AbstractID: 9528 Title: Treatment Responses Monitored by Estimated Returning-To-Origin Probability for Clinical High Diffusion Image

Background: The usefulness of diffusion magnetic resonance imaging (MRI) to monitor treatment response has been recognized. For more specific information like extra-/intracellular space, and water exchange, an extensive diffusion encoding with high diffusion weighting is required. However the intrinsic low signal-to-noise with eddy-current contamination prohibits the high diffusion weighting imaging from becoming a useful clinical tool in spite of its great clinical potentials. **Purpose:** We proposed a novel expression to represent high diffusion encoded image based on q-space analysis for clinical purpose. Our q-space analysis is to approximate the probability theory of ensemble averaged water molecules "returning" to their original spot at the beginning diffusion observation for a given diffusion time. **Method:** The 14-minute MRI sequence employed a high-diffusion encoding with 9 b-values ranging as: $1\sim 4x10^3$ sec/mm^2, and a re-focused diffusion gradient waveform is to balance eddy-current effect, and the diffusion gradient is set in 6 directions for uniformly sampling in 3 dimensions to provide the information for returning-to-origin (RTO) probability as well as diffusion tensor imaging (DTI). In q-space, the 9-point diffusion encoding values from each voxel are interpolated before spatial domain conversion. The fractional anisotropy (FA) map is derived from the Eigenvalue of a given DTI. The giloblastoma patient's image is presented in this study. **Results/Conclusion:** A better signal-to-noise RTO map demonstrates its superior image quality than any diffusion images derived from the conventional apparent diffusion coefficient (ADC) analysis because the q-space analysis uses the integration over q-space instead of differentiating used in ADC analysis. The RTO also highlights the slower water diffusion along white matter as FA map, and it also shows the slow diffusion in fiber-deteriorated part in GBM tumor location that FA map cannot. The slow diffusion helps to identify the high-grade glioma due to its higher cellularity.