



HAL
open science

Atlases and generic priors for multi-compartment mapping with diffusion MRI

Marie Poirier, Aymeric Stamm, Emmanuel Caruyer

► **To cite this version:**

Marie Poirier, Aymeric Stamm, Emmanuel Caruyer. Atlases and generic priors for multi-compartment mapping with diffusion MRI. ESMRMB 2024 - 40th Annual Meeting scientific European Society for Magnetic Resonance in Medicine and Biology, ESMRMB, Oct 2024, Barcelona, Spain. hal-04843311

HAL Id: hal-04843311

<https://hal.science/hal-04843311v1>

Submitted on 15 Jan 2025

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License

Atlases and generic priors for multi-compartment mapping with diffusion MRI

The specificity of microstructure models in diffusion MRI is limited by the quality of clinical protocols. We propose a generic statistical framework to build priors for multicompartment models, to inform estimations made from clinical acquisitions; we illustrate on a standard model of diffusion.

Introduction: In diffusion MRI, our ability to estimate the microstructure parameters of brain tissue models depends on the acquisition protocol. With standard clinical acquisitions, only simple models can be estimated [2].

We hereby propose an integrated method for deriving priors for multi-compartment model (MCM) estimation from high-quality databases, such as the Human Connectome Project (HCP). We present firstly the model we chose to compute priors, then the different statistical distributions adapted for each parameter, and finally the atlas we obtained.

Methods:

MC model

We focus on an MCM in which the anisotropic compartments are modeled according to diffusion tensors with fixed diffusivities, $d_{\text{parallel}} = 1.7 \times 10^{-3} \text{ mm}^2/\text{s}$ and $d_{\text{perp}} = 1.7 \times 10^{-4} \text{ mm}^2/\text{s}$, ensuring the anisotropic compartments cannot be made isotropic during estimation. For the isotropic compartments, we opted to include a compartment for modeling free water diffusion (F) with $d_F = 3.0 \times 10^{-3} \text{ mm}^2/\text{s}$ and one for modeling isotropic restricted diffusion (IR) in glial cells as in [3]. The MR signal predicted by such a model reads:

$$S(i, b) = w_F e^{-bd_F} + w_R S_{IR}(b, \delta, \Delta; d_S, R_S) + \sum_{j=1}^M w_j e^{-bd_{\text{perp}}} e^{-b(d_{\text{parallel}} - d_{\text{perp}})(\mu_j^T g)^2}$$

where (i) w_j 's are the volume fractions, (ii) b and g are respectively the b-value and direction defining the diffusion gradient, δ and Δ are the pulses duration and separation (iii) S_{IR} is the MR signal predicted by the IR diffusion model proposed in [3] which has two parameters: the IR diffusivity (in mm^2/s) and the average cell radius (in μm) and (iv) μ_j is the direction of diffusion in the j-th anisotropic compartment.

Data

We chose such a model in regards of our data that comes from the HCP105 database [4], from the Human Connectome Project.

Model for the priors

We define priors for the parameters of this model that are common to many MCM. We used parametric distributions with appropriate support, each prior depending on the number of anisotropic compartments. The whole pipeline process is described in Figure 1. We calculated them for 0, 1, 2 and 3 anisotropic compartments. Doing this ensures that the users will ultimately be able to select the most appropriate number of compartments given the data.

For the two IR parameters d_s and R_s , we used a Gamma distribution, being the natural distribution for positive-valued data, estimated by a closed form estimator.

The prior for the volume fraction parameters, w_{FW} , w_{IRW} , w_A , where w_A is the sum of the volume fraction of each anisotropic compartment, was computed using a Dirichlet distribution, being the most common distribution on the simplex (each weight is non-negative and the weights sum to 1).

Last, the direction of diffusion μ_j of the j -th compartment follows a Watson distribution, a specific case of the Bingham distribution [8].

Results:

We present here the priors we were able to obtain, for clarity we only report the specific case of $M=1$ anisotropic compartment. We also optimized the number M of anisotropic compartments as described in [1]. We provide a map of the mean of the model selection for our 105 subjects in Figure 2.

Figure 3 exhibits the mean and variance for IR diffusivity d_s and cell radius R_s , calculated thanks to our Gamma prior.

Figure 4 shows the prior on the weight distribution parameter. The results are well related to the underlying anatomy, with a high volume fraction of free water, IR and anisotropic compartments in CSF, gray matter and white matter, respectively.

The whole pipeline shows conclusive results, therefore we are confident in the priors obtained, and we are currently working on validating the improvement they provide on our MCM estimations.

Discussion & Conclusions:

As a first step, we hereby provide atlases and priors for parameters characterizing free water, isotropic restricted diffusion and anisotropic diffusion. Our goal is to ultimately render it available and usable in a clinical context, with the most generic priors possible, usable for many different compartment models. It could also be used in a framework with deep-learning, as suggested in [7]. We expect those atlases to improve the MCM estimation, as suggested by [6].

