Tissue separation of multi-shell DW-MRI with a physiologically constrained multi compartment model and spherical deconvolution

Alberto De Luca[1,2], Marco Castellaro[1], Stefania Montemezzi[3], Massimiliano Calabrese[4], and Alessandra Bertoldo[1]
[1]*Department of Information Engineering, University of Padova, Padova, PD, Italy,* [2]*Department of Neuroimaging, Scientific Institute, IRCCS "Eugenio Medea", Bosisio Parini, LC, Italy,* [3]*Radiology Unit, Azienda Ospedaliera di Verona, Verona, Italy,* [4]*Neurology Section, Department Of Neurological and Movement Sciences, University Hospital of Verona, Verona, Italy*

TARGET AUDIENCE – Scientist and clinicians with interest in diffusion weighted imaging and application of advanced models to multiple sclerosis

PURPOSE – .

In the last years diffusion weighted imaging (DWI) sequences evolved first increasing the number of acquired directions, then introducing the concept of multi-shell acquisition. Sequences acquired with b-values above 1500s/mm^2 cannot be correctly quantified with the classic mono-exponential diffusion tensor model, as the signal deviates from its theoretical assumptions due to the contribution of restricted diffusion. Acquisitions with multiple gradient strengths allow the adoption of more complex modelling approaches such as the use of multi compartmental models. In this study we propose a diffusion model able to disentangle the contribution of white matter (WM) and gray matter (GM) and to quantify their diffusivity properties.

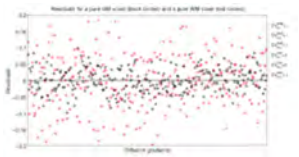

Figure 1 Residuals for a pure WM voxel (red dots) and a pure GM voxel (black dots).

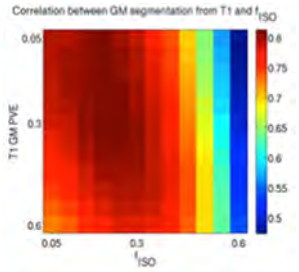

Figure 2 Correlation matrix between binarized GM PVE map from FSL FAST and the binarized f_{ISO} map with variable threshold.

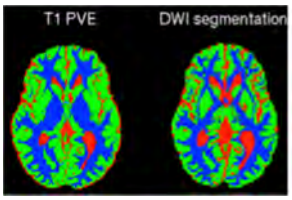

Figure 3 Comparison between the PVE map from FAST and the segmentation from our diffusion model. In green GM, in blue WM, in red CSF.

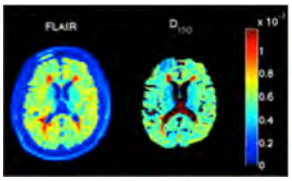

Figure 4 On the left a FLAIR scan of a MS patient, with some visible lesions. On the right the same slice on the D_{ISO} map.

