A simple and efficient method for acceleration and denoising of multi-contrast diffusion data: application to q-space and HARDI

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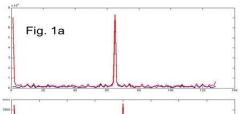
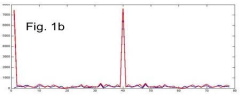
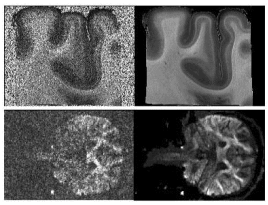
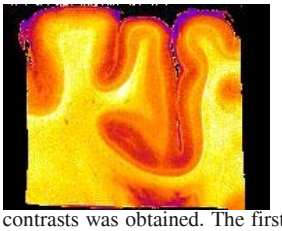
Introduction The water signal decay in diffusion experiments in neuronal tissues was shown to deviate from mono-exponentiality at high enough b-values [1]. This deviation holds promise for new insights into tissue microstructure and also points to the need to characterise diffusion with as few assumptions as possible. Q-space analysis provides a means to extract structural information on the sample without resorting to complicated models [2]. However, for *in vivo* brain imaging, experiments involving a large number of b-values, ideally also in conjunction with a large number of angular samples to allow for reconstruction of the full 3D diffusion propagator, are very time consuming. Moreover, measurements at high b-values are generally very noisy. We propose in the following a simple and efficient method to alleviate these two shortcomings of q-space imaging. Because the q-space information is extracted from the shape of the Fourier transform of the signal as a function of the q-value, we find acceleration based on UNFOLD ideally matched to this application. Indeed, the q-space information is contained to a large extent in the centre of the q-space, which is a region unaffected by aliasing at moderate UNFOLD acceleration (2,4). The relevant q-space parameters can therefore be retrieved without the need to perform dealiasing in image space. Independent of acceleration, denoising is performed by using singular value decomposition (SVD) of the multi-q data set and keeping only a (very small) number of components which are found to account for most of the variability of the signal. This very efficient, model-free denoising allows for very good access to the shape of the signal decay. We present applications of the method to q-space data acquired on fixed brain tissue. We also investigate the potential of the UNFOLD + SVD method on HARDI data acquired *in vivo*.









Materials and methods A piece of tissue with linear dimension of 2.5cm was dissected from the left visual cortex of a fixed post mortem brain. All procedures were approved by the local ethics committee. Measurements were performed on a 9.4T animal scanner equipped with a 12cm ID, 600mT/m, 100µs rise time gradient coil and interfaced to a Siemens TIM Trio console. A birdcage coil with ID of 7cm was used for transmit and a 2-coil receiver array of 3cm diameter was used for signal reception. A 2D spin-echo sequence was modified to include a diffusion preparation module. Q-space data were acquired for a single diffusion gradient orientation and on a single slice for 128 b-values ranging between 0 and 40,000 s/mm^2 (giving equidistant q values). Each diffusion-weighted scan was accompanied by a b=0 reference scan. The measurement parameters included: FOV 20x26mm^2, matrix 192x148 (resolution of 136x136x400µm^3), TR=1000ms, TE=40ms, Δ=20ms, δ=10ms, α=90^o, 4 averages. The total measurement time was 42 hrs. The HARDI acquisition was performed on a healthy volunteer after securing informed consent. Measurements were performed on a 3T Tim-Trio Siemens scanner, equipped with a gradient coil capable of 40mT/m/axis with a slew rate of 200 T/m/s. A body coil was used for RF transmit and a 32-channel phased-array coil for signal detection. A doubly-refocused diffusion weighted EPI sequence was used, with parameters: FOV 152x220mm^2, matrix 104x150 x74 slices (resolution of 1.47x1.47x1.5mm^3), TR=12600ms, TE=102ms, α=90^o, b=1900 s/mm2, 1 average, 78 directions and six b=0 acquisitions. The full k-q or k-direction space was acquired; resampling corresponding to an acceleration factor of two and reconstruction using UNFOLD was performed off-line as follows. For each contrast (b-value for q-space imaging or diffusion weighting direction for HARDI) the k-space was reconstructed starting from magnitude and phase DICOM images via a 2D inverse Fourier transform. Every second line of each of the k-spaces was eliminated such that k-spaces corresponding to odd points had all even k-space lines zeroed and k-spaces corresponding to even points had all odd lines zeroed. The total measurement time for such an UNFOLD-accelerated acquisition with k-spaces undersampled by a factor of two would therefore be reduced to half of its original value. Image data were reconstructed from the undersampled k-spaces by two-dimensional Fourier transform for each contrast and slice. The stack of images corresponding to the contrasts, for each slice, was Fourier transformed in the 'contrast dimension' (q-value or direction #) resulting in a spectrum for each voxel. The central half only of each spectrum was kept and the rest of the spectrum set to zero. For a quick q-space analysis, the information is already accessible. The height and FWHM of the spectrum in each voxel represent the probability of zero displacement and the mean displacement, respectively. For a more involved q-space analysis, and also for the HARDI data, the reconstruction of unfolded images is necessary. An inverse Fourier transform was performed in the contrast dimension and a stack of UNFOLDed images corresponding to the contrasts was obtained. The first and last image of the series were found to show artefacts due to the truncation in the spectrum and were not included in the further analysis. For the SVD-based denoising, the amplitudes corresponding to individual components were plotted on a logarithmic scale. The cut-off was determined by visual inspection to correspond to a value after which the contribution of individual components flattens out. All data processing was performed using Matlab.

