reactive' Astrocyte

### In UCL, London (UK)

#### Simulate the whole brain $\rightarrow$ Cells growth and context aware interactions



Vanherpe L., et al. PRE (2016); 94, 023315





Torben-Nielsen B., et al. Front. NeuroAnatomy (2014); **8**, 92







# THANK YOU ALL FOR YOUR KIND ATTENTION!!!



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## RESULTS EFFECTS OF MORPHOMETRIC PARAMETERS ON ADC TIME DEPENDENCE



Similar impact was found for  $N_{\mbox{\scriptsize branch}}$  and  $\mbox{\scriptsize SD}_{\mbox{\scriptsize Nbranch}}$ 

### RESULTS EFFECTS OF MORPHOMETRIC PARAMETERS ON ADC TIME DEPENDENCE



 $(N_{branch} \times L_{segment})$ , but specifically depends on  $L_{segment}$  and  $N_{branch}$ .



Strong g (short t<sub>d</sub>)

**×** Segments length

imes Number of consecutive bifurcation

→ Segments Diameter

### HIGH G EXPERIMENTS AND MODELING

#### RESULTS



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## HIGH G EXPERIMENTS AND MODELING

#### RESULTS



→ Randomly oriented cylinders model <u>well describes metabolites' diffusion at high b</u> <u>values</u>

→ Randomly oriented cylinders model allows <u>estimation of reasonable values</u> for <u>cell</u> <u>processes diameter</u>

Metabolite	D <sub>intra</sub> <sup>cyl</sup> (μm²/ms)	a (µm)
NAA	0.339	0.00
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Myo-Inositol	0.325	1.67



# HIGH G EXPERIMENTS AND MODELING RESULTS



→ Modified randomly oriented cylinders model <u>well describes NAA diffusion at high b</u> <u>values</u>, allowing <u>estimation of reasonable values</u> for <u>cell processes diameter and small</u> <u>compartments size</u>.