METHODS AND RESULTS –

Recently the MSMT-SD[1] model has been introduced. It addresses the tissue segmentation problem by assuming: $S = S_0(f_{GM}X_{GM} + f_{WM}X_{WM} + f_{CSF}X_{CSF})$, where S is the DW signal, X are the tissue response functions of each voxel class (CSF is the cerebrospinal fluid) picked from representative voxels, and f are the coefficients of each class, estimated with linear least squares. We have modified this model expressing the diffusion signal as the sum of three compartments based on physiological assumptions: a compartment for free diffusing water, one for isotropic diffusing water and an anisotropic diffusion compartment. The latter is modeled as the sum of a single fiber response derived with constrained spherical deconvolution (SD) and an isotropic exponential term to mimic perpendicular diffusivity: $S = S_0 \cdot \left(f_{FREEWATER}e^{-\mathbf{q}\cdot 0.003} + (1 - f_{FREEWATER})\left(f_{ISO}e^{-\mathbf{q}D_{ISO}} + (1 - f_{ISO})(SD_{ANISOTROPIC} + e^{-\mathbf{q}D_{ISO}})\right)\right)$, where $\mathbf{q}$ is the product between the b-values and the corresponding diffusion vectors. Unlike the MSMT-SD model, only the WM response, i.e. $SD_{ANISOTROPIC}$, is picked from the data for deconvolution purposes while $f_{FREEWATER}, f_{ISO}, D_{ISO}$ are estimated. Our assumption is that the free water compartment explains most of the CSF signal, the isotropic compartment can be thought as the GM while the anisotropic compartment models WM. We have used our model to fit the data of 5 healthy subjects downloaded from the Human Connectome Project (HCP)[2]. More specifically the data consisted in 3 DW volumes (270 directions at b=1000,2000,3000s/mm^2, voxel resolution 1x1x1mm^3, 18 B0s) and a T_{1w} scan. The model has been voxel-wise fitted using the "Trust-Region Reflective" non-linear least squares optimizer shipped with Matlab, bounding the parameters to physiologically acceptable values, i.e. the fractional parameters f are constrained between 0 and 1 and the diffusion coefficient D_{ISO} between 0 and 0.002 s/mm^2. To assess the goodness of the fit we have computed voxel-wise residuals and precision of the estimates (expressed as percentage coefficient of variation, $CV_{\%}$) for the three estimated parameters. The residuals are randomly dispersed around the zero, except some spurious voxels in the ventricles. Figure 1 shows the residuals for a pure WM voxel (red) and pure GM voxel (black). To assess the model ability to separate the tissue information from GM, WM and CSF, we have compared the f maps with those obtained by segmentation[3] of the T_{1w} images. In particular, we have evaluated the correlation between the partial volume maps (PVE) from FSL FAST, f_{ISO}, $1 - f_{ISO}$ and $f_{FREEWATER}$ binarizing them above a variable threshold. In Figure 2 the correlation matrix for f_{ISO} vs GM segmentation is shown. The correlation between GM and f_{ISO} is over 80%, between WM and $1 - f_{ISO}$ is 75%, between CSF and $f_{FREEWATER}$ about 70% for a wide range of selected thresholds. An example of segmentation for an axial slice is presented in Figure 3, where the thresholds for both T_{1w} PVE and f maps is 0.5. The $CV_{\%}$ precision of the parameter estimates in the three tissue types are very good with average values: $\overline{CV}(f_{FREEWATER}) = 4\%, \overline{CV}(f_{ISO}) = 24\%, \overline{CV}(D_{ISO}) = 6\%$. As additional assessment of the model performance, we have acquired and analyzed a FLAIR volume and a DWI scan (7 B0s, 32 directions at b=700s/mm^2, 64 directions at b=2000s/mm^2) of a multiple sclerosis (MS) patient (male, 42 yrs). The DWI data has been pre-processed with Tortoise[4], then the FLAIR image has been rigidly co-registered to the DWI space for visual comparison. Figure 4 reports the comparison of a middle axial slice between a FLAIR slice and the corresponding D_{ISO} map. It is noticeable that MS lesions recognizable from the FLAIR scan are also identifiable on the D_{ISO} map in correspondence of abnormally high diffusion values.

DISCUSSION AND CONCLUSION–

The presented model is able to describe multi-shell DW data providing parametric maps that are highly correlated to the segmentation from T_{1w} data. Thus, the model provided adequately separation of GM, WM and CSF based on the diffusion state of the tissues. Unlike the MSMT-SD model, that assumes all voxels of a specific tissue type to share the same response to diffusion weighting, our model fits the isotropic diffusivity parameter D_{ISO}, and therefore seems promising for application also in case of alterations of the WM and eventually of the GM, although further work is needed to address the validation of these features. Nevertheless, when applied to MS data as first attempt to evaluate the model performance in presence of pathological tissues, it has been able to detect the WM alterations in the lesion area. As additional result, we can suggest its use as an alternative segmentation method when a T_{1w} scan is not available or the pathologic tissue could influence the segmentation process. If the T_{1w} sequence has been acquired, the f_{ISO} and $f_{FREEWATER}$ maps can be used to guide the registration from the T1 space to the DWI space, while D_{ISO} can be useful for, lesion detection purpose.

REFERENCES –

1. B Jeurissen B, JD Tournier, T Dhollander, A Conelly, J Siibers, Multi-tissue constrained spherical deconvolution for improved analysis of multi-shell diffusion MRI data. Neuroimage, 14: S1053-8119 (2014).
2. DC Van Essen, SM Smith, DM Barch, TEJ. Behrens, E Yacoub, K Ugurbil, The WU-Minn Human Connectome Project: An overview. NeuroImage 80:62-79 (2013).
3. Y Zhang and M Brady, S Smith, Segmentation of brain MR images through a hidden Markov random field model and the expectation-maximization algorithm. IEEE Trans Med Imag, 20(1):45-57 (2001).
4. C Pierpaoli, L Walker, MO Irfanoglu, A.Barnett, P Basser, LC Chang, C Koay, S Pajevic, G Rohde, J Sarlls, and M Wu,, TORTOISE: an integrated software package for processing of diffusion MRI data, ISMRM 18th annual meeting (2010)