Results and discussion We illustrate in Fig. 1 the effect of SVD-based denoising, obtained when keeping only 3 components for q-space data and 15 components for HARDI data. Fig. 2 shows, for selected voxels, spectra obtained after Fourier transformation in the "contrast direction" of the original (blue) and undersampled data (red, magnified by 2 for better comparison). Fig. 2a illustrates q-space data and Fig. 2b HARDI data. In both cases the signal is concentrated in a narrow central portion of the spectral range. The probability for zero displacement obtained from UNFOLDed data reconstructed for the piece of fixed tissue is included in Fig. 3. We mention that it is identical to the similar information obtained from fully sampled data. This is due to the fact that the centre of the q-space, from which this information is extracted, is practically unaffected by the acceleration. As can also be appreciated from Fig. 2, the FWHM of the q-space spectrum obtained after acceleration is practically identical to that obtained from fully sampled data. Due to space limitations, we enunciate the following results without the possibility to present accompanying figures. SVD-based denoising of q-space data was found to have a dramatic beneficial effect on the further analysis of the information (biexponential fitting, kurtosis and mean diffusivity analysis). The signal attenuation was found to be very well described by a biexponential fit with slow diffusion roughly a factor of 10 slower than the fast diffusion. The distribution of amplitudes of the two components were different from those found in vivo [1] with the slow component being the largest one in the white matter. Polynomial fitting of the attenuation curve up to b-values of 40,000 required 6 terms. Denoising of HARDI data, while clearly beneficial for data appearance, has reduced influence on maps such as mean diffusivity and fractional anisotropy. The factor of 2 acceleration was found in both cases to be unproblematic and lead to images and quantities consistent with those obtained from the fully sampled information. In conclusion, an ideally-matched acceleration technique (UNFOLD) is proposed for q-space imaging. The relevant information can be recovered from undersampled data without the need for further reconstruction. HARDI data can also be accelerated with this technique. The same technique should therefore work very well for combined q-space and HARDI methods (diffusion spectrum imaging, multiple q-shell diffusion propagator imaging, etc) with crucial applications to the study of tissue microstructure in vivo. Denoising based on SVD decomposition is extremely successful on q-space data but has a smaller influence on ADC and FA maps obtained with HARDI.

References [1] R.V. Mulkern, S.J. Hacker, S.E. Maier, Magn Reson Imaging 27 (2009); [2] Y. Cohen and Y Assaf, NMR Biomed (2002) ; [3] Madore B, Glover GH, Pelc NJ. Magn Reson Med. 42 (1999); [4] M. Menzel et al., Magn Reson Med 66 (2011).