Our work fits in with the priors developed by [9]. We wish to extend this approach by focusing on the brain microstructure, giving our results clear biological relevance. We also plan to compare our statistical-based approach to deep learning approaches such as [10]; we hypothesize that building priors with parametric distribution may help in the interpretation of results.

As for the next steps we are currently investigating, we will be using the HCP105 tracts, all reviewed by clinicians. We think we should be able to use them to improve the atlas for our anisotropic compartments priors. [5] We also are looking into the HCP MGH database, with lengthier acquisition, that may allow us to develop priors on more complex models, such as CHARMED, with a focus on the axon density.

References:

- [1]: Fast identification of optimal fascicle configurations from standard clinical diffusion MRI using Akaike information criterion, Stamm *et al*, ISBI, 2014
- [2]: Compartment models of the diffusion MR signal in brain white matter: a taxonomy and comparison, Panagiotaki *et al*, Neuroimage, 2012
- [3]: An analytical model of restricted diffusion in bovine optic nerve, Stanisiz *et al*, MRM, 1997
- [4]: Advances in diffusion MRI acquisition and processing in the Human Connectome Project, Sotiropoulos *et al*, Neuroimage, 2013
- [5]: TractSeg - Fast and accurate white matter tract segmentation, Waaserthal *et al*, NeuroImage, 2018
- [6] : Taquet M, Scherrer B, Boumal N, Peters JM, Macq B, Warfield SK. Improved fidelity of brain microstructure mapping from single-shell diffusion MRI. Medical image analysis. 2015 Dec 1;26(1):268-86.
- [7]: Karimi, D. and Gholipour, A., 2022, September. Atlas-powered deep learning (adl)-application to diffusion weighted mri. In International Conference on Medical Image Computing and Computer-Assisted Intervention (pp. 123-132). Cham: Springer Nature Switzerland.
- [8]: Statistics of Directional Data, K. V. Mardia, Academic Press, 1972
- [9]: Taquet M, Scherrer B, Boumal N, Peters JM, Macq B, Warfield SK. Improved fidelity of brain microstructure mapping from single-shell diffusion MRI. Med Image Anal. 2015
- [10]: Davood Karimi, Ali Gholipour, Atlas-Powered Deep Learning (ADL) - Application to Diffusion Weighted MRI, MICCAI 2022

Figures:

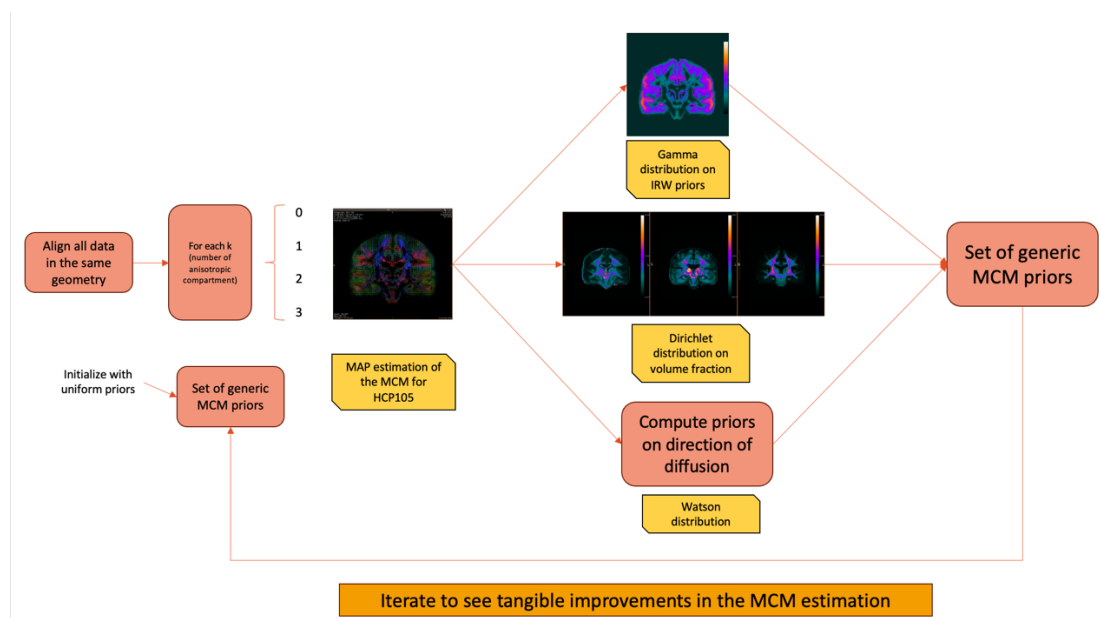


Figure 1 : Description of the process pipeline. The iteration process is a way to validate our process and the improvements we get from our priors. We could ultimately get the Aikake Information Criteria to have a measure of the improvement.

