

A model for diffusion spectra and restoration

P. Hagmann^{1,2}, S. Masip¹, C-P. Lin³, I. Tseng⁴, R. Meuli², V. J. Wedeen⁵, J-P. Thiran¹

¹Signal Processing Institute, Swiss Federal Institute of Technology, Lausanne, VD, Switzerland, ²Department of Radiology, University Hospital, Lausanne, VD, Switzerland, ³Institute of Neuroscience, National Yang-Ming University, Taipei, Taiwan, Taiwan, ⁴Center for Optoelectronic Biomedicine, National Taiwan University College of Medicine, Taipei, Taiwan, Taiwan, ⁵MGH Martinos Center for Biomedical Imaging, Harvard Medical School, Charlestown, MA, United States

Introduction

Diffusion Spectrum Imaging (DSI) is a powerful diffusion MR technique that allows to image diffusion spectra (DS), $\bar{p}(\mathbf{r})$, which are voxel averaged diffusion pdfs (eq. 1) [1]. In particular it affords the capacity of resolving several diffusion orientational maxima related to the shape of the underlying fibrous tissue structure. However, because of water exchange between the various compartments, noise and finite mixing time, the measured pdfs are blurred versions of the compartment shape functions, which as a consequence limit the separation power of the imaging technique. Furthermore the relation between the observed signal and the tissue structure is sufficiently complex that it has only been modeled for simple structural configurations [2]. We propose a simplified analytic model that relates the compartment shapes to the MR signal. It allows easy DSI modeling of various fiber configurations. We then use the model to design a restoration technique to diminish the angular uncertainty of the fiber orientations by sharpening the diffusion spectra.

Theory

Modeling the diffusion spectrum. When compartments have perfectly reflecting wall, so that spins do not exchange across barriers, the voxel DS can be written as the sum of the DS of their individual compartments (eq. 2). We know from Callaghan [3] that in this case, and if the diffusion time is sufficiently long, the individual DS tend to the autocorrelation (eq. 3.a) of their compartment shape functions. In biological tissues however restriction is only partial and the experimental mixing time is finite so that the voxel DS is not simply the sum of the individual compartment autocorrelations. A simple way to qualitatively model this situation is to convolve the individual compartment shape functions or their autocorrelations by a low pass filter (eq. 3.b); practically we use a Gaussian function. The voxel DS can then be seen as the results of the smoothed sum of the individual compartment autocorrelations.

Modeling the MR signal. We remember that in a diffusion encoding experiment the MR signal is made proportional to the inverse Fourier transform of the DS ($S \sim \mathcal{F}^{-1}\{\bar{p}\}$) [1]. According to our model we express the observed MR signal as the sum between the inverse Fourier transform of the voxel DS that is multiplied by the degradation filter frequency response and noise (eq. 4). The observed DS is then reconstructed by taking the Fourier transform of $S^{obs}(\mathbf{q})$ [1].

Restoration. Eq. 4 fits the classical formulation of an inverse filtering problem, where an image, degraded by blurring and additive noise, is optimally (in the least square sense) restored by a Wiener filter $H_r(\mathbf{q})$ (eq. 5, NSR is the Noise to Signal ratio).

Material and Methods

For all following experiments we use a similar DSI scheme where $S^{obs}(\mathbf{q})$ is sampled over 515 values of \mathbf{q} comprising the interior of a sphere of radius $r=5$ grid units in a 3D grid. The DS is reconstructed by taking the Fourier transform of the signal modulus and represented as an Orientation Diffusion Function (ODF): radial projection of the DS. (Exp. 1) The above proposed model is used to create a synthetic dataset of the MR signal, $S^{obs}(\mathbf{q})$. It represents a pair of 30° crossing fibertracts embedded into an isotropic medium. Fibertracking is based on a streamline approach and is described in [4]. (Exp. 2) We use an MR phantom made of a stack of plastic capillaries placed orthogonally and scanned it according to a DSI scheme [1] (3T Bruker with a spatial resolution of $0.72 \times 0.72 \times 3.5 \text{ mm}^3$, $TR/TE/\Delta/\delta = 2000/20/250/6 \text{ ms}$ and $b\text{-max} = 8000 \text{ s/mm}^2$ for details see [5]). (Exp. 3) 5 coronal slices were obtained on a healthy volunteer with a DSI scheme (3T Philipps scanner with a spatial resolution of $2 \times 2 \times 3 \text{ mm}^3$, $TR/TE/\Delta/\delta = 3000/154/47.6/35 \text{ ms}$ and $b\text{-max} = 12000 \text{ mm}^2/\text{s}$).

Results

(Exp. 1) We notice that, on the original synthetic dataset (1.a), the two directional maxima related to the fiber crossings are confounded because of noise and the blurring effect of the water exchange between compartments, i.e. the convolution of the compartments autocorrelations with a Gaussian kernel. As a consequence the tractography results are aberrant. If the data is filtered by our proposed Wiener method the bimodal shape of the odf is restored and as a consequence tractography result is correct (1.b). (Exp. 2) We also validate the restoration method on the MR phantom (2.a). The result shows that the distribution of the ODF tightens around the capillary main axes that are aligned with the image frame. Furthermore some orientational bias in the horizontal component is reduced by the deconvolution (2.b). (Exp. 3) Finally we run the algorithm on the brain images (3.b). The zoom on the corona radiate shows that as a result of the deconvolution the orientational maxima are sharpened, potentially revealing new orientational components (3.c).

Conclusion

We have constructed an analytical model of DSI measurement in fibrous tissue. It allows simple conceptualization of DSI and a straightforward implementation for further simulation. We used this model in order to design a restoration algorithm that sharpens the odfs to potentially enhance the separation power of the DSI.

References

[1]Wedeen VJ, et al. Proc. Intl. Soc. Mag. Reson. Med.. 8:82 (2000). [2] Lori NF et al. J Magn Reson. 165:185-95 (2003). [3] Callaghan PT. Principles of Nuclear Magnetic Resonance Microscopy (1991). [4] Proc. Intl. Soc. Mag. Reson. Med. 11:623 (2004). [5] Lin CP, et al. Neuroimage. 19:482-95 (2003).

Acknowledgments

This work was financially supported by NIH 1R01-MH64044 grant, the Swiss National Science Foundation grant number 3235B0-102868 and Mr Yves Paternot.

$$(1) \bar{p}(\mathbf{r}) = \int_{\mathbf{r}' \in \text{voxel}} p(\mathbf{r}' + \mathbf{r} | \mathbf{r}') p(\mathbf{r}') d^3 \mathbf{r}'$$

$$(2) \bar{p}(\mathbf{r}) = \sum_{i=1}^I \bar{p}_i(\mathbf{r})$$

$$(3) \bar{p}_i(\mathbf{r}) = \begin{cases} \chi^i(\mathbf{r}) & \text{(a)} \\ (\chi^i * h_d)(\mathbf{r}) & \text{(b)} \end{cases}$$

$$(4) S^{obs}(\mathbf{q}) = H_d(\mathbf{q}) \mathcal{F}^{-1} \left\{ \sum_{i=1}^I \chi^i \right\}(\mathbf{q}) + N(\mathbf{q})$$

$$(5) H_r(\mathbf{q}) = \frac{H_d^*(\mathbf{q})}{|H_d(\mathbf{q})|^2 + NSR}$$

