Magnetic Resonance Characterization of General Compartment Size Distributions

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INTRODUCTION

The influence of molecular diffusion on the MR signal can be exploited to estimate compartment size distributions in heterogeneous specimens [1]. There has been recent interest in adopting this idea to characterize axon diameter distributions in white matter [2]. To this end, previous studies have assumed a known statistical distribution of compartment sizes (such as log-normal or gamma distributions). However, neural tissue does not necessarily conform to such parametric distributions. In this study, we describe an alternative strategy to measure all moments of the compartment size distribution directly from a single diffusion-weighted MR signal decay curve, hence obviating the assumed existence of a known parametric size distribution.

THEORY & IMPLEMENTATION

When an ensemble of compartments with different sizes is examined via MR, each compartment's contribution to the overall signal is proportional to the number of spins that reside within the pore. Using this principle, it is possible to relate all moments of the size distribution, $\langle r_0^n \rangle_e$, for a population of cylinders to the q-space MR signal decay, $E(q)$, through the expressions

$$\begin{aligned}
\langle r_0^2 \rangle_e &= (\pi \mathcal{R}_2 E_2(q))^{-1} \\
\langle r_0 \rangle_e &= \frac{3\pi^2}{16} \langle r_0^2 \rangle_e \mathcal{R}_1 E_2(q) \\
\langle r_0^{2l+2} \rangle_e &= \frac{(l+1)!\,(l+2)!}{2\,(2l-1)!!\,(2l+1)!!} \langle r_0^2 \rangle_e \mathcal{D}_l E_2(q) \\
\langle r_0^{2m+1} \rangle_e &= \frac{(-1)^m\,(2m+1)!!\,(2m+3)!!}{2^{5m+3}\pi^{2m-2}\,m!} \langle r_0^2 \rangle_e \mathcal{K}_m E_2(q)
\end{aligned}$$

$$\begin{aligned}
\mathcal{R}_k E(q) &= \beta_k \int_0^\infty dq\, q^{k-1} E(q)\,, \quad k = 1, 2\,, \beta_1 = 2, \beta_2 = 2\pi \\
\mathcal{D}_l E(q) &= \frac{(-1)^l}{(2\pi)^{2l}} \frac{d^{2l} E(q)}{dq^{2l}}\bigg|_{q=0}\,, \quad l = 1, 2, 3, \ldots \\
\mathcal{K}_m E(q) &= \int_0^\infty dq \left(\frac{1}{q}\frac{d}{dq}\right)^m E(q)\,, \quad m = 1, 2, 3, \ldots
\end{aligned}$$

For an accurate estimate of the moments, one needs an analytical representation of the MR signal decay. To this end, we employed the one-dimensional simple harmonic oscillator based reconstruction and estimation (1D-SHORE) framework [3], which represents the $E(q)$ profile as the sum of a series of Hermite functions. Once the estimation is performed, the moments can be computed by using analytical expressions relating them to the series coefficients.

SIMULATIONS

To validate the derived expressions for the moments and assess the accuracy of the 1D-SHORE technique, we simulated ensembles of cylindrical pores whose radii are distributed according to beta distributions with parameters $(\alpha;\ \beta) = (3.5;\ 6.5)$, and $(\alpha;\ \beta) = (6.5;\ 3.5)$. For the first distribution, the predicted values were 7.0±2.9μm, while the estimates yielded 7.3±2.6μm. For the second distribution, the predicted and estimated values were 13.0 ± 2.9μm and 13.2 ± 2.3μm, respectively. It was not possible, however, to obtain accurate estimates for the skewness of these distributions.

EXPERIMENTS

One phantom comprising only 19±1μm tubes and three size distribution phantoms were prepared by mixing different sized microcapillaries (Polymicro Technologies, Phoenix, AZ, USA) in one NMR tube. The distribution phantoms were designed to have variations in both the mean diameter values and the variance of the distributions [4]. Pulsed field gradient experiments were performed using the stimulated echo sequence with the following parameters: 48 q-values were collected with a maximum gradient strength of 1600mT/m and with Δ/δ=150/3ms, resulting in a maximum q-value of 204.3mm^{-1} and with a number of scans of 32.

The inner diameter (ID) distributions weighted by the enclosed number of spins, and the MR data along with its 1D-SHORE estimates are provided in Fig. 1. Also provided in this figure are the predicted and estimated ID values. Note that the predicted values are obtained by assuming that the nominal ID values provided by the manufacturer are correct. Additional inaccuracy in the predicted values is expected because some capillaries may be only partially filled with water. Despite these potential problems, comparing the results for different phantoms, it is clear that the trends in the mean and standard deviation values are consistent with the trends in their predicted values.

DISCUSSION & CONCLUSION

A new method to compute the moments of a general compartment size distribution from diffusion-weighted MR data is presented. The simulations as well as the experimental data obtained from phantoms demonstrate the ability of this technique to create meaningful contrast based on the mean and standard deviation of compartment size distributions without making any *a priori* assumption about the form of the distribution. The 1D-SHORE framework appears to be well-suited to represent the signal decay profiles and provides accurate estimates of the mean and standard deviation values.

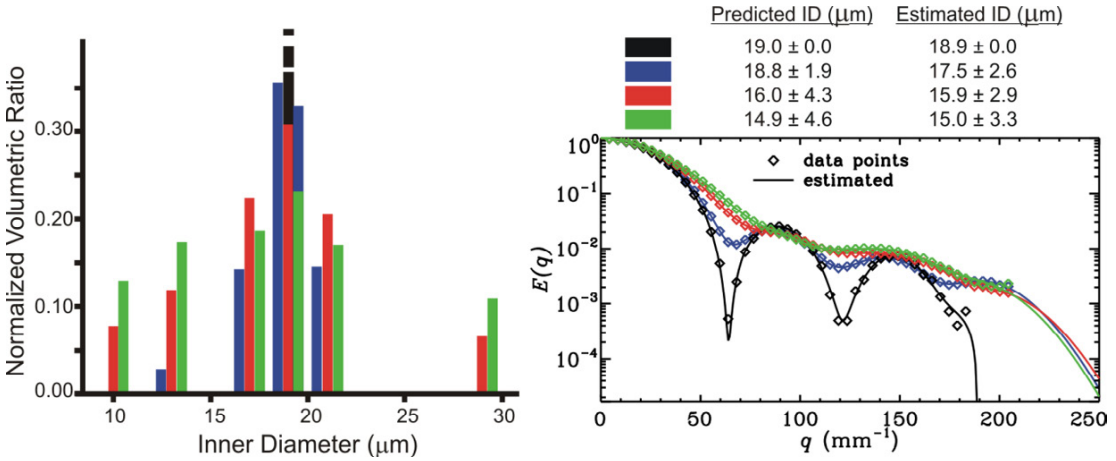

Figure 1. Left: Histograms for the four different size distribution phantoms. The black distribution comprises only 19μm tubes. Right: Symbols represent experimental data points while the 1D-SHORE estimates of the signal decay curves are depicted with continuous lines (bottom). The predicted and estimated values for the mean and standard deviation of the inner diameter (ID) distributions (top).

References: [1] Packer and Rees, J Colloid Interface Sci, 40:206-218, 1972. [2] Assaf et al., Magn Reson Med, 59:1347-1354, 2008. [3] Ozarslan et al., Proc Intl Soc Mag Reson Med, 16:35, 2008. [4] Shemesh et al., J Chem Phys, 132:034703, 2010.