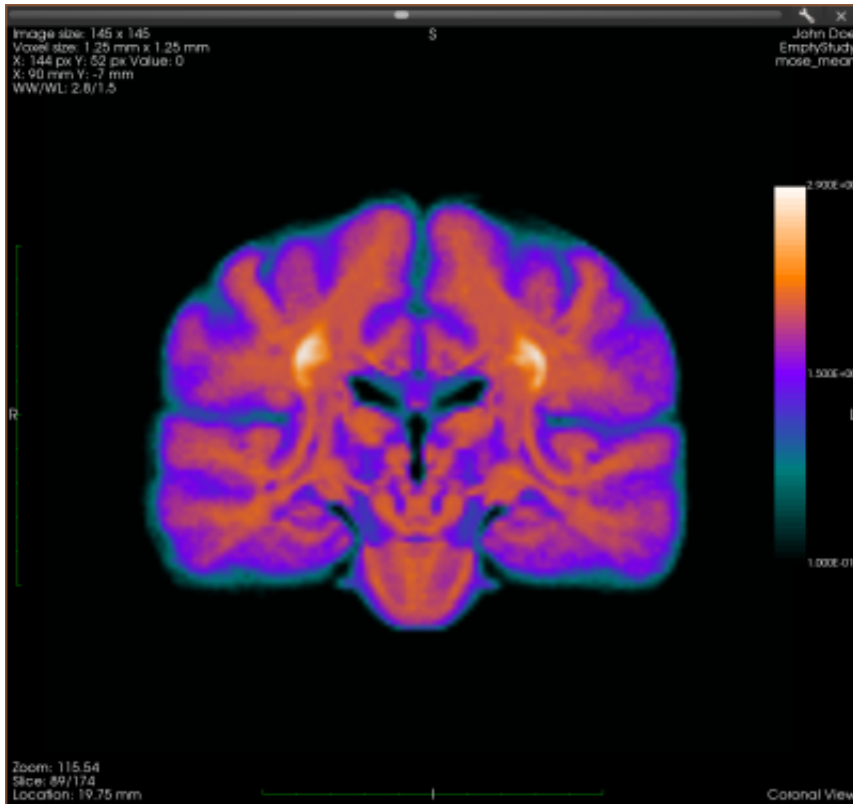


Figure 2 : Map of the mean optimized number of anisotropic compartments for the 105 subjects. Gray matter and CSF have an average close to zero, while white matter voxels show a number of anisotropic compartments from 1 to 3 in complex white matter regions.

