Entropy as a Measure of Non-Gaussian Diffusion in Porous Tissues

R.L Magin[a], C. Ingo[a], L. Colon-Perez[b], W., and T.H. Mareci[c]

[a] Dept. of Bioengineering, University of Illinois at Chicago, Chicago, IL; [b] Dept. of Physics, University of Florida, Gainesville, FL; [c] Dept. of Biochemistry, University of Florida, Gainesville, FL

Fractional-order dynamic models (e.g., systems of ordinary and partial differential equations of non-integer order in time and space) are becoming more popular for simulating the behavior of complex systems. Justification for such models is typically based on improved fits to experimental data and a recognition that fractional-order models work better at describing the electrical, mechanical and dielectric properties of multi-scale, heterogeneous materials. In order to address this issue and to offer a new approach for the utility of fractional-order models, we solve the fractional order diffusion equation in terms of the Mittag-Leffler function and then calculate the total Shannon spectral entropy for the case of anomalous diffusion. This fractional-order representation of the continuous time, random walk model of diffusion gives a spectral entropy minimum for normal, or Gaussian diffusion, with all surrounding values leading to greater values of spectral entropy.

Recently, a stretched exponential decay model has been fit to NMR measurements of anomalous diffusion performed in solutions of dispersed microbeads. Here, we extend this work via a new, generalized diffusion model for the NMR propagator, $p(q,\Delta)$:

$$p(q,\Delta) = E_\alpha\left(-D_{\alpha,\beta}\ q^\beta \Delta^{\alpha`}\right)_,$$ [1]

where E_α is the single parameter Mittag-Leffler function, $D_{\alpha,\beta}$ is the the diffusion coefficient, q is the spatial frequency, Δ is the mixing time, and α and β are the fractional order parameters in time and space, respectively. When $\alpha = 1$ and $\beta = 2$, eq. [1] recovers the classical Gaussian form. And, as a new method to quantify the complexity of the media explored by $p(q,\Delta)$, we proposet q-space entropy, $H(q,\Delta)$:

$$H(q,\Delta) = -\sum_{i=1}^{N} \frac{\hat{p}(q,\Delta)_i ln[\hat{p}(q,\Delta)_i]}{ln(N)}$$ [2]

where $\hat{p}(q,\Delta)_i$ is the individual contribution to the normalized power spectrum of $p(q,\Delta)$ defined in eq. [1], and the term, $ln(N)$, is a normalization factor such that $0 < H(q,\Delta) < 1$.

To apply eqs. [1] and [2], we examined water diffusion in heterogenous white matter (WM) and homogenous gray matter (GM) regions of a fixed rat brain using a modified Pulsed Gradient Stimulated Echo pulse sequence on a Bruker spectrometer (17.6 T, 750 MHz, 89 mm bore). The signal decay plots for the ROIs selected in the corpus callosum, thalamus, and cortex show clear divergence from the mono-exponential decay on the linear-log scale (Fig. 1). The MLF parameter, α, separated the central corpus callosum (0.42 ± 0.04), the thalamus (0.57 ± 0.07), and the cerebral cortex (0.76 ± 0.05) (Fig. 2a). The entropy, $H(q,\Delta)$, distinguished the central corpus callosum (0.93 ± 0.01), the thalamus (0.86 ± 0.01), and the cerebral cortex (0.81 ± 0.01) (Fig. 2b). We observed the best image contrast in the constant D =17.5 ms PGSTE DWI experiment, in which q was arrayed over the largest range of gradient strengths.
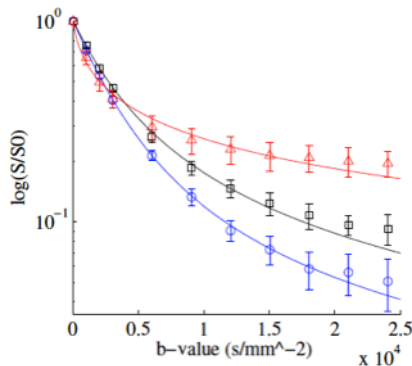

Fig. 1: Signal plots and MLF fits for the corpus callosum (red triangles), thalamus (black squares), and cortex
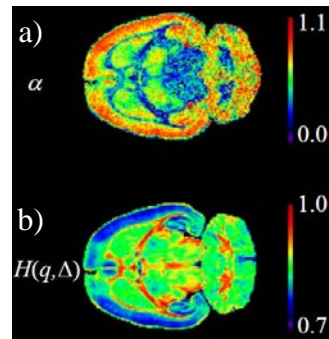
Fig. 2: Parameter maps for a) α, and b) $H(q,\Delta)$ in an axial slice through a fixed rat brain.

We present these MLF and entropy parameters as biomarkers for morphology in neural tissue. Furthermore, our study suggests the experimental setup should minimize the diffusion time such that protons have enough time to explore the environment, while the gradient strength is maximized in order to resolve the tissue microstructure within the imaging voxel. Finally, we believe the CTRW approach will be able to distinguish regimes of Brownian, sub-, and super-diffusion.