Novel Strategy for Accelerated Diffusion Imaging

S. E. Maier[1], and B. Madore[1]
[1]Radiology Department, Brigham and Women's Hospital, Harvard Medical School, Boston, MA, United States

Introduction: Acceleration methods such as parallel imaging prove very helpful in diffusion imaging, to reduce echo-train lengths in single-shot acquisitions and to reduce imaging time in multi-shot acquisitions. An approach is introduced and tested here that also aims at accelerating diffusion imaging applications, by exploiting inherent redundancies in multi-*b* (or multi-*q*) and multi-direction datasets. The approach is not meant as an alternative to established methods such as parallel imaging and partial-Fourier imaging, but instead as a supplement to these methods, to further increase acceleration. Different sets of *k*-lines are acquired for different *b* factors and different directions, in a scheme that could be understood as a 2D version of the UNFOLD method [1]. While UNFOLD involves changing the sampling function along one (temporal axis), the present approach involves changes across a 2D (*b*-*d*) plane.

Theory: For example, Fig. 1 shows a 6-direction 32-*b* factors datasets, as represented in a k_b-k_d plane, without (top) and with (bottom) the proposed acceleration scheme. One cannot help but notice from the non-accelerated case that most of the information is found on a cross at k_b=0 and/or k_d=0. As a consequence, all other locations in the k_b-k_d plane become available for acceleration purposes. With only one line every 6 in *k*-space (i.e., acceleration of 6), and shifting the sampling function from one *b* value to the next and from one diffusion direction to the next, the effect in k_b-k_d space can be seen in Fig. 1 (bottom): One non-aliased component (see green lines) and five aliased components (see red squares) now share a same k_b-k_d plane. Non-aliased signals are recovered as follows: 1) Signal in the four quadrant (outside the green-marked 'corridors') is zeroed, 2) corruption along k_d = 0 (see red arrows in Fig. 1) is removed by exploiting smoothness properties along k_b, and 3) corruption along k_b = 0 is removed as artifacts can be shown to simply be spatially-shifted versions of those previously removed in step '2' above. As a result, a de-aliased k_b-k_d plane is obtained (not shown here) which appears nearly identical to the non-accelerated case. If so desired, the missing quadrants in the k_b-k_d plane can be re-generated through either a mono- or biexponential model, and a de-aliased *b*-*d* space is then obtained through FFT. In the presence of motion, the approach proved compatible with the multi-shot motion-correction scheme by Atkinson *et al.* [2], once this scheme is modified to act on *k*-space rather than image data. Figure 2 shows a simulated case where motion effects prevented the shifts in sampling function to create the multiple-replica effect seen in Fig. 1. With corrections, R = 4 replica can clearly be seen in the plot in Fig. 2b, while only noise-like variations could be seen in Fig. 2a without motion corrections.

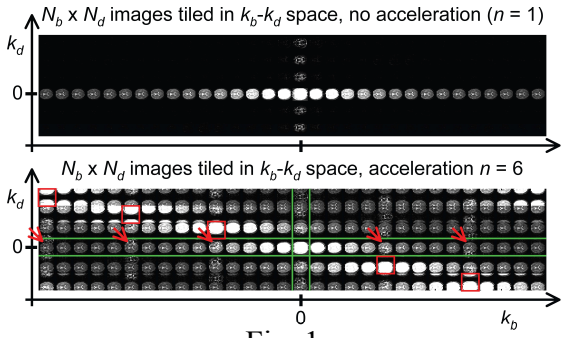

Fig. 1

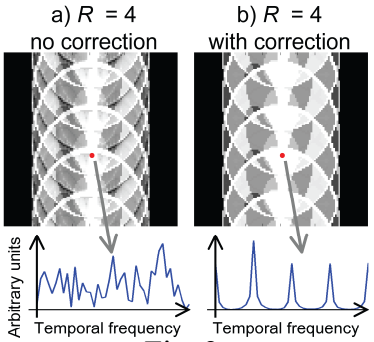

Fig. 2

Results: Diffusion-weighted brain image data were collected in normal volunteers with LSDI [5] and the standard single-shot echo-planar diffusion imaging sequence of 1.5 T and 3 T General Electric whole body MR systems. All datasets included six non-collinear and non-coplanar diffusion encoding directions. The number of *b*-factors obtained for the different datasets ranged between 6 and 32 and the maximum *b*-factor between 1000 s/mm^2 to 5000 s/mm^2. Spatial resolution varied between 0.9x1.7x2.0 mm^3 for data sets with a maximum b-factor of 1000 s/mm2 and 3.4x3.4x6.0 mm^3 for data sets with a maximum b-factor of 5000 s/mm^2. Moreover, simulated data was produced to study the noise characteristics of the novel acceleration method. Image data was reconstructed with the standard reconstruction software for LSDI and the single-shot echo-planar imaging sequence. Diffusion-weighted image data sets then underwent Fourier transform along the *b*-factor and encoding direction parameter axes. Processing was performed in k_b-k_d space, and final results were obtained by transforming back to a *b*-*d* space. An example can be seen in Fig. 3, with biexponential diffusion signal processing. Fractional anisotropy maps of both the fast (a, b) and slow (c, d) diffusion components are shown, for an example where a fully sampled dataset (shown in a, c) was subsampled by a factor R = 6 (shown in b, d). Notice that original and accelerated results appear very similar. Analysis of the simulated data demonstrated that the new acceleration method produced diffusion data with slightly better SNR than if acceleration had been achieved simply by reducing the number of sampled b-factors.

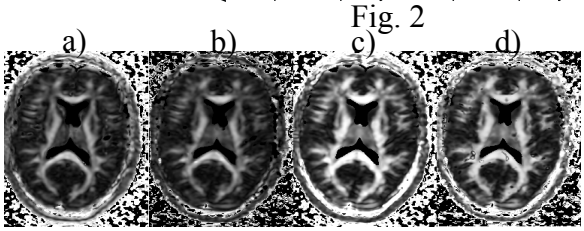

Fig. 3

Conclusion: The presented approach for reduced sampling promises to be useful for acceleration of navigated diffusion-weighted imaging sequences, especially in conjunction with non-monoexponential diffusion-analysis experiments, where a simple reduction in the number of sampled b-factors would result in fitting instability. The proposed method is also completely compatible with traditional acceleration methods, such as parallel imaging and partial-Fourier imaging. It is anticipated that the combined acceleration will be particularly attractive if used together with an otherwise time consuming segmented acquisition, to obtain images with less distortion.

References: [1] Madore et al, MRM 1999;42:813. [2] Atkinson et al, MRM, 2006;56:1135. [3] Gudbjartsson et al, MRM 1996;36:509.