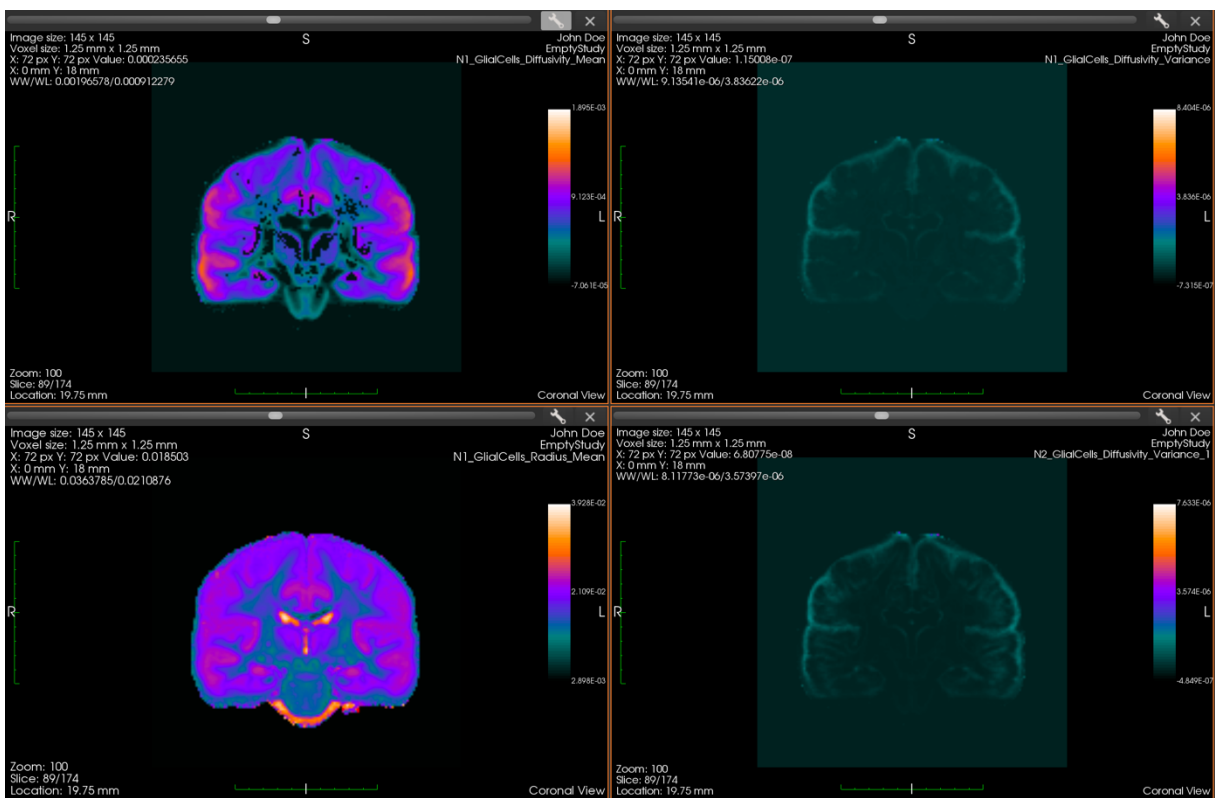


Figure 3 : Mean (left) and variance (right) of diffusivity (top, in mm^2/s) and radius (bottom, in mm) of the isotropic restricted compartment.

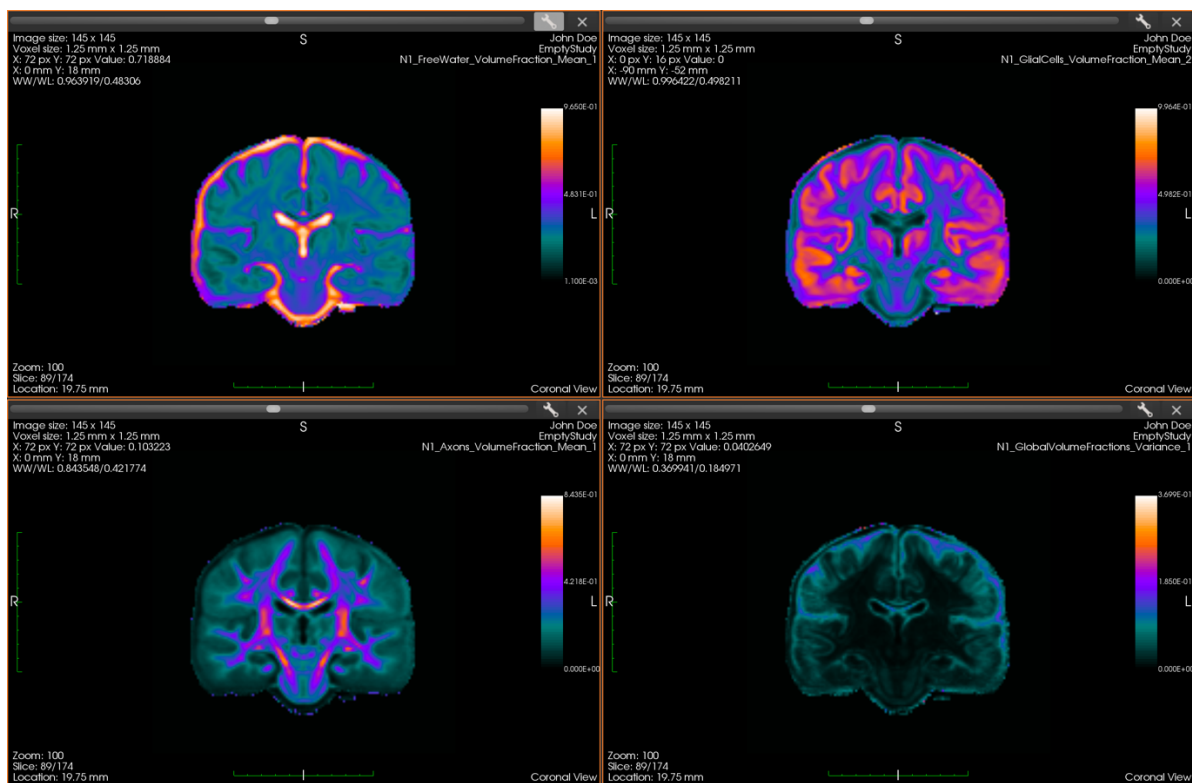


Figure 4 : Mean volume fraction of the free water (top left), IR water (top right) and axons compartment (bottom left). On the bottom right, we plotted the global variance of the volume fractions. As expected, the CSF shows high free water volume fraction on average. Similarly, the cortex and deep gray matter structures exhibit a large IR volume fraction. And the white matter shows a large axons volume fraction.