INTRODUCTION: Diffusion-weighted magnetic resonance (MR) signals reflect information about underlying tissue microstructure and cytoarchitecture. We propose a quantitative, efficient, and robust mathematical and physical framework for representing diffusion-weighted MRI data obtained in “q-space,” and the corresponding “mean apparent propagator (MAP)” describing molecular displacements in “r-space.” We also define and map novel quantitative descriptors of diffusion that can be computed robustly using this MAP-MRI framework.

MAP-MRI: We describe efficient analytical representation of the three-dimensional q-space MR signal in a series expansion of Hermite functions that accurately describes diffusion in many complex geometries. The lowest order term in this expansion contains a diffusion tensor that characterizes the Gaussian displacement distribution, equivalent to diffusion tensor MRI (DTI). Inclusion of higher order terms enables the reconstruction of the true apparent propagator whose projection onto the unit “displacement” sphere provides an orientation distribution function (ODF) that contains only the orientational dependence of the diffusion process.

The MAP-MRI framework represents the propagator as a vector in an abstract space. Therefore, it is meaningful to measure the (dis)similarity of two propagators via an angular metric. Such a measure was used to introduce several scalar indices. The dissimilarity between the MAP and its isotropic counterpart is used to define the propagator anisotropy (PA) index. Since MAP-MRI subsumes DTI, the PA index can be computed from DTI as well, which enables measurement of the contribution of the non-Gaussian terms to overall anisotropy. The dissimilarity of the full MAP and the Gaussian propagator leads to measures of non-Gaussianity (NG). Due to the separability of the basis, NG can be quantified along directions parallel and perpendicular to the principal eigenvector of the diffusion tensor.

Other important measures this representation provides include the return-to-the-origin probability (RTOP), and its variants for diffusion in one- and two-dimensions—the return-to-the-plane probability (RTPP), and the return-to-the-axis probability (RTAP), respectively. These zero net displacement probabilities measure the mean compartment (pore) volume and cross-sectional area in distributions of isolated pores irrespective of the pore shape.