Double-Wave-Vector Diffusion-Weighting Experiments with Multiple Concatenations

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Introduction

In double wave vector experiments [1] two diffusion-weighting periods are applied successively in a single experiment. They have been used to observe microscopic diffusion anisotropy [2] or estimate compartment sizes [3] in biological tissue. In the latter experiment, which involves a short mixing time between the two diffusion weightings, a cosine-shaped signal modulation is observed when varying the angle between the two wave vectors. However, the detection of this effect on a whole-body MR system is challenging because the modulation amplitude is reduced for the long gradient pulse durations [4,5] required to obtain a sufficient diffusion weighting and may be close to the noise level. In this work, an extension of the experiment is analyzed that involves multiple concatenations of the two diffusion weightings in a single experiment (Fig. 1). It is shown theoretically and in numerical simulations that this approach increases the amplitude of the signal modulation which may help to improve its detectability on whole-body MR systems.

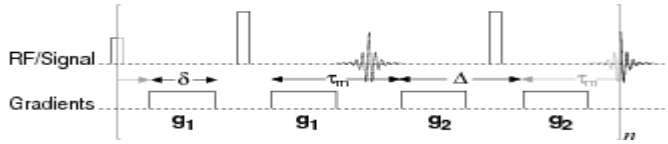


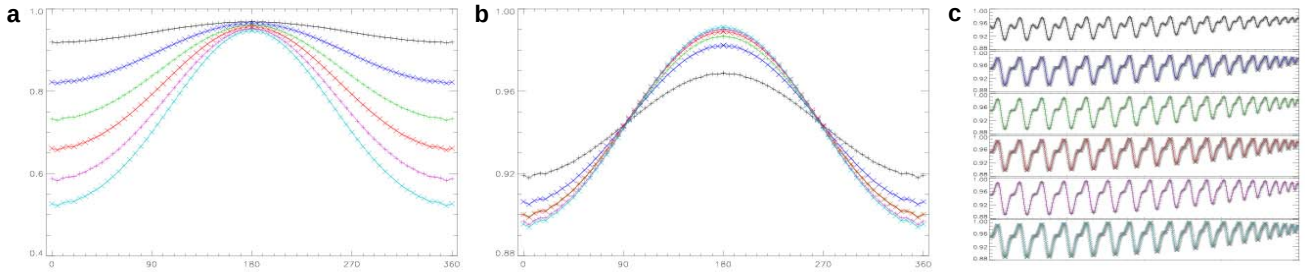
Figure 1: Basic pulse sequence for the double wave vector experiment with n concatenations. The diffusion gradient directions g_1 and g_2 enclose an angle θ which is varied in the experiment.

Theory

A tensor approach to describe the signal modulation observed at short mixing times τ_m for arbitrary orientation distributions of the cells has been proposed recently [6]. For multiple concatenations of the two wave vectors (as shown in Fig. 1), a generalization of the corresponding signal equation $M \propto 1-\vec{Q}^T \underline{\underline{T}} \vec{Q}/2$ is obtained by using the tensor $\underline{\underline{T}}_n = \begin{pmatrix} 2n\underline{\underline{R}} & (2n-1)\underline{\underline{R}} \\ (2n-1)\underline{\underline{R}} & 2n\underline{\underline{R}} \end{pmatrix}$ with $R_{ij} = \int_{cell} r_i r_j d\vec{r}$ where n is the number of concatenations, $Q = (\vec{q}_1^T, \vec{q}_2^T)^T$, and $\vec{q}_1$ and $\vec{q}_2$ the two wave vectors. For an isotropic orientation distribution of the cells and $q_2 = q_1 = q$, the signal expression yields $M = 1-\langle R^2 \rangle q^2 (2n+(2n-1)\cos\theta)/3$ where θ is the angle between the two wave vectors and $\langle R^2 \rangle$ the mean radius of gyration of the cell. Thus, the ratio of the modulation amplitude and the average signal decay is given by $1-1/(2n)$, i.e. it increases with the number of concatenations n.

Methods

Numerical simulations of the MR signal in spheroidal cells (principle axes 1.5µm, 1.5µm, 2.8µm) for the experiment shown in Fig. 1 were performed for n=1–6 and 5000 spins using a Monte-Carlo IDL algorithm [6]. Minimum gradient pulse durations δ and mixing times τ_m were used, the diffusion time Δ was chosen large compared to the time a spin typically needs to cross the long axis of the cell. The signal was either calculated for an isotropic



orientation distribution of the cells or cells of a single orientation and fitted to the extended signal equation using a Levenberg-Marquardt algorithm.

Figure 2: Results of the numerical simulations for 1–6 concatenations using (a) a fixed gradient amplitude or (b,c) a fixed averaged signal decay ($ng^2\delta^2$ constant). (a) and (b) show the signal amplitude vs. θ for an isotropic orientation distribution of the cells, (c) the signal (symbols) and its fit to the signal equation (solid lines) for a single cell orientation and different orientations of the wave vectors.

Results and Discussion

For an isotropic orientation distribution of the spheroidal cells and a fixed integral of the diffusion gradients (Fig. 2a), the simulated signal for the parallel orientation (0°) decreases with increasing number of concatenations while the signal for the antiparallel orientation (180°) remains rather constant. Both observation are consistent with the theoretical considerations. For a comparable averaged signal decay (Fig. 2b), the modulation amplitude increases with the number of concatenations and approaches asymptotically about twice the value observed for a single concatenation (black) which is also expected from the theory. For a single cell orientation (Fig. 2c), the complex signal modulation observed for a variety of wave vector orientation combinations can be well described by the generalized tensor expression. The corresponding fits yield principle axes between 96% and 102% of the nominal values for all axes and concatenations which further supports the validity of the theoretical results. In summary, multiple concatenations may help to improve the detectability of the signal modulation for short mixing times, in particular on whole-body MR systems.

References

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