Framework for Task-Based Assessment of MR Image Quality

Christian G. Graff¹

¹Division of Imaging and Applied Mathematics, U. S. Food and Drug Administration, Silver Spring, MD, United States

Target Audience: Researchers developing imaging sequences or iterative reconstruction algorithms and others who would like to have tools for evaluating MR sequences and reconstructions in terms of clinically-relevant image quality metrics.

Purpose: The versatility of MRI has permitted the development of numerous acquisition techniques, trajectories and reconstruction algorithms. Traditionally these techniques are either evaluated qualitatively in terms of artifact and noise properties, or by metrics such as SNR and CNR. Modern compressed sensing (CS) reconstructions cannot be characterized by CNR or SNR due to their inherent nonlinearity and de-noising properties which also may remove important diagnostic information. Furthermore, studies with non-anthropomorphic phantoms may not reflect in vivo performance as the effectiveness of CS is strongly dependent on the complexity of the object being imaged. The purpose of this work is to develop a framework of practical image quality metrics based on basic tasks which act as surrogates for clinical MR uses. A complete simulation environment has been developed for rapidly producing large amounts of realistic synthetic data for image quality comparison between sequences, trajectories and reconstructions.



Fig. 1: Evaluation methodology

Methods: Measuring task performance involves the entire imaging process as summarized in Fig. 1. Here we concentrate on two tasks. 1. A signal localization task: correctly identify a small low-contrast object from a set of candidate locations; representative of clinical tasks such as counting MS brain lesions. 2. A shape discrimination task: determine where the spicule perturbation is on the edge of an otherwise uniform circular object; representative of tumor boundary and shape determination The signals are randomly embedded in a high-resolution tasks. (0.17x0.17x0.33 mm) voxelized brain phantom which contains segmented tissue classes and associated MR parameter distributions. For each task,

sets of randomized images are produced Fig. 2: Sample and analyzed. A T2-weighted spin-echo shape sequence (TR = 3000ms, TE = 20ms, $BW = \pm 64$ kHz, 256x256 matrix) was modeled with a fully sampled Cartesian acquisition (FFT recon.), 256-view radial (FBP recon.) and a sub-sampled radial (128 views, CS recon.). The CS algorithm was an implementation of the Split-Bregman method with wavelet and



total variation constraints (regularization parameters chosen empirically). K-space data generation and reconstruction were Task performance was assessed based on a template-matching approach. implemented in C with MPI on a 3500 core computer cluster and data analysis was performed in Matlab.



Fig 3: Cartesian vs. radial (left) and under-sampled radial (right) results for lesion localization task (4 mm lesion diameter, 95% confidence intervals

Results: Figure 2 shows representative images for each task. Figure 3a compares lesion localization results for 256 view Cartesian and radial acquisitions (4 mm signal diameter, in white matter) indicating a statistically significant advantage for radial at T2 = 100ms. Figure 3b compares equal-spaced 128 view radial subsampling/CS with random subsampling/CS (same task), indicating equal spacing results in superior performance. Comparing equal-spaced vs.

random for the shape discrimination task found no significant differences in performance, (0.444±0.031 vs. 0.440±0.032 probability of correct perturbation detection respectively, $T_2 = 120$ ms, perturbation length 4 mm, 1000 images per case), indicating multiple tasks may be necessary to adequately characterize performance. Discussion: These results highlight some of the analyses possible with this tool that cannot be performed with physical phantoms due to the numbers of images and object complexity necessary. Conclusion: A framework for comparing (and potentially optimizing) MR sequences using clinically relevant tasks has been developed. This is particularly important for CS reconstructions, which are not amenable to other more traditional types of